

GenCore version 5.1.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 04:07:47 ; Search time 6559 Seconds  
(without alignments)  
4543.570 Million cell updates/sec

Title: US-09-697-089-2  
Perfect score: 1024  
Sequence: 1 MNFIKDNKRALIQRMGTRVI.....WQFDDDLVITGAFKLVT 1024

Scoring table:  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106490

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
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-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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37: em.htg\_vrt.\*  
38: em.sy.\*  
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40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1024	100.0	3133	9	AY032589 Homo sapi
2	923	90.1	3219	9	AY035391 Homo sapi
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4	822	80.3	3355	9	AK095467 Homo sapi
5	822	80.3	3581	9	AF376061 Homo sapi
6	721	70.4	3396	6	AX318091 Sequence
7	721	70.4	3396	9	AY027787 Homo sapi
8	589	57.5	160583	2	AC010968 Homo sapi
9	559	54.6	138909	9	CNS01DS3
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12	271	26.5	1395	9	AY027788 Homo sapi
13	232	22.7	891	6	AX318174 Sequence
14	206	20.1	618	6	AX318176 Sequence
15	154	15.0	768	6	AX318097 Sequence
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20	89	8.7	578	9	AY027790 Homo sapi
21	87	8.5	261	6	AX318172 Sequence
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23	36	3.5	165	6	AX318178 Sequence
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ALIGNMENTS

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VERSION AY032589.1 GI:13899172  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 3133)  
Geddes,B.J., Wang,L., Huang,W.-J., Lavelles,M., Manji,G.A.,  
Brown,M., Jurman,M., Morganstern,J., Merriam,S., Glucksmann,A.,  
Distefano,P.S. and Bertin,J.  
Human CARD12 is a novel CED4/Apaf-1 family member that induces  
apoptosis  
JOURNAL Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)  
MEDLINE 21268963  
PUBMED 11374873  
REFERENCE 2 (bases 1 to 3133)  
AUTHORS Bertin,J.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals  
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA  
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Score: 1024.00 Matches: 1024  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
  
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## RESULT 2

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LOCUS Homo sapiens ICE-protease activating factor mRNA, complete cds.  
DEFINITION  
ACCESSION AY035391  
VERSION AY035391.1 GI:14334214  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 3219)

## AUTHORS

Poyet, J.-L., Srinivasula, S.M., Thani, M., Razmama, M.,  
Fernandes-Alnemri, T. and Alnemri, E.S.  
Identification of Ipaf, a human caspase-1-activating protein  
related to Apaf-1  
J. Biol. Chem. 276 (30), 28309-28313 (2001)  
21359454  
11390368  
PUBMED  
REFERENCE  
2 (bases 1 to 3219)  
Poyet, J.-L., Srinivasula, S.M., Fernandes-Alnemri, T. and  
Alnemri, E.S.  
Direct Submission  
Submitted (16-MAY-2001) Microbiology and Immunology, Thomas  
Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,  
USA

## FEATURES

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BASE COUNT 934 a 696 c 748 g 841 t  
ORIGIN

## Alignment Scores:

Pred. No.: 0 Length: 3219  
Score: 923.00 Matches: 1023  
Percent Similarity: 99.80% Conservative: 0  
Best Local Similarity: 99.80% Mismatches: 1  
Query Match: 90.14% Indels: 2  
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AY035391 (1-3219)

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Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTirAsnTyrProLeu 80  
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Qy 181 ArgIleAlaMetLeuTirGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
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## RESULT 3

BC031555

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC031555 Homo sapiens, caspase recruitment domain protein 12, clone  
MGC:35330 IMAGE:5179909, mRNA, complete cds.  
BC031555 BC031555.1 GI:21594975  
MGC.  
human.

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 3360)  
Direct Submission  
Strausberg, R.  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: amg@bcm.tmc.edu  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
Series: IPAK Plate: 50 Row: a Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis.

## FEATURES

Location/Qualifiers

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BASE COUNT 1011 a 718 c 768 g 863 t

## ORIGIN

## Alignment Scores:

Pred. No.:	0	Length:	3360
Score:	923.00	Matches:	1023
Percent Similarity:	99.80%	Conservative:	0
Best Local Similarity:	99.80%	Mismatches:	1
Query Match:	90.14%	Indels:	2
DB:	9	Gaps:	0

US-09-697-089-2 (1-1024) x BC031555 (1-3360)

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Qy	421	LeuLeuThrThrGlyLeuLeuLysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440

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## RESULT 4

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ACCESSION AK095467  
VERSION AK095467.1 GI:21754727  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens CD34+ Cells cDNA to mRNA, clone\_lib:D9OST2  
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## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1  
AUTHORS  
Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,  
Kodaïra,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,  
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,  
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,  
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Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,  
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,  
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.  
NEDO human cDNA sequencing project

## TITLE

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3355)  
 AUTHORS Isogai, T. and Yamamoto, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
 Kazusa-Kamatari, Kisarazu, Chiba 252-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 key technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and  
 RAB; annotation: HRI and RAB.

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BASE COUNT 986 a 726 c 774 g 869 t

ORIGIN

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 Score: 822.00 Matches: 1022  
 Percent Similarity: 99.61% Conservative: 0  
 Best Local Similarity: 99.61% Mismatches: 2  
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AUTHORS	Gingras, M.-C., Qiu, J. and Margolin, J.F.		
TITLE	Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3581)		
AUTHORS	Gingras, M.-C., Qiu, J. and Margolin, J.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center, Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX 77030, USA		
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US-09-697-089-2 (1-1024) X AF376061 (1-3581)

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1
REFERENCE
AUTHORS
Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,
Oliveira, V.A., Hayashi, H. and Pawlowski, K.
TITLE
Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL
Patent: WO 0190156-A 96 29-NOV-2001;
The Burnham Institute (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
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JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 3396)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
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Score: 721.00 Matches: 1021
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Query Match: 70.41% Indels: 6
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LOCUS 11 unordered pieces.
DEFINITION AC010968
ACCESSION AC010968
VERSION AC010968.5 GI:9845170
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 160583)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 160583)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Aug 18, 2000 this sequence version replaced gi:8439959.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
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----- Project Information -----
Center project name: H_NH0093002
----- Summary Statistics -----
Sequencing vector: M13; 59%
Chemistry: Dye-primer Et; 47% of reads
Assembly: Dye-terminator Big Dye; 53% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q30
Consensus quality: bases at least Q20
Insert size: 147000; agarose-fp
Insert size: 159583; sum-of-contigs
Quality coverage: 6.64 in Q20 bases; agarose-fp
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs, the true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1080: contig of 1080 bp in length
* 1081 1380: gap of unknown length
* 1181 2476: contig of 1296 bp in length
* 2477 2576: gap of unknown length
* 2577 5035: contig of 2459 bp in length
* 5036 5135: gap of unknown length
* 5136 9606: contig of 4471 bp in length
* 9607 9706: gap of unknown length
* 9707 17078: contig of 7372 bp in length
* 17079 17178: gap of unknown length
* 17179 27158: contig of 9980 bp in length
* 27159 27258: gap of unknown length
* 27259 45137: contig of 17879 bp in length
* 45138 45237: gap of unknown length
* 45238 65522: contig of 20285 bp in length
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Percent Similarity: 99.70% Conservative: 0  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 57.52% Indels: 2  
DB: 2 Gaps: 0

US-09-697-089-2 (1-1024) x AC010968 (1-160583)

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of library CITB_978_SKB from chromosome 2 of Homo sapiens (human).
ACCESSION AL121653
VERSION AL121653.2 GI:7159616
KEYWORDS SPG4 genomic DNA interval.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 138909)
Hazan, J., Fonknechten, N., Mavel, D., Paternotte, C., Samson, D.,
Artiguenave, F., Davoine, C.S., Cruaud, C., Durr, A., Wincker, P.,
Brottier, P., Catolico, L., Barbe, V., Burgunder, J.M.,
Prud'Homme, J.F., Brice, A., Fontaine, B., Heilig, R. and
Weissenbach, J.
TITLE Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
JOURNAL Nat. Genet. (1999) In press
REFERENCE 2 (bases 1 to 138909)
AUTHORS Genoscope.
DIRECT SUBMISSION
Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.
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ORIGIN

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QY 489 SerLeuLeuArgTyrThrCysGlySerValGluAlaThrArgAlaValMetLysHis 508
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QY 529 TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla 548
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LOCUS Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005417.  
DEFINITION AL389934  
ACCESSION AL389934.1 GI:9367839  
VERSION FLI\_CDNA.  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1355)  
AUTHORS Auffray,C., Ansoorge,W., Ballabio,A., Estivill,X., Gibson,K.,  
Lehrach,H., Poustka,A. and Lundberg,J.  
TITLE The European IMAGE consortium for integrated Molecular analysis of  
human gene transcripts  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1355)  
AUTHORS Pluvinet,R., Estivill,X., Escarceller,M. and Sumoy,L.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de  
Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via  
s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,  
SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:  
http://www.iro.es e-mail enquiries: lsumoy@iro.es  
COMMENT EURO-IMAGE Consortium Contact: Auffray C  
CNRS UPR 420 - Genetique Moleculaire et Biologie du Developement  
IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8

94801 Villejuif Cedex, FRANCE  
Tel: ++33-1-49 58 34 98  
Fax: ++33-1-49 58 35 09  
e-mail: auffray@irobio.gen.fr  
This clone is available royalty-free through IMAGE Consortium  
Distributors.  
IMPORTANT: This sequence represents the full insert of this IMAGE  
cDNA clone. No attempt has been made to verify whether this  
corresponds to the full-length of the original mRNA from which it  
was derived.

FEATURES  
source

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Qy 606 AlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTrpGlu 625  
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Qy 646 SerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArgThrLeuGluValThr 665  
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Qy 666 LeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSe 685  
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Qy 705 rLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuTh 725  
Db 361 TTTGGTCTCAGCACCTGTGAAGACATTTATTTCTCATGTGTGAAGCCAGTCCCTCCAC 420



QY	725	rileGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAs	745	AUTHORS	Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Db	421	CATAGAAGATGAGAGGCACATCATCTGTACAAACACCTGAAACCTTGAGTATTCATGA	480	TITLE	Oliveira,V.A., Hayashi,H. and Pawlowski,K.
QY	745	pLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLe	765	JOURNAL	Card domain containing polypeptides, encoding nucleic acids, and
Db	481	CCTACAGAAATCAACGGCTCCGGGTGGTCTGACTGACAGCTTGGTAACTTGAAGAACCT	540	Patent:	WO 0190156-A 98 29-NOV-2001;
QY	765	uThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaG1	785	FEATURES	The Burnham Institute (US)
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Db	601	AGSCCTGAAACACCTCAAGAAGATGTTATTATTCATTGACCCACTTGTCTGACATTGG	660		/organism="Homo sapiens"
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Db	901	GTGCCCCCTGGGGCTGTGAGCTGCAAGCGACCTGTGAGCAGCCTGTTGAAACATTTGGAGGA	960		QLVSCCLSANAVKILAQNLHNLVKLSILDLSNLYLEKDGNEALHELIDRMNVLKQLTA
QY	905	uValProGlnLeuValLysLeuGlyLeuLysAsnTrrpArgLeuThrAspThrGluIleAr	925		LMLPWGCDVQGSLSLLKHLLEVQPLVKLGNLWRLTDTETIRILGAFGKPKLNKFOQ
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QY	945	aGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLy	965		ORIGIN
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QY	1005	pGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLysLeuValThrAla 1024			Query Match: 26.46% Indels: 0
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AX318093					
LOCUS	AX318093	1395 bp	DNA	linear	PAT 14-DEC-2001
DEFINITION	Sequence 98 from Patent WO0190156.				
ACCESSION	AX318093				
VERSION	AX318093.1	GI:17900822			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
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 AY027788

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 ACCESSION AY027788  
 VERSION AY027788.1 GI:14324114

KEYWORDS  
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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1395)  
 Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C.  
 JOURNAL Genomics 75 (1-3), 77-83 (2001)  
 MEDLINE 21365712  
 PUBMED 11472070

REFERENCE 2 (bases 1 to 1395)  
 Stehlik, C., Damiano, J.S., Pio, F., Godzik, A. and Reed, J.C.  
 AUTHORS Direct Submission  
 TITLE Submitted (21-FEB-2001) Program on Apoptosis and Cell Death  
 JOURNAL Research, The Burnham Institute, 10901 North Torrey Pines Road, La  
 Jolla, CA 92037, USA

FEATURES  
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BASE COUNT 436 a 248 c 327 g 384 t  
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Alignment Scores:  
 Pred. No.: 3.37e-274 Length: 1395  
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 Query Match: 26.46% Indels: 0

DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AY027788 (1-1395)

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LOCUS AX318174 891 bp DNA linear PAT 14-DEC-2001  
 DEFINITION Sequence 179 from Patent WO0190156.  
 ACCESSION AX318174  
 VERSION AX318174.1 GI:17900865  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,

Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
Patent: WO 0190156-A 179 29-NOV-2001;  
The Burnham Institute (US)  
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BASE COUNT 237 a 228 c 217 g 209 t  
ORIGIN

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Pred. No.: 2,1e-233 Length: 891  
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US-09-697-089-2 (1-1024) x AX318174 (1-891)

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LOCUS  
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ACCESSION AX318176  
VERSION AX318176.1 GI:17900867  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 181 29-NOV-2001;  
The Burnham Institute (US)  
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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 03:11:25 ; Search time 486 Seconds

(without alignments)  
4744.951 Million cell updates/sec

Title: US-09-697-089-2

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Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	922	90.0	3213	22	AAH78219 Nucleotide sequenc
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6	663	64.7	2215	22	AAH78218 Nucleotide sequenc
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ALIGNMENTS

RESULT 1

AAS03945

ID AAS03945 standard; cDNA; 3133 BP.

XX AAS03945;

XX AAS03945;

DT 12-SEP-2001 (first entry)

DE Human caspase recruitment domain 12 (CARD-12) cDNA.

XX

KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;

KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;

KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;

KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;

KW aplastic anaemia; myocardial infarction; inflammatory disorder;

KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;

KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;

KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;

KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
 XX excitotoxic brain damage; liver disease.

OS Homo sapiens.

PH Key Location/Qualifiers  
 FT CDS 36..3110  
 FT /\*tag= a  
 FT /product= "Human CARD-12"

PN W0200130971-A2.  
 XX 03-MAY-2001.  
 PD 26-OCT-2000; 2000WO-US29643.  
 XX 27-OCT-1999; 99US-0161822.  
 PR (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J, Robison KE;  
 PI WPI: 2001-308628/32.  
 DR P-PSDB; AAU02880.

XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
 encoding them, useful for treating and diagnosing disorders associated  
 with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
 disease -  
 PS Claim 2; Fig 1; 93pp; English.  
 XX The sequence represents a cDNA which encodes the human caspase  
 recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
 number of proteins that transmit signals that activate apoptosis and  
 inflammatory pathways in response to stress and other stimuli. Therefore,  
 CARD-12 and its corresponding nucleic acid may be used in treatment and  
 diagnosis of patients suffering from disorders associated with an  
 abnormal level (an increase or a decrease) of apoptotic cell death or  
 abnormal activity of stress-related pathways. The disorders include  
 cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
 autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
 neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
 sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
 infarction, stroke), inflammatory and immune system disorders (e.g.  
 Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
 psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
 lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
 ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
 meningitis and liver disease.

XX Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

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QY 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
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QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
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RESULT 2
AAH78219
ID AAH78219 standard; DNA; 3213 BP.
XX
AC AAH78219;
XX
DT 26-NOV-2001 (first entry)
XX
DE Nucleotide sequence of a human secreted polypeptide.
XX
KW Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW gastrointestinal ulceration; spinal cord disease; trachea disease;
KW thyroid gland disease; ovary disease; prostate disease; heart disease;
KW renal gland disease; small intestine disease; thymus disease;
KW lymph node disease; muscular system disease; colon disease;
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
KW microbial disease; immune disorder; inflammation; transplant rejection;
KW bone thickness; bone density; ferroxidase loss; apoptosis;
KW vascular smooth cell proliferation; vaccine; ss.
XX
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Homo sapiens.

Key	Location/Qualifiers
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/product= "secreted polypeptide"

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WO200166690-A2.

13-SEP-2001.

05-MAR-2001: 2001WO-US07143.

06-MAR-2000: 2000US-0187107.

13-MAR-2000: 2000US-0188916.

03-OCT-2000; 2000US-0236874;

03-OCT-2000; 2000US-0237846.

(SMIK ) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

Aqarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z:

WPI: 2001-570768/64.

P-PSDB; AAG67527;

Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection -

Claim 2; Page 53-54; 102pp; English.

Claim 2; Page 53-54; 102pp; English.

The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation such as myocardial infarction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating liver diseases, coagulation disorders and microbial diseases, for treating immune disorders, for treating inflammation and transplant rejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines.

Sequence 3213 BP; 916 A; 704 C; 756 G; 837 T; 0 other;

ment Scores:

Length:	0	3213
Matches:	922.00	1022
Percent Similarity:	99.80%	0
Local Similarity:	99.80%	1
Mismatches:	90.04%	2
Indels:	22	0
Gaps:	0	0

NO. 1

ent similarity.

Local similarity:

Local similarity: 9

22

9-697-089-2 (1-1024) x AAH78219 (1-3213)

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22 GlnIleThrAspAspLeupheValTrpAsnValLeuAsnArgGluGluValAsnIleIle 41

202 CAAATCACAGATGACCTATTTTGTATGGAATGTTCTGAATCGGAGCAAGTAAACATCAT 261

42 CysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLys 61

262 TGCTGCGAGAGGTGGAGCAGCATGCTGCTAGAGGATCATTCACATGATTTTGAAAAAG 321

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Qy	102	AlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGly121 
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Qy	142	LysAspGlnHisHisArgValGluGlnIleuThrLeuAsnGlyLeuLeuAlaLeu161 
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Qy	182	IleAlaMetLeuTrpGlySerglyLysCysLysAlaLeuThrLysPheLysPheValPhe201 
Db	682	ATTGCCATGTCTCGGGCTCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTCTTC 
Qy	202	PheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuLeu221 
Db	742	TTCCTCCGTCTCAGCAGGGCCCCAGGGTGGACTTTTGAACCCTCTGTGATCAACCTCGTG 
Qy	222	AspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGln241 
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Qy	262	GluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr281 
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Qy	302	GluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeu321 
Db	1042	GAAGACAGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGCTGAAGGCTTG110 
Qy	322	LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheVal341 
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Qy	342	ValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThr361 
Db	1162	GTATCATCTTGTGCATTCAGATGGGTGAAGTAGTTCACCTCTCACACACAAACACG122 
Qy	362	LeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyVal381 
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Db	1282	GCTGCAAGTACTTTCATTTCGGAGCCTGGACCATCTGGAGACCTTAGTCTCTGGAGGGTGTG134 
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Db 1402 CTGACAACCTGGGCTCCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTC 1461  
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QY 522 SerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrThr 541  
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Db 1702 TCCATCGCCAGAGGCCCTCTCTGGACACAGGAATCTTTGCAAGTGTGAAACACCACT 1761  
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Db 2002 GCTTCATGGGAAAAGGCTCGAAGACACAGGTGGAATCCACATGAAGAGGCCCCAGAA 2061  
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AC AAS03946;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.  
XX  
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
KW systemic lupus erythematosus; arthritis; neurologic disorder; stroke;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;  
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
KW excitotoxic brain damage; liver disease.  
XX  
OS Homo sapiens.  
XX

FH Key Location/Qualifiers  
 FT 1..3615  
 FT /\*tag= a  
 FT /product= "Human CARD-12"  
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 XX  
 PN WO200130971-A2.  
 XX  
 XX 03-MAY-2001.  
 XX  
 XX 26-OCT-2000; 2000WO-US29643.  
 XX  
 XX 27-OCT-1999; 99US-0161822.  
 PR (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PA Bertin J, Robison KE;  
 XX  
 XX  
 XX WPI: 2001-308628/32.  
 DR P-PSDB: AAU02881.  
 XX  
 XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
 PT encoding them, useful for treating and diagnosing disorders associated  
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
 PT disease -  
 XX  
 PS Disclosure; Fig 2; 93pp; English.  
 XX  
 CC The sequence represents a genomic DNA which encodes the human caspase  
 CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
 CC number of proteins that transmit signals that activate apoptosis and  
 CC inflammatory pathways in response to stress and other stimuli. Therefore,  
 CC CARD-12 and its corresponding nucleic acid may be used in treatment and  
 CC diagnosis of patients suffering from disorders associated with an  
 CC abnormal level (an increase or a decrease) of apoptotic cell death or  
 CC abnormal activity of stress-related pathways. The disorders include  
 CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
 CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
 CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
 CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
 CC infarction, stroke), inflammatory and immune system disorders (e.g.  
 CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
 CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
 CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
 CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
 CC meningitis and liver disease.  
 XX  
 SQ Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

## Alignment Scores:

Pred. No.: 0 Length: 3615  
 Score: 827.00 Matches: 927  
 Percent Similarity: 99.78% Conservative: 0  
 Best Local Similarity: 99.78% Mismatches: 1  
 Query Match: 80.76% Indels: 2  
 DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAS03946 (1-3615)

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Db	1096	CAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCGATATACCTGCACAATCAGG	1155
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Db	1156	AAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGCAGAGGGTCTCTTCTCTTGTAT	1215
QY	249	GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGluAsn	268
Db	1216	GGCTACAAATGAATTCAGAGCCCAAGACTGCCAGAAATCGAAGCCCTGATAAAGGAAAC	1275
QY	269	HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg	288
Db	1276	CACCGCTTCAAGAACATGGTCACTGCTCACCCTACCACTGAGTGCCTGAGGCACATACGG	1335
QY	289	GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu	308
Db	1336	CAGTTTGGTGCCTGACTGCTGAGTGGGGATATGACAGAGACACGCGCCAGGCTCTC	1395
QY	309	IleArgGlnValLeuLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer	328
Db	1396	ATCCGAGAAGTGCCTGATCAAGAGGCTTGCCTCAAGGCTTGTGCTCCAAATTCAGAAATCC	1455
QY	329	ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln	348
Db	1456	AGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTGTGTCATCACTTGTGCATCCAG	1515
QY	349	MetGlyGluSerGluPheHisSerHisThrThrThrLeuPheHisThrPheTyrAsp	368
Db	1516	ATGGGTGAAAGTGAGTTCCTCACTCTCACACACAAACACGCTGTTCCTCATATGAT	1575
QY	369	LeuLeuIleGlnLysAsnLysHisLysHisGlyValAlaAlaSerAspPheIleArg	388
Db	1576	CTGTGTGATACAGAAAAACAAACACAAATAAAGGTGTGGCTGCAAGTCACTTCATTCGG	1635
QY	389	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe	408
Db	1636	AGCTGGACCACCTGTGGAGACCTAGCTCTGGAGGGTGTGTCTCCACACAGTTGATTTC	1695
QY	409	GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys	428
Db	1696	GAACCTGCAGGATGTGTCCAGCGTGAATGAGGATGCTCTGCTGCACAACTGGGCTCTGT	1755
QY	429	LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu	448
Db	1756	AAATATACAGCTCAAGAGTTCAAGCCAAAGTATAAAATCTTTTCAAAAGTCAATCCAGAG	1815
QY	449	TyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr	468
Db	1816	TACACAGCAGCAGACACTCAGCAGGTTTATTGACGCTCTATGAGCAGGAGGAGTGAACC	1875
QY	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
Db	1876	AAGGGGAATGTTTACTTTCAGAAAAATGTTTCCATTTTCGGACATTTACATCCACTATAGC	1935
QY	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
Db	1936	AGCCTGCTCGGTACACCTGTGGGTCTATCTGTGGAAGCCACCAGGGGTGTATTATGAAGC	1995
QY	509	LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
Db	1996	CTCGACAGCTGTATCAACACAGGCTGCCTTCTCGGACTTTTCCATTCGCAAGAGGCTCTC	2055

QY 529 TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla 548  
|||||  
Db 2056 TGGAGACAGGAATCTTTGCAAGAGTGTGAACACACCCACCTGAGCAAGAAATCTGAAGCC 2115  
QY 549 IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568  
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Db 2116 ATAACATCAATTCCTTTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAA 2175  
QY 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer 588  
|||||  
Db 2176 TCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTCAAGGTAAGAGCTTATATCAACTCA 2235  
QY 589 GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla 608  
|||||  
Db 2236 GGGAAACATCCCGATTACTTTATTGACTTCTTTGAACATTTGCCCAATTTGCAAGTGCC 2295  
QY 609 LeuAspPheIleLysLeuAspPheTyrGlyAlaMetAlaSerTrpGluLysAlaAla 628  
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Db 2296 CTGGACTTCATTAACCTGGACTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCA 2355  
QY 629 GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla 648  
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Db 2356 GAGACACAGGTGAATCCACATCGAAGAGAGGCCCAAGAACCTTACATCCCAGCAGGGCT 2415  
QY 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgasp 668  
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Db 2416 GTATCTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGGAT 2475  
QY 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh 688  
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Db 2476 TTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGGAATAATTCAGCTCTGCCAC 2534  
QY 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValle 708  
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Db 2535 AGCCTCAGCTGCGAAATGAAGAGATGCTGTGTGGCTGAAGCTCAGTTTGTCTC 2594  
QY 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728  
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Db 2595 CAGCACCTGTAAGACATTTATCTCTCATGTGTGAAGCCAGCTCCCTCACCATAGAAGA 2654  
QY 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs 748  
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Db 2655 TCAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAGTATTTCATGACTACAGAA 2714  
QY 748 nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768  
|||||  
Db 2715 TCACCGCTGCCGGTGGTCTGACTGACAGCTTGGTAACTTGAAGAACCTTACAAAGCT 2774  
QY 768 uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuTy 788  
|||||  
Db 2775 CATAATGGATAACATAAAGATGAATGAAGAAGATGCTATAAAACTAGCTGAAGGCCGAA 2834  
QY 788 sasnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyMe 808  
|||||  
Db 2835 AAACCTGAAGAAGATGTGTTATTTTCATTTGACCCACTTGTCTGACATTTGGAGAGGAAT 2894  
QY 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828  
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Db 2895 GGATTCATAGTCAGTCTCTGCAAGTGAACCCCTGTGACCTTGAAGAAATTCATTTAGT 2954  
QY 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848  
|||||  
Db 2955 CTCCTGCTGTTGTCGAAATGCAGTGAATAATCCTAGCTCAGAAATCTTCACAAATTTGCT 3014  
QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868  
|||||  
Db 3015 CAAACTGAGCATCTTGATTTATCAAGAAATTTACCTGGAAAAAGATGGAAATGAAGCTCT 3074  
QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888  
|||||  
Db 3075 TCATGAACATGATCGACAGAGTAAGCTGTAGAAGAGCTCACCGCACTGATGCTGCCG 3134  
QY 888 pGlyCysaspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluValProGln 908

Db 3135 GGGCTGTGAGCTGCAAGGCAGCGCTGAGAGCCCTGTTGAAACATTTGGAGGAGGTCCCA 3194  
QY 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928  
|||||  
Db 3195 ACTCGTCAAGCTGGGTTGAAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAG 3254  
QY 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948  
|||||  
Db 3255 TGCATTTTTTTGAAAGAACCCCTCTGAAAAACTTCCAGCAGTTGAATTTGGCGGGAATCG 3314  
QY 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968  
|||||  
Db 3315 TGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTTGAGAAATCTTTAAGCAATTAGT 3374  
QY 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988  
|||||  
Db 3375 GTTTTTTGACTTTAGTACTTAAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAACTTAG 3434  
QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008  
|||||  
Db 3435 CCAAGTGTTATCCAGTTAACTTTCTGCAAGAAAGCTAGGCTTGTGGTGGAATTTGA 3494  
QY 1008 pAspAspAspLeuSerValIleThr 1016  
|||||  
Db 3495 TCATGATGATCTCAGTGTATTATACA 3519  
RESULT 4  
ABK22731  
ID ABK22731 standard; cdna; 3396 BP.  
XX  
AC ABK22731;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human cDNA encoding CLAN A.  
XX  
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
OS Homo sapiens.  
XX  
PN WO200190156-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US17158.  
XX  
PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
PA (BURN-) BURNHAM INST.  
XX  
PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
DR WPI; 2002-083086/11.  
XX  
PT P-PSDB; AAU80861.  
PT New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke

XX Claim 1; Page 166-171; 216pp; English.

CC The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

SQ Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;

#### Alignment Scores:

Pred. No.:	0	Length:	3396
Score:	721.00	Matches:	1021
Percent Similarity:	99.42%	Conservative:	0
Best Local Similarity:	99.42%	Mismatches:	3
Query Match:	70.41%	Indels:	6
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABK22731 (1-3396)

QY	1	MetAsnPhelLeuLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle	20
DB	277	ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACITGTATA	336
QY	21	LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle	40
DB	337	AAGCAAAATCACAGATGACATATTCTGTATGGAATGCTTGAATCGCGAAGAAATGAATC	396
QY	41	IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys	60
DB	397	ATTGCTCGGAGAGGTGGACAGATGCTGCTAGAGGGATCATTCACATGATTTTGAA	456
QY	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu	80
DB	457	AAGGTTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAGGAGTGAACATATCTCTA	516
QY	81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp	100
DB	517	TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACCAT	576
QY	101	LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu	120
DB	577	TGGCTCAGGATTTAAGAGACTTGACCATCCCATCTTTCTGAACTTTATCCCTT	636
QY	121	GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProVal-LeuTr	140
DB	637	GGTGAAGATATTGACATATTATTTAACTTGAAGACACCTTCACAGAACCTAT-CTGTG	695
QY	140	PARGLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAl	160
DB	696	GAGGAAGACCAACACCATCACCGCGTGGAGCAGCTGACCTGATGCGCTCTCGACGC	755
QY	160	aLeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuLeuGln	180
DB	756	TCTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCATCTGCTGCA	815
QY	180	nArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVa	200

DB	816	GCGCATTCGCCATGCTCTGGGGCTCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATCGT	875
QY	200	lPhePheLeuArgLeuSerArgAlaGlnGlyClyLeuPheGluThrLeuCysAspGlnIe	220
DB	876	CTTCTTCTCCGTCTCAGCAGGGCCCGAGGTGGACCTTTTGAACCCCTCTGTGATCAACT	935
QY	220	uLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuAr	240
DB	936	CCTGGATATACCTGGCAACAATCAGGAAGCAGACATTCATGCCATGCTGCTGAAGCTGG	995
QY	240	gGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProG	260
DB	996	GCAGAGGGTCTCTTTCCTCTTGTATGGCTACAATGAATTAAGCCCCAGAGCTGCCAGA	1055
QY	260	uIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrTh	280
DB	1056	AATCGAAGCCCTGATAAAGGAAACCCCGCTTCAAGAACATGGTCATCGTCACCACTAC	1115
QY	280	rThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMe	300
DB	1116	CACGTAGTGCCTGAGGCACATACGCGACGTTGGTGCCCTGACTGCTGAGTGGGGGATAT	1175
QY	300	tThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluG	320
DB	1176	GACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGCTGAAGG	1235
QY	320	yLeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPh	340
DB	1236	CTTGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCT	1295
QY	340	eValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnTh	360
DB	1296	TGTGGTCACTACTGTGCAATCCAGATGGTGAAGTAGTTCCTACTCTCACACACAAC	1355
QY	360	rThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysG	380
DB	1356	AACGCTGTTCATACCTCTCTATGATCTCTGTATACAGAAAAACAACAACAATAAAGG	1415
QY	380	yValAlaAlaSerAspPheIleArgSerLeuAspHisCys-GlyAspLeuAlaLeuGluG	400
DB	1416	TGTGGCTCAAGTACTTTCATTCGGAGCTGGACCCAGC-TGGAGACCTAGCTCTGGAGG	1474
QY	400	lyValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspV	420
DB	1475	GTGTGTTCTCCCAAGTTTGATTTTCGAACTGCAGAGTGTGTCCAGCGTGAATGAGGATG	1534
QY	420	alLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrL	440
DB	1535	TCCTGCTGACAACCTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCAAAGTATA	1594
QY	440	ysPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuT	460
DB	1595	AATTTCTTTCAAGTCAATTCAGGAGTACACAGCAGGAGAGACTCAGCAGCTTTATTGA	1654
QY	460	hrSerHisGluProGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerI	480
DB	1655	CGTCTCATGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAATATGGTTTCCA	1714
QY	480	leSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValG	500
DB	1715	TTTCGGACATTTACATCCACTTATAGCAGCCTGCTCCGCTACACCTGTGGTCTCATCTGG	1774
QY	500	luAlaThrArgAlaValaMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuG	520
DB	1775	AAGCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGCGCTCTTCG	1834
QY	520	lyLeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnT	540
DB	1835	GACTTTCCATCGCCCAAGAGGCTCTCTGAGACACAGGAATCTTTGCAAAAGTGTGAAAA	1894
QY	540	hrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH	560

Db 1895 CCACCTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCC 1954  
Qy 560 IsLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheG 580  
Db 1955 ATTTATATACAGAGAGTACATCCAATCAGCCCTGAGCCAGAATTTGAAGCTTCTTCCTTC 2014  
Qy 580 InGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheG 600  
Db 2015 AAGGTAAAAGCTTATATATCAACTCAGGGAACATCCCGATTACTATTGACTTCTTTG 2074  
Qy 600 LuHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyA 620  
Db 2075 AACATTTCCCAATTTGTCAAGTGCCTCGACTTCATTAACCTGGACTTTTATGGGGAG 2134  
Qy 620 LaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaP 640  
Db 2135 CTATGGCTTCATGGAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGAAGAGGCC 2194  
Qy 640 roGluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheA 660  
Db 2195 CAGAAACCTACATCCAGCAGGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTC 2254  
Qy 660 rgThrLeuGluValThrLeuArgaspPheSerLysLeuAsnLysGlnAspIleThr-Tyr 679  
Db 2255 GGACTCTGGAGGTCACATCCCGGATTTTCAGCAAGTTCAATAAGCAAGATATCAG-ATAT 2313  
Qy 680 LeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGly 699  
Db 2314 CTGGGAAATATTCAGCTCTGCCACAAGCTCAGGCTGCAATAAAGAGATGCTGGT 2373  
Qy 700 ValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetVal 719  
Db 2374 GTGGCTGGAAGCCTCAGTTTGTCTCAGCACCTGTAAGAACATTTATCTCTCATGTG 2433  
Qy 720 GluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLys 739  
Db 2434 GAAGCCATGCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAAACAACCTGAAA 2493  
Qy 740 ThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeu 759  
Db 2494 ACCITGATTTATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTG 2553  
Qy 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAsp 779  
Db 2554 GGTAACTTGAAGAACCTTACAAAGCTCATATGGATACATAAAGATCAATGAAGAAGAT 2613  
Qy 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799  
Db 2614 GCTATAAAACCTAGCTGAAGGCTGAAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACC 2673  
Qy 800 HisLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluPro 819  
Db 2674 CACTTGCTGCACATGGAGAGGAATGATATACATAGTCAAGTCTCTCTCAAGTGAACCC 2733  
Qy 820 CysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIle 839  
Db 2734 TGTGACCTTGAAGAAATTCATTTAGTCTCCTGCTGCTGCTGCAAAATGCAGTGAATC 2793  
Qy 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859  
Db 2794 CTAGCTCAGAATCTTCACAAATTTGGTCAAACTGGACATCTTGAATTTATCAGAAATATAC 2853  
Qy 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879  
Db 2854 CTGGAAAAGATGGAATGAAGCTCTTCATGAATCATGCACAGGATGAAGCTGTAGAA 2913  
Qy 880 GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu 899  
Db 2914 CAGCTCACCGCACATGATCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTG 2973  
Qy 900 LeuLysHisLeuGluGluValIleProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu 919  
Db 2974 TTGAACATTTTGGAGGAGTCCCACTCGTCAAGCTTGGGTTGAAATACTGGAGACTC 3033

Qy 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939  
Db 3034 ACAGATACAGAGATTAGAAATTTTAGTGCAATTTTGGAAAGAACCTCTGAAAACATTC 3093  
Qy 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 959  
Db 3094 CAGCAGTTGAATTTGGCGGAAATCGTGTGACAGCTGATGGATGCTTGCCTTCATGGGT 3153  
Qy 960 ValPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuPro 979  
Db 3154 GTATTTGAGAATCTTAAGCAATTTAGTGTTTTGTACTTTAGTACTAAAAGAATTTTACCT 3213  
Qy 980 AspProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlu 999  
Db 3214 GATCCAGCATTAGTCAGAAACCTTAGCCCAAGTGTATCCAGTTAACTTTCTGCAAGAA 3273  
Qy 1000 AlaArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPhe 1019  
Db 3274 GCTAGGCTTGTGGGTGCAATTTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTT 3333  
Qy 1020 LysLeuValThrAla 1024  
Db 3334 AAACCTAGTAACGTCT 3348  
RESULT 5  
AAH98254  
ID AAH98254 standard; cDNA; 3545 BP.  
XX  
AC AAH98254;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Murine EST-derived coding sequence SEQ ID NO: 111.  
XX  
Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition; ss.  
XX  
OS Mus musculus.  
XX  
PN WO200154477-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02687.  
XX  
PR 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX  
XX WPI; 2001-476164/51.  
DR P-PSDB; AAM23595.  
XX  
Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use -  
XX  
XX Claim 1; Page 250-251; 1275pp; English.  
XX  
The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA

CC of the invention.

XX Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;

## Alignment Scores:

Pred. No.: 0 Length: 3545  
Score: 721.00 Matches: 1021  
Percent Similarity: 99.42% Conservatives: 0  
Best Local Similarity: 99.42% Mismatches: 3  
Query Match: 70.41% Indels: 6  
DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAH98254 (1-3545)

QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB ATGAATTCATAAGGACAAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATA 291  
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40  
DB AAGCAATACACATGACCTATTGTATGAATGTTCTGAATCGCGAAGAAGTAACATC 351  
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLys 60  
DB ATTTGCTGCGAGAGGTTGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 411  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80  
DB AAGGTTACAGAGTCCTGTAACCTTTCTTTAAATCCCTTAAGGAGTGGAACTATCCCTA 471  
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 100  
DB TTTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGAG 531  
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
DB TTGGCTCAGGATTTAAAGGACTTGTACATACCCCATCTTTTCTGAACTTTTATCCCT 591  
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140  
DB GTTGAAGATATTGACATATTATTTTAACTTGAAAGACCTTTCAGAACCTGCTCTGTGG 651  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
DB AGGAAGACCAACACCATCATCCCGTGGAGCAGTGAACCTGTAATGGCCCTCCCTGCA 711  
QY 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysSerThrLeuLeuGln 180  
DB CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 771  
QY 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
DB CGCATTCGCATGCTCTGGGCTCCGGAAGTGGCAAGCTCTGACCAAGTTCAAATTCGTC 831  
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220  
DB TTCTTCCTCGCTCAGCAGGGCCAGGCTGGACTTTTGTAAACCCCTCTCTGTATCAACT 891  
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240  
DB CTGGATATACCTGGCAATCAGAGAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGG 951  
QY 241 GlnArgValLeuPheLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
DB CAGAGGTTCTTTTCTTCTTGTATGCTACAATGAATTCAGCCCCCAAGACTGCCAGAA 1011  
QY 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280  
DB ATCGAGCCCTGTAAAGGAAAAACCCGCTTCAAGAACATGCTCATCGTCACCACTACC 1071  
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyValaLeuThrAlaGluValGlyAspMet 300  
DB ACTGAGTGCCTGAGGCACATACGCGAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 1131

QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
DB ACAGAGACAGCGCCAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTGAAGGC 1191  
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
DB TTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1251  
QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
DB GTGGTCATCACTTGTGCAATCCAGATGGTGCAAGTGCAGTCTCCACTCTCACACAAACA 1311  
QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGly 380  
DB ACGTGTCTCATCTCTTCTATGATCTGTTGATACAGAAAACAAACAACATAAAGGT 1371  
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAsp-LeuAlaLeuGlu 400  
DB GTGGCTGCAAGTGACTTCATTCGAGGCTGGACCACCTGTGGATA-CCTAGCTCTGGAGG 1430  
QY 400 YValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420  
DB TGTGTTCTCCACAAAGTTTGAATTCGAACCTGCAGGATGTCTCCAGCGTGAATGAGGATG 1490  
QY 420 lLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLy 440  
DB CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGGCCAAGATATAA 1550  
QY 440 sPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuTh 460  
DB ATTCCTTCACAAGTCAATTCAGGAGTACACAGCAGGAGCAAGACTCAGCAGTTTATTGAC 1610  
QY 460 rSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIl 480  
DB GTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTACTTGCAGAAAAATGTTTCCAT 1670  
QY 480 eSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGl 500  
DB TTCGGACATTTACATCCACTTATAGCAGCTGCTCCGCTACACCTGTGGGTCTCTGTGGA 1730  
QY 500 uAlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGl 520  
DB AGCCACAGGCGCTGTATGAAGCACCTCGCAGCAGTGTATCAACACAGCGCTCCCTTCGG 1790  
QY 520 yLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnTh 540  
DB ACTTTCATCGCCCAAGAGGCTCTCTGGAGACAGGAATCTTGCAGAGTGTGAAAAACAC 1850  
QY 540 rThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH1 560  
DB CACTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCA 1910  
QY 560 sLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGl 580  
DB TTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCAAGAAATTTGAAGCTTTCTTTCA 1970  
QY 580 nGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGl 600  
DB AGGTAAAGCTTATATATCAACTCAGGGAACATCCCGCATTTACTTATTTGACTTCTTTGA 2030  
QY 600 uHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAsp-PheTyrGlyGly 620  
DB ACATTTGCCCAATTTGTCAAGTCTCTGGACTTCATTAAACTGGG-CTTTTATGGGGGAG 2089  
QY 620 lMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaP 640  
DB CTATGGCTTCAATGGAAAAAGGCTGCAGAGACACAGGTGGAATCCACATCGAAGAGGCC 2149  
QY 640 roGluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheA 660  
DB CAGAAACCTACATTCACAGCGGCTGTATCTTTGTTCTTCAACTGGAAACAGCAATTC 2209





XX  
SQ Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;

Alignment Scores:			
Pred. No.:	0	Length:	2215
Score:	663.00	Matches:	737
Percent Similarity:	99.73%	Conservative:	0
Best Local Similarity:	99.73%	Mismatches:	1
Query Match:	64.75%	Indels:	2
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAH78218 (1-2215)

Qy	15	MetGlyMetThrValIleLysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsn	34
Db	1	ATGGGAATGACTGTATTAAGCAAAATCACAGATGACCTATTTGTATGGAAATGTTCTGAAT	60
Qy	35	ArgGluGluValAsnIleIleCysGlyGluLysValGluGlnAspAlaAlaArgGlyIle	54
Db	61	CGCGAAGAAGTAACATCATTTGCTGGGAGAAGGTGGACGAGATGCTGCTAGAGGGATC	120
Qy	55	IleHisMetIleLeuLysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLys	74
Db	121	ATTACATGATTTTGA AAAAGGTTGAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAG	180
Qy	75	GluTrpAsnTrpProLeuPheGlnAspLeuAsnGlyClnSerLeuPheHisGlnThrSer	94
Db	181	GAGTGGAACTATCTCTATTTCAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCA	244
Qy	95	GluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPhe	114
Db	241	GAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGACTTGTACCATACCCCATCTTTT	300
Qy	115	LeuAsnPheTrpProLeuGlyGluAspIleAspIlePheAsnLeuLysSerThrPhe	134
Db	301	CTGAACCTTTATCCCTTGTGTGAAGATATTGACATATTATTTAACTTGAAGACACCTTC	360
Qy	135	ThrGluProValLeuTrpArgLysAspGlnHisHisArgValGluGlnLeuThrLeu	154
Db	361	ACAGAACCTGCTCTGTGGAGGAAGGACCAACACCATCCCGGTGGAGCAGCTGACCCGT	420
Qy	155	AsnGlyLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGluSerGlyLysGly	174
Db	421	AATGGCCCTCTCGAGGCTCTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGC	480
Qy	175	LysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeu	194
Db	481	AAGTCCACTCTGCTGACGGAATTGCCATGCTCTGGGGCTCCGGAAGTGCAGGCTCTG	540
Qy	195	ThrLysPheLysPheValPhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlu	214
Db	541	ACCAAGTTCAAATTCGTCTTCTTCCTCCGCTCTCAGCAGGGCCCGAGGGTGGACTTTTGA	600
Qy	215	ThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAla	234
Db	601	ACCTCTGTGATCACTCTCTGGATATACCTGGCCAAATCAGGAAGCAGACATTCATGGCC	660
Qy	235	MetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLys	254
Db	661	ATGCTGTGAAGCTGGCGCAGAGGGTTCTTTTCTTCTTGATGGCTACAAATGAATTCAG	720
Qy	255	ProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet	274
Db	721	CCCCAGAACTGCCAGAAATCGAAGGCCCTGATAAAGGAAACACCGCTTCAGAACATG	780
Qy	275	ValIleValThrThrThrThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThr	294
Db	781	GTCACTGTCACCACTACCACTGAGTGCCTGAGGCACATACGGCAGCTTTGGTGCCTGACT	840
Qy	295	AlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIle	314
Db	841	GCTGAGTGGGGATATGACAGAAGACAGCCCGCCGGCTCTCATCCGAGAAGTGTGATC	900



Db 1981 CAAGATATCAG-ATATCTGGGAAATATTCAGCTCGCACAAAGCCTCAGGCTGCAAT 2039  
QY 694 eLysArgCysAlaGlyValAlaGlySerLeuValLeuSerThrCysLysAsn11 714  
Db 2040 AAAGAGATGTGGTGGTGGGAGAGCCTCAGTTGGTCCAGCACCTGTAAGAAT 2099  
QY 714 eTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspGluArgHisIleThrSe 734  
Db 2100 TTATTTCTCTCAGTGGAGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCACC 2159  
QY 734 rValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuPro 752  
Db 2160 TGTAAACAAACCTGAAACCTTGAGTATTATCATGACCTACAGAAATCAACGGCTGCCG 2214

RESULT 7

AAH99581  
ID AAH99581 standard; cDNA; 2950 BP.  
AC AAH99581;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human protein encoding cDNA sequence SEQ ID NO:416.  
XX  
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
KW anti-HIV; fungicide; antitumagen; cardiovascular; antianemic; anaemia;  
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;  
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200153455-A2.  
XX  
PD 26-JUL-2001.  
XX  
PF 22-DEC-2000; 2000WO-US35017.  
XX  
PR 23-DEC-1999; 99US-0471275.  
XX  
PR 21-JAN-2000; 2000US-0488725.  
XX  
PR 25-APR-2000; 2000US-0552317.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-457603/49.  
XX  
DR P-PSDB; AA25640.

Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
Claim 1; Page 511-512; 1217pp; English.  
XX  
CC AAH99166 to AAH99904 encode the human proteins given in AA25225 to  
CC AA25963. The proteins can have activities based on the tissues and  
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
CC central nervous system; virucide; anti-HIV; fungicide; antitumagen;  
CC cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary;  
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
XX

CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders.  
XX

SQ Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;

Alignment Scores: 0 Length: 2950  
Pred. No.: 0 Matches: 625  
Score: 425.00  
Percent Similarity: 99.36% Conservative: 0  
Best Local Similarity: 99.36% Mismatches: 2  
Query Match: 41.50% Indels: 4  
Db: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAH99581 (1-2950)

QY 398 LeuGluGlyValPheSerHisLysPheAspPheGluLeuGlnAspValSerValAsn 417  
Db 47 CTGGAGGGTGTCTCCCAAGTTGATTTCGAACTCAGATGTGTCCAGCGTGAAT 106  
QY 418 GluAspValLeuLeuThrThrGlyLeuLeuLysLysTyrThrAlaGlnArgPheLysPro 437  
Db 107 GAGGATGCTCTGCTGACAACTGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCA 166  
QY 438 LysTyrLysPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457  
Db 167 AAGTATAAATCTTTTCCAAAGTCATTCAGGAGTACACAGCAGGAGGAGAGCTCAGCAGT 226  
QY 458 LeuLeuThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMet 477  
Db 227 TTATTGACGCTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTCAGAAAAATG 286  
QY 478 ValSerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySer 497  
Db 287 GTTTCATTCGACATTCATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCA 346  
QY 498 SerValGluAlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCys 517  
Db 347 TCTGTGGAAGCCACCCAGGGCTGTATTGAAGCACCTCGCAGCAGTGTATCAACACGCGTGC 406  
QY 518 LeuLeuGlyLeuSerIleAlaLysArgProLeuTyrArgGlnGluSerLeuGlnSerVal 537  
Db 407 CTTCTGGGACTTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGAAAGTGTG 466  
QY 538 LysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCys 557  
Db 467 AAAACACACCTGAGCAAGAAATCTGAAAGCCATAAATCAATTCCTTTGTAGAGTGT 526  
QY 558 GlyIleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAla 577  
Db 527 GGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCT 586  
QY 578 PhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAsp 597  
Db 587 TTCTTTCAAGGTAAGAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTTATTGAC 646  
QY 598 PhePheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAsp-PheTy 617  
Db 647 TTCCTTGAACATTTGCCCAATTTGCAAGTGTCTGGACTTTCATTAACCTGGG-CTTTTA 705  
QY 617 rGlyGlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetG1 637  
Db 706 TGGGGGAGCTATGGCTTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGA 765

Qy	637	uGluAlaProGluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGln	657
Db	766	AGAGGCCCCAGAAACCTACATTTCCAGCAGGCGCTGTATCTTGTGTTCTTCAACTGGAAGCA	825
Qy	657	nGluPheArgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIle	677
Db	826	GGAAATTCAGGACCTCTGGAGGTACACTCCGGGATTTCAGCAAGTTGGAATAAGCAAGATAT	885
Qy	677	eThr-TyrLeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgC	697
Db	886	CAG-ATATCTGGGAAATATTTCAGCTCTGCCACAAAGCTCAGGCTGCAATAAAGAGAT	944
Qy	697	ysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerL	717
Db	945	GTGCTGTGTGTGGTGAAGCCTCAGTTTGGTCTCCTCAGCACCTGTGAAGAACATTTATTCTC	1004
Qy	717	eMetValGluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrA	737
Db	1005	TCATGGTGGGAAGCAGTCCCTCCACNTAGAAGATGAGAGGCACATCATCTGTACAA	1064
Qy	737	snLeuLysThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrA	757
Db	1065	ACCTGAAACCTTGAGTATTTCATGACCTACAGAATCAACGGCTGCCGGGTGTGCTGACTG	1124
Qy	757	spSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnG	777
Db	1125	ACAGCTTGGGTAACTTTGAAGAACCTTACAAAGCTTCATAATGATGAACATAAAGATGAATG	1184
Qy	777	luGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheH	797
Db	1185	AAGAGATGCTATAAACTAGCTGAAGCGCTGAAAACCTGAAGAAGATGTGTTATTTC	1244
Qy	797	isLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerS	817
Db	1245	ATTTGACCCACTTGTCTGCATTTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAA	1304
Qy	817	erGluProCysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlav	837
Db	1305	GTGAACCTCTGTACCTTGAAGAAATTCAAATTAGTCTCTGCTGTCTGTCTGCAAAATCGAG	1364
Qy	837	allysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerG	857
Db	1365	TGAATFCCCTAGCTCAGAATCTTCACAATTTGGTCAAACTGAGCATTTCTGATTATTCAG	1424
Qy	857	luAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnV	877
Db	1425	AAAATTACCTGGAAAAAGATGGAATGAAGCTCTTCATGAAGTATGTCGACAGGATGAACG	1484
Qy	877	alLeuGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeus	897
Db	1485	TGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCGACGCTGA	1544
Qy	897	erSerLeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnT	917
Db	1545	GCAGCCTGTGTGAACATTTGGAGGAGGTCCCAACACTCGTCAAGCTGGGTTGAAAAACT	1604
Qy	917	rpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuL	937
Db	1605	GGGACTCACAGATACAGAGATTAGAAATTTAGGTGCATTTTTTGGAAAGAACCCCTCTGA	1664
Qy	937	ysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlap	957
Db	1665	AAAATTCACAGCATTTGAATTTGGCGGGAAATCGTGTGAGCAGTGATGGATGGCTTCGCT	1724
Qy	957	heMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluP	977
Db	1725	TCATGGGTGTTATTGAGAATCTTAAGCAATTAGTCTTTTTGACTTTAGTACTAAAGAAT	1784
Qy	977	heLeuProAspProAlaLeuValArgLysLeuSerGlnValIleuSerLysLeuThrPheL	997
Db	1785	TTCTACTGATCCGACATTAGTCAGAAACTTAGCCCAAGTGTATPCCAAGTAACTTTTC	1844

Qy	997	eugInGluAlaArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleHrg	101
Db	1845	TGCAAGAAGCTAGGCTGTGTGGGTGGCAATTTGATGATGATCTCAAGTCTTATTACAG	1904
Qy	1017	lyAlaPheLysLeuValThrAla	1024
Db	1305	GTGCTTTTAACCTAGTACTGCT	1927
RESULT 8			
ABK22732			
ID	ABK22732	standard; cDNA; 1395 BP.	
XX	AC	ABK22732;	
XX	XX		
DT	26-MAR-2002	(first entry)	
XX	XX		
DE	Human cDNA encoding CLAN B.		
XX	XX		
KW	Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;		
KW	abnormal cell proliferation; cancer; abnormal cell death; apoptosis;		
KW	autoimmune disease; inflammation; keratinocyte hyperplasia;		
KW	inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;		
KW	balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;		
KW	leukemia; allergy; arthritis; lupus; Schrogen's syndrome;		
KW	Crohn's disease; graft-versus-host disease; stroke;		
KW	myocardial infarction; heart failure; neurodegenerative disease;		
KW	Parkinson's disease; Alzheimer's disease; HIV;		
KW	human immunodeficiency virus infection.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FN	WO200190156-A2.		
XX	XX		
PD	29-NOV-2001.		
XX	XX		
PF	24-MAY-2001; 2001WO-US17158.		
XX	XX		
PR	24-MAY-2000; 2000US-0579240.		
PR	10-OCT-2000; 2000US-0686347.		
PR	14-MAR-2001; 2001US-275980P.		
PR	23-MAY-2001; 2001US-0864921.		
XX	XX		
PA	(BURN-) BURNHAM INST.		
XX	XX		
PI	Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;		
PI	Oliveira VAM, Hayashi H, Pawlowski K;		
XX	XX		
DR	WPI; 2002-093086/11.		
DR	P-PSDB; AAU80862.		
XX	XX		
PT	New caspase recruitment domain (CARD)-containing polypeptides and		
PT	encoding nucleic acids, useful for treating abnormal cell proliferation		
PT	or cell death, autoimmune diseases or inflammation, e.g. carcinomas,		
PT	arthritis or stroke		
XX	XX		
PS	Claim 1; Page 174-176; 216pp; English.		
XX	XX		
CC	The invention relates to an isolated caspase recruitment domain (CARD)		
CC	-containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain		
CC	from it, and the polynucleotides encoding them. Also included are a		
CC	recombinant vector comprising the polynucleotide, recombinant cells		
CC	containing the vector (e.g. bacteria, yeast, plant, animal, mammalian		
CC	and insect cells) and an anti-CARD antibody. The CARD-containing		
CC	polypeptide and CARD-encoding nucleic acid are useful for treating a		
CC	pathology characterised by abnormal cell proliferation (e.g. cancer),		
CC	abnormal cell death (apoptosis), autoimmune diseases or inflammation.		
CC	Particular, the polypeptide and nucleic acid are useful for treating		
CC	keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth		
CC	muscle cell proliferation in arteries following balloon angioplasty		
CC	(restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,		
CC	allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,		
CC	graft-versus-host disease, stroke, myocardial infarction, heart failure		
CC	neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's		

CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

## Alignment Scores:

Pred. No.: 1.88e-254 Length: 1395  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 26.46% Indels: 0  
DB: 24 Gaps: 0

US-09-697-089-2 (1-1024) x ABK22732 (1-1395)

Qy 754 GlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIle 773  
Db 541 GGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGCTCATATGGATAACATA 600  
Qy 774 LysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysMet 793  
Db 601 AAGATGAATGAAGAGATGCTATAAACTAGCTGAAGGCCCTGAAACCTGAAGAAGATG 660  
Qy 794 CysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleValLys 813  
Db 661 TGTATTATTCATTGACCCACTGTCTGACATTGGAGAGGGAATGGATTACATGTCAG 720  
Qy 814 SerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValSerCysLeuSer 833  
Db 721 TCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCATTAAGTCTCTGCTGTGCT 780  
Qy 834 AlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeu 853  
Db 781 GCAATGCAAGTGAATCCTAGCTCAGAACTTTCACAAATTTGGTCAAACTGAGCATCTT 840  
Qy 854 AspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAsp 873  
Db 841 GATTTATCAGAAATTAACCTGGAAAAAGATGGAATGAAGCTTTCATGAACATGTCAC 900  
Qy 874 ArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTyrGlyCysAspValGln 893  
Db 901 AGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCA 960  
Qy 894 GlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLysLeuGly 913  
Db 961 GCGAGCCTGAGCAGCTGTTGAACATTTGGAGGAGGTCCACAACTCGTCAAGCTTGGG 1020  
Qy 914 LeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLys 933  
Db 1021 TTGAAAAACTGGAGACTCACAGATACAGAGATTAGAATTTTAGTGCATTTTGGGAAG 1080  
Qy 934 AsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 953  
Db 1081 AACCTCTGAAAAAATCTCCAGCAGTTGAATTTGGCGGAAATCTGTGAGCAGTGATGGA 1140  
Qy 954 TrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPheSer 973  
Db 1141 TGGCTTGCTTCATGGGTGATTTTGGAGAACTTAAAGCAATTAGTGTTTTGGACTTAGT 1200  
Qy 974 ThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuSerLys 993  
Db 1201 ACTAAAGAATTTTACCTGATCCAGCATTAAGCAAACTTACCAAGAGTGTATCCCAAG 1260  
Qy 994 LeuThrPheLeuGlnGlnAlaArgLeuValGlyTrpGlnPheAspAspAspLeuSer 1013  
Db 1261 TTAACCTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATTTGATGATGATGATCTCAGT 1320  
Qy 1014 VallileThrGlyAlaPheLysLeuValThrAla 1024  
Db 1321 GTTATTACAGGTGCTTTTAAACTAGTAACCTGCT 1353

## RESULT 9

ABK22766

ID ABK22766 standard; cDNA; 891 BP.

XX AC ABK22766;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN NACHT.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNHAM INST.

XX PI Read JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX PI Oliveira VAM, Hayashi H, Pawlowski K;

XX DR WPT; 2002-083086/11.

XX DR P-PSDB; AAU80872.

XX PT New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke

XX PS Claim 1; Page 200-201; 216pp; English.

XX CC The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX SQ Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other;

Alignment Scores:

Pred. No.: 1.5e-216 Length: 891  
Score: 232.00 Matches: 296  
Percent Similarity: 99.33% Conservative: 0  
Best Local Similarity: 99.33% Mismatches: 1  
Query Match: 22.66% Indels: 2  
DB: 24 Gaps: 0

US-09-697-089-2 (1-1024) x ABK22766 (1-891)

Qy 161 LeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuLeuGln 180  
Db 1 CTTGAGAGCCCTGTCATCATGAGGGGAATCTGGCAAGGCAAGTCCATCTGCTGCAG 60  
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
Db 61 CGCATTCGCATCTCTGGGGCTCGGAAAGTCAAGAGCTCTGACCAAGTCAAAATTCGTC 120  
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220  
Db 121 TTCTTCCTCCGCTCTACAGAGGCCCGGAGGTGGACTTTTGGAAACCCCTCTGTGATCAACT 180  
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240  
Db 181 CTGATATACCTGGCACAATCAGGAACGACACATTCATGGCCATGCTCTGAAGCTCGG 240  
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
Db 241 CAGAGGGTCTCTTTCCCTCTCTGATGGCTACAATGAATCAAGGCCCAAGACTGCCAGAA 300  
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280  
Db 301 ATCGAAGCCCTGATAAGAGAAACCCAGCTTCAAGAACATGTGTCATCGTCACCACTAAC 360  
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
Db 361 ACTGAGTGCCTGAGGCACATACGGCAGTTGGTGCCTGACTGCTGAGGTGGGGGATG 420  
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
Db 421 ACAGACACAGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGGTGCTGAAGGC 480  
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
Db 481 TTGTGTCTCAAAATTCAGAAATCAGGTGCTTGAAGAAATCTCATGAAGACCCCTCTCTT 540  
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
Db 541 GTGGTCAATCACTGTGCAATCCAGATGGGTGAAGTGAAGTTCACCTCACACAAACA 600  
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGly 380  
Db 601 ACGCTGTCCATACCTTCTATGATCTGTGATACAGAAACAAACAAACATAAAGGT 660  
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCys-GlyAspLeuAlaLeuGlu 400  
Db 661 GTGGCTCAAGTCACTTCATTCGAGGCTGGACACCG-TGGAGACCTAGCTCTGGAGGG 719  
Qy 400 YValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420  
Db 720 TGTGTTCTCCCAAGTTGATTCGAATTCGAAGTGCAGAGTGTCTCAGCGTGAATGAGATGT 779  
Qy 420 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyr 440  
Db 780 CCGTCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGTTCAAGCCAAAGTATAA 839  
Qy 440 sPhePheHisLysSerPheGlnGluThrThrAlaGlyArgArgLeuSerSer 457  
Db 840 ATTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGACGAAGACTCAGCAGT 891

RESULT 10  
ABK22767  
ID ABK22767 standard; cDNA; 618 BP.  
XX

AC ABK22767;  
XX 26-MAR-2002 (first entry)  
XX Human cDNA encoding CLAN LRR.  
DE  
XX  
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
XX Homo sapiens.  
OS  
XX WO200190156-A2.  
PN  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
PF  
XX 24-MAY-2000; 2000US-0579240.  
PR  
XX 10-OCT-2000; 2000US-0686347.  
PR  
XX 14-MAR-2001; 2001US-275980P.  
PR  
XX 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURNHAM INST.  
XX  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX WPI; 2002-083086/11.  
DR P-PSDB; AAU08073.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke -  
XX  
XX Claim 1; Page 202-203; 216pp: English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer), In  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

SQ Sequence 618 BP; 194 A; 113 C; 148 G; 163 T; 0 other;

Alignment Scores:  
Pred. No.: 2,61e-191 Length: 618  
Score: 206.00 Matches: 206  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0

```
Query Match: 20.12% Indels: 0
DB: 24 Gaps: 0
US-09-697-089-2 (1-1024) x ABK22767 (1-618)
QY 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAsp 779
Db 1 GGTAACTTGAAGAACCCTTACAAAGCTCATATGGATAACATAAGATGAATGAAGAAGAT 60
QY 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799
Db 61 GCTATAAACTAGCTGAAGCCCTGAAAAACCTGAAGAAGATGTTTATTTTCATTGGACC 120
QY 800 HisLeuSerAspIleGlyGluMetAspTyrIleValLysSerLeuSerGluPro 819
Db 121 CACTTCTGTGACATGGACAGGGAATGGATTACATAGTCAAGTCTCTGTCAGTGAACCC 180
QY 820 CysAspLeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIle 839
Db 181 TGTGACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGCTGCTGCAAAATGCAGTGAATC 240
QY 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859
Db 241 CTAGCTCAGAAUCTTCACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAAATTAC 300
QY 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879
Db 301 CTGGAAGAAAGATGGAATGAAGCTCTTCATGAACGTGACAGGATGAACGTGTAGAA 360
QY 880 GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeu 899
Db 361 CAGCTCACCGCACTGATGCTGCGCTGGGCTGTGAGTCAAGGCAAGCCTGTGAGCAGCTG 420
QY 900 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu 919
Db 421 TTGAAACATTTGGAGAGGTCCACAACTCGTCAAGCTTGGGTGAAAACCTGGAGACTC 480
QY 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939
Db 481 ACAGATACAGAGATTAGAATTTTAGTGCATTTTGGGAAGAACCCTCTGAAAAACTTC 540
QY 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 959
Db 541 CAGCAGTTGAATTTGGCGGAAATCGTGTGACGAGTGGATGGATGGCTTCCCTTCATGGGT 600
QY 960 ValPheGluAsnLeuLys 965
Db 601 GTATTTGAGAACTTAAAG 618
RESULT 11
AAH34171/c
ID AAH34171 standard; cDNA; 2735 BP.
AC AAH34171;
XX
DT 03-SEP-2001 (first entry)
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1253.
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
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(HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
DR P-PSDB; AAG74766.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX Claim 1; Page 3017; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate p
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing P.
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 2735 BP; 791 A; 555 C; 512 G; 876 T; 1 other;

Alignment Scores:
Pred. No.: 2,67e-165 Length: 2735
Score: 180.00 Matches: 180
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.58% Indels: 0
DB: 22 Gaps: 0
US-09-697-089-2 (1-1024) x AAH34171 (1-2735)
QY 845 HisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGly 864
Db 2727 CACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAAATTTACCTGGAAAAGATGGA 2668
QY 865 AsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeu 884
Db 2667 AATGAAGCTCTTCATGAACGTGACAGAGATGAAGCTGCTAGAACAGCTCACCCGACTG 2608
QY 885 MetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLysHisLeuGlu 904
Db 2607 ATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCTGAGCAGCTTGTGTGAACATTTGGAG 2548
QY 905 GluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIle 924
Db 2547 GAGGTCCCACTCGTCAAGCTTGGTTGAAAACCTGGAGACTCACAGATACAGAGATT 2488
QY 925 ArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeu 944
Db 2487 AGAATTTTAGGTGCATTTTGTGAAAAGAACCCCTCTCAAAAACCTCCAGCAGTTGAATTTG 2428
QY 945 AlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetClyValPheGluAsnLeu 964
Db 2427 GCGGGAAATCGTGTGACAGATGATGGATGGCTTGCCTTCATGGGTGATTTGAGAAATCTT 2368
QY 965 LysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuVal 984
Db 2367 AAGCAATTAGTGTGTTTTTGCATTTAGTACTAAGAATTTTCTACCTGATCCAGCATTAGTC 2308
QY 985 ArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGly 1004
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|||||  
Db 2307 AGAAACCTAGCCAAAGTGTATCCCAAGTAACTTTCTGCAAGAGCTAGGCTTGTGGG 2248  
Qy 1005 TrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLeuValThrAla 1024  
Db 2247 TGGCAATTGATGATGATGATCTCACTGCTTATTACAGGTGCTTTTAAACTAGTAACTGCT 2188  
RESULT 12  
ABK22734  
ID ABK22734 standard; cDNA; 768 BP.  
XX AC ABK22734;  
XX DT 26-MAR-2002 (first entry)  
XX DE Human cDNA encoding CLAN D.  
XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX OS Homo sapiens.  
XX PN WO200190156-A2.  
XX PD 29-NOV-2001.  
XX PF 24-MAY-2001; 2001WO-US17158.  
XX PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX PA (BURN-) BURNHAM INST.  
XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX WPI: 2002-083086/11.  
DR P-PSDB: AAU0864.  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke -  
XX Claim 1; Page 178-179; 216pp; English.  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human

CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX Sequence 768 BP; 218 A; 157 C; 180 G; 213 T; 0 other;  
Qy  
Alignment Scores:  
Pred. No.: 1.95e-140 Length: 768  
Score: 154.00 Matches: 154  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 15.04% Gaps: 0  
DB: 24  
US-09-697-089-2 (1-1024) x ABK22734 (1-768)  
Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
Db 277 ATGAATTTTCATAAAGGACATAGCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA 336  
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40  
Db 337 AAGCAATTCACAGATGACCTATTGTATGGAATGTTCTGAATCGGAAGAAGTAACATC 396  
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
Db 397 ATTTGCTGCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGAA 456  
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80  
Db 457 AAGGGTTTCAGAGTCTCTTAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCTCT 516  
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
Db 517 TTTTCAGGACTTGAATGGCAAGAGCTTTTTCATCAGACATCAGAGGAGACTTGGACCAT 576  
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
Db 577 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCT 636  
Qy 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140  
Db 637 GGTGAAGATATTGACATTTATTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG 696  
Qy 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeu 154  
Db 697 AGGAAGGACCAACACCATCATCCGCGTGGAGCAGCTGACCCCTA 738  
RESULT 13  
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ID AAS26160 standard; cDNA; 608 BP.  
XX AC AAS26160;  
XX DT 07-NOV-2001 (first entry)  
XX DE Human cDNA encoding a novel secreted protein, Seq ID 339.  
XX KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;  
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulnary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX OS Homo sapiens.  
XX PN WO200155322-A2.  
XX PD 02-AUG-2001.

XX	17-JAN-2001;	2001WO-US01341.	PR	29-SEP-2000;	2000US-0236369.
PF			PR	29-SEP-2000;	2000US-0236370.
XX			PR	02-OCT-2000;	2000US-0236802.
PR	31-JAN-2000;	2000US-0179065.	PR	02-OCT-2000;	2000US-0237037.
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PR	02-MAR-2000;	2000US-0186350.	PR	02-OCT-2000;	2000US-0237040.
PR	16-MAR-2000;	2000US-0189874.	PR	13-OCT-2000;	2000US-0239935.
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PR	28-JUN-2000;	2000US-0214886.	PR	20-OCT-2000;	2000US-0241786.
PR	30-JUN-2000;	2000US-0215135.	PR	20-OCT-2000;	2000US-0241787.
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PR	11-JUL-2000;	2000US-0217487.	PR	20-OCT-2000;	2000US-0241826.
PR	11-JUL-2000;	2000US-0217496.	PR	01-NOV-2000;	2000US-0244617.
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PR	22-AUG-2000;	2000US-0226681.	PR	17-NOV-2000;	2000US-0249207.
PR	22-AUG-2000;	2000US-0226868.	PR	17-NOV-2000;	2000US-0249208.
PR	22-AUG-2000;	2000US-0227182.	PR	17-NOV-2000;	2000US-0249209.
PR	23-AUG-2000;	2000US-0227009.	PR	17-NOV-2000;	2000US-0249210.
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PR	01-SEP-2000;	2000US-0229287.	PR	17-NOV-2000;	2000US-0249212.
PR	01-SEP-2000;	2000US-0229343.	PR	17-NOV-2000;	2000US-0249213.
PR	01-SEP-2000;	2000US-0229344.	PR	17-NOV-2000;	2000US-0249214.
PR	01-SEP-2000;	2000US-0229345.	PR	17-NOV-2000;	2000US-0249215.
PR	05-SEP-2000;	2000US-0229509.	PR	17-NOV-2000;	2000US-0249216.
PR	05-SEP-2000;	2000US-0229513.	PR	17-NOV-2000;	2000US-0249217.
PR	06-SEP-2000;	2000US-0230437.	PR	17-NOV-2000;	2000US-0249218.
PR	06-SEP-2000;	2000US-0230438.	PR	17-NOV-2000;	2000US-0249244.
PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000;	2000US-0231243.	PR	17-NOV-2000;	2000US-0249264.
PR	08-SEP-2000;	2000US-0231244.	PR	17-NOV-2000;	2000US-0249265.
PR	08-SEP-2000;	2000US-0231413.	PR	17-NOV-2000;	2000US-0249297.
PR	08-SEP-2000;	2000US-0231414.	PR	17-NOV-2000;	2000US-0249299.
PR	08-SEP-2000;	2000US-0232080.	PR	17-NOV-2000;	2000US-0249300.
PR	08-SEP-2000;	2000US-0232081.	PR	01-DEC-2000;	2000US-0250160.
PR	12-SEP-2000;	2000US-0231968.	PR	01-DEC-2000;	2000US-0250391.
PR	14-SEP-2000;	2000US-0232397.	PR	05-DEC-2000;	2000US-0251030.
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PR	14-SEP-2000;	2000US-0232400.	PR	06-DEC-2000;	2000US-0251479.
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PR	14-SEP-2000;	2000US-0233065.	PR	08-DEC-2000;	2000US-0251889.
PR	21-SEP-2000;	2000US-0234223.	PR	08-DEC-2000;	2000US-0251990.
PR	21-SEP-2000;	2000US-0234274.	PR	11-DEC-2000;	2000US-0254097.
PR	25-SEP-2000;	2000US-0234997.	PR	05-JAN-2001;	2001US-0259678.
PR	25-SEP-2000;	2000US-0234998.	XX		
PR	26-SEP-2000;	2000US-0235484.	XX		
PR	27-SEP-2000;	2000US-0235834.	XX		
PR	27-SEP-2000;	2000US-0235836.	XX		
PR	29-SEP-2000;	2000US-0236327.	XX		
PR	29-SEP-2000;	2000US-0236367.	XX		
PR	29-SEP-2000;	2000US-0236368.	XX		
			PA	(HUMA-)	HUMAN GENOME SCI INC.
			XX		
			XX		
			PI	Rosen CA,	Barash SC,
			XX		Ruben SM;
			XX		
			DR	WPI;	2001-488783/53.
			DR	P-PSDB;	AAU16173.



XX New nucleic acid molecules encoding 461 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives -

XX PS Claim 1: SEQ ID No 339; 980pp: English.

XX The invention relates to isolated nucleic acid molecules and their  
CC encoded secreted proteins. The nucleic acids and proteins are used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
CC are also used in diagnosing a pathological condition or susceptibility  
CC to a pathological condition. Antibodies to the proteins can also  
CC be used in alleviating symptoms associated with the disorders and in  
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
CC include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischaemia, angioneurosis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection, and many other  
CC disorders listed in the specification. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence encodes a novel secreted protein of the invention.

Alignment Scores:  
Pred. No.: 1-26e-136 Length: 608  
Score: 150.00 Matches: 150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 14.65% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAS26160 (1-608)

QY 499 ValGluAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeu 518  
DB 88 GTGAAGCCACCCAGGCGTGTATGAAGCACCCTCGACAGCTGTATCAACACGGCTGCCTT 147  
QY 519 LeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLys 538  
DB 148 CTCGGACTTTCATCGCCAAAGAGCGCTCTCTGGAGACAGGAATCTTTGCCAAAGTGTGAAA 207  
QY 539 AsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGly 558  
DB 208 AACACCACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGC 267  
QY 559 IleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhe 578  
DB 268 ATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTC 327  
QY 579 PheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhe 598  
DB 328 TTTCAAGGTAAAGCTTATATATCACTCAGGAAACATCCCGATTACTTATTGACTTC 387  
QY 599 PheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGly 618  
DB 388 TTTGAACATTGCCCAATTGTGAAGTGTCTGGACTTCATTAACTGGACTTTTATGGG 447  
QY 619 GlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGlu 638  
DB 448 GGAGCTATGGCTTCATGGGAAAGGCTGCAGAGACACAGGCGGAATCCACATGGAAGAG 507  
QY 639 AlaProGluThrTyrIleProSerArgAla 648  
DB 508 GCCCCAGAAACCTACATTCCAGCAGGGCT 537

RESULT 14

AAS26575  
ID AAS26575 standard; cDNA; 522 BP.  
XX AC  
XX AAS26575;  
XX AC  
XX 07-NOV-2001 (first entry)  
DE Human cDNA encoding a novel secreted protein, Seq ID 754.  
XX  
XX Human; immunosuppressive; antiarthritic; ss; antirheumatic;  
KW cytostatic; cardiac; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulnery; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX  
OS Homo sapiens.  
XX  
XX WO20015322-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01341.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
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PR 14-AUG-2000; 2000US-0224518.  
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PR 22-AUG-2000; 2000US-0226681.  
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PR 23-AUG-2000; 2000US-0227182.  
PR 30-AUG-2000; 2000US-0227009.  
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PR 20-OCT-2000; 2000US-0241785.  
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PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
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PR 08-NOV-2000; 2000US-0246478.  
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PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
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PR 17-NOV-2000; 2000US-0249207.  
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PR 17-NOV-2000; 2000US-0249209.  
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PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.

PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
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PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
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PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI; 2001-488783/53.  
XX P-PSDB; AAU16588.  
XX  
PT New nucleic acid molecules encoding 461 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
XX used as food additives or preservatives -  
XX  
PS Claim 1; SEQ ID No 754; 980pp; English.  
XX  
CC The invention relates to isolated nucleic acid molecules and their  
CC encoded secreted proteins. The nucleic acids and proteins are used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
CC are also used in diagnosing a pathological condition or susceptibility  
CC to a pathological condition. Antibodies to the proteins can also  
CC be used in alleviating symptoms associated with the disorders and in  
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
CC include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection, and many other  
CC disorders listed in the specification. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence encodes a novel secreted protein of the invention.

Alignment Scores:  
Pred. No.: 6.26e-85 Length: 522  
Score: 97.00 Matches: 97  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.47% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAS26575 (1-522)

Qy 80 LeuPheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 99  
Db 3 CTTATTCAGGACTTGAATGACAAAGCTTTTCATCAGACATCAGAGAGACTTGGAC 62  
Qy 100 AspLeuAlaGlnAspLeuLysAspLeuTyHisThrProSerPheLeuAsnPhetyrPro 119

Db 63 GATTGGCTCAGGATTTAAAGACTGTACCATACCCCATCTTTCTGAACCTTTATCCC 122  
Qy 120 LeuGlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeu 139  
Db 123 CTGTGTGAAGATATGACATATTTTAACTTGAAAGACCTTCACAGAACCTGTCTG 182  
Qy 140 TrpArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGln 159  
Db 183 TGGAGGAAGGACCAACCATCATCCGCGCTGGAGCAGCTGACCTGAATGGCTCTCGCAG 242  
Qy 160 AlaLeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSer 176  
Db 243 GCTCTTCAGAGCCCTGCATCATTTGAAGGGAATCTGCGAAAGCAAGTCC 293  
RESULT 15  
ABK22733  
ID ABK22733 standard; cDNA; 578 BP.  
AC ABK22733;  
XX  
XX  
XX 26-MAR-2002 (first entry)  
XX Human cDNA encoding CLAN C.  
XX  
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrodgen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
OS Homo sapiens.  
XX  
XX PN WO200190156-A2.  
XX  
XX PD 29-NOV-2001.  
XX  
XX PF 24-MAY-2001; 2001WO-US17158.  
XX  
XX PR 24-MAY-2000; 2000US-0579240.  
XX PR 10-OCT-2000; 2000US-0686347.  
XX PR 14-MAR-2001; 2001US-275980P.  
XX PR 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURNHAM INST.  
XX  
XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
XX PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX DR WPI; 2002-083086/11.  
XX DR P-PSDB; AAU80863.  
XX  
XX PT New caspase recruitment domain (CARD)-containing polypeptides and  
XX PT encoding nucleic acids, useful for treating abnormal cell proliferation  
XX PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX PT arthritis or stroke  
XX  
XX PS Claim 1; Page 177; 216pp; English.  
XX  
XX CC The invention relates to an isolated caspase recruitment domain (CARD)  
XX CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
XX CC from it, and the polynucleotides encoding them. Also included are a  
XX CC recombinant vector comprising the polynucleotide, recombinant cells  
XX CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
XX CC and insect cells) and an anti-CARD antibody. The CARD-containing  
XX CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
XX CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
XX CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In

CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrodgen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX  
SQ Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;

#### Alignment Scores:

Pred. No.:	4.48e-77	Length:	578
Score:	89.00	Matches:	89
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	8.69%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABK22733 (1-578)

Qy	1	MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle	20
Db	277	ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGAATGACTGTATA	336
Qy	21	LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle	40
Db	337	AAGCAAAATCACAGATGACCTATTTGTATGGAATGTCGAATCGCGAAGAAGTAAACATC	396
Qy	41	IleCysCysGluLysValGluGlnAspAlaLaArgGlyIleIleHisMetIleLeuLys	60
Db	397	ATTTGCTCGAGAAGGTGGACGAGATGCTGCTAGAGGATCATTCACATGATTTTGAA	456
Qy	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu	80
Db	457	AAGGTTTCAGAGTCTCTTAAGCTCTTTCTTAAATCCCTTAAGGAGTGAAGTATCTCTCTA	516
Qy	81	PheGlnAspLeuAsnGlyGlnSerLeu	89
Db	517	TTTCAGGACTTGAATGGACAAGTCTT	543

Search completed: January 31, 2003, 04:26:58

Job time : 528 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 04:09:41 ; Search time 3285 Seconds  
(without alignments)  
5048.456 Million cell updates/sec

Title: US-09-697-089-2  
Perfect score: 1024  
Sequence: 1 MNFIKNSRALIQRMGTVI.....WQFDDDDLSVITGAFKLWTA 1024

Scoring table:

OLIGO	
Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 16154066 seqs, 8097743376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-Q/cgn2\_l1/USPto\_spool/US09697089/runat\_29012003\_091154\_13480/app\_query.fasta\_1.1223  
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HEAPSIZE=500 -MINLEN=2000000000  
-USER=US09697089 -CGEN\_1\_1\_2475 -runat\_29012003\_091154\_13480 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIME=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	183	17.9	552	17	AQ309404	AQ309404 CITBI-E1-
C 2	156	15.2	480	10	AV719179	AV719179 AV719179
C 3	121	11.8	741	13	BI824482	BI824482 603038854
C 4	116	11.3	748	13	BI908869	BI908869 603066455
C 5	114	11.1	364	9	AI263294	AI263294 qx57b01.x
C 6	74	7.2	261	10	AW337918	AW337918 he12h11.x
C 7	60	5.9	371	10	AV656315	AV656315 AV656315
C 8	56	5.5	553	17	AQ320928	AQ320928 RPI111-93
C 9	55	5.4	476	12	BG210375	BG210375 RST29913
C 10	48	4.7	630	17	AQ112439	AQ112439 CIT-HSP-2
C 11	45	4.4	509	10	AW418826	AW418826 ha21e11.x
C 12	35	3.4	470	17	AQ624020	AQ624020 HS-5378.B
C 13	34	3.3	650	10	BB627584	BB627584 BB627584
C 14	33	3.2	219	17	AQ283886	AQ283886 RPI111-78
C 15	32	3.1	412	14	H25984	H25984 YL56907.r1
C 16	30	2.9	499	9	AI023795	AI023795 ox08d03.x
C 17	23	2.2	518	17	BH348412	BH348412 CH230-42F
C 18	23	2.2	602	17	AZ360053	AZ360053 LM0103H11
C 19	21	2.1	697	17	BH293386	BH293386 CH230-44G
C 20	18	1.8	635	17	B58691	B58691 CIT-HSP-201
C 21	18	1.8	840	12	BF207840	BF207840 601862546
C 22	15	1.5	775	13	BI854236	BI854236 603381263
C 23	14	1.4	619	17	BH267158	BH267158 CH230-19B
C 24	14	1.4	675	10	BB108531	BB108531 BB108531
C 25	14	1.4	817	17	BH358172	BH358172 CH230-18E
C 26	13	1.3	719	14	BQ204082	BQ204082 UI-R-DNI-
C 27	11	1.1	251	12	BF903662	BF903662 IL2-MT018
C 28	10	1.0	221	10	BB593094	BB593094 BB593094
C 29	10	1.0	375	10	BB575989	BB575989 BB575989
C 30	10	1.0	389	10	AW401018	AW401018 Landigest
C 31	10	1.0	446	9	AI222422	AI222422 qh04f06.x
C 32	10	1.0	826	12	BF185320	BF185320 601844132
C 33	10	1.0	1765	17	AG068034	AG068034 Pan trogl
C 34	9	0.9	54	10	AW307272	AW307272 sf54hd07.y
C 35	9	0.9	187	9	AU166132	AU166132 AU166132
C 36	9	0.9	217	10	AW326139	AW326139 18288.MAR
C 37	9	0.9	237	14	BQ458950	BQ458950 HA02M04r
C 38	9	0.9	237	14	BQ656632	BQ656632 HA02M04u
C 39	9	0.9	240	9	AJ460952	AJ460952 AJ460952
C 40	9	0.9	240	9	AJ461386	AJ461386 AJ461386
C 41	9	0.9	245	10	AW458474	AW458474 sh09f07.y
C 42	9	0.9	248	13	BM101090	BM101090 EBP101.SQ
C 43	9	0.9	251	13	BM374011	BM374011 ERna03.SQ
C 44	9	0.9	285	14	BQ761907	BQ761907 EBP101.SQ
C 45	9	0.9	294	10	BB330264	BB330264 BB330264

ALIGNMENTS

RESULT 1  
AQ309404/c  
LOCUS  
DEFINITION AQ309404 CITBI-E1-2528J13.TF CITBI-E1 Homo sapiens genomic clone 2528J13,  
DNA sequence.  
ACCESSION AQ309404  
VERSION AQ309404.1 GI:4041438  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 552)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and

Venter, J.C.  
Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
Unpublished (1998)  
Other GSSs: CITBI-E1-2528J13.TR  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html).  
Seq primer: M13-21  
Class: BAC ends.

FEATURES  
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Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="2528J13"  
/clone\_lib="CITBI-E1"  
/sex="male"  
/cell\_type="sperm"  
/notes="Vector: pBelOBAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
Caltech Human BAC Library D"

BASE COUNT 144 a 121 c 130 g 157 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 7,61e-178 Length: 552  
Score: 183.00 Matches: 183  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 17.87% Indels: 0  
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x AQ309404 (1-552)

Qy 477 MetValSerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly 496  
|||||  
Db 550 ATGGTTTCCATTTCGGACATTACATCCATTATAGCAGCTGCTCCCGGTACACCTGTGGG 491  
Qy 497 SerSerValGluAlaThrArgAlaValMetIleHisLeuAlaValTyrGlnHisGly 516  
|||||  
Db 490 TCATCTGTGGAAGCCACAGCGCTGTTATGAAGCACCTCGCAGCAGTGATCAACACGCG 431  
Qy 517 CysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSer 536  
|||||  
Db 430 TGCCTTCTCGGACTTTCATCGCCAAAGGCTCTCTGGAGACAGGAATCTTTGCAAGT 371  
Qy 537 ValLysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlu 556  
|||||  
Db 370 GTGAARAACACCACTGAGCAGAAGTAATCTGAAGCCATAACATCAATCTTTGTAGAG 311  
Qy 557 CysGlyIleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlu 576  
|||||  
Db 310 TGTGGCATCCATTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAA 251  
Qy 577 AlaPheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPhe 596  
|||||  
Db 250 GCTTTCTTCAAGGTAAAGCTTATATCAACTCAGGAACATCCCGGATTACTTATT 191  
Qy 597 AspPheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPhe 616  
|||||  
Db 190 GACTTCITTTGAACATTTGCCCAATGTGCAAGTGCTCTGGACTTCATTAACATGGACTTT 131  
Qy 617 TyrGlyGlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMet 636  
|||||  
Db 130 TATGGGGAGCTATGGCTTCATGGAAAGGCTCAGACAGACAGGTGGATCCACATG 71  
Qy 637 GluGluAlaProGluThrThrIleProSerArgAlaValSerLeuPhePheAsnTrpLys 656  
|||||

Db 70 GAAGAGCCCCAGAAACCTACATTCCAGGAGGCTGATCTTTGTTCTTCACTGAAG 11  
Qy 657 GlnGluPhe 659  
|||||  
Db 10 CAGGAATTC 2  
RESULT 2  
LOCUS AV719179/c 480 bp mRNA linear EST 16-OCT-2000  
DEFINITION AV719179 GLC Homo sapiens cDNA clone GLCEQA10 5', mRNA sequence.  
ACCESSION AV719179  
VERSION AV719179.1 GI:10816331  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 480)  
AUTHORS Qian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,  
Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,  
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang  
Y., Gu,Y., Chen,Z. and Han,Z.  
Homo sapiens cDNA GLC clones  
Unpublished (2000)  
CONTACT: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.  
FEATURES  
source  
1..480  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GLCEQA10"  
/clone\_lib="GLC"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 138 a 120 c 85 g 137 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 4,66e-150 Length: 480  
Score: 156.00 Matches: 156  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 15.23% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x AV719179 (1-480)

Qy 869 HisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrp 888  
|||||  
Db 480 CATGAACGTATGACAGAGTGACGTGTAGAACAGCTCACCGCCTGATGCTCCCTGG 421  
Qy 889 GlyCysAspValGlnGlnGlySerLeuSerSerLeuLeuLysHisLeuGluValProGln 908  
|||||  
Db 420 GGCTGTGACGTGCAAGCAGCGCTGAGCAGCCTGTTGAACATTTGGAGGAGGTCCCAAA 361  
Qy 909 LeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGly 928  
|||||  
Db 360 CTCGTCGAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGATTTTAGT 301  
Qy 929 AlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArg 948  
|||||  
Db 300 GCATTTTTTGAAGAAGAACCCCTCTGAAAAAACTTCAGCAGTTGAATTTGGCGGGAATCGT 241  
|||||



cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."

BASE COUNT 236 a 148 c 166 g 198 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1.41e-108 Length: 748  
Score: 116.00 Matches: 136  
Percent Similarity: 98.55% Conservative: 0  
Best Local Similarity: 98.55% Mismatches: 0  
Query Match: 11.33% Indels: 2  
DB: 13 Gaps: 0

US-09-697-089-2 (1-1024) x BI08869 (1-748)

Qy 1 MetAsnPhelLeuLysAspAsnSerArgAlaLeuLeuGlnArgMetGlyMetThrValille 20  
Db 252 ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 311  
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40  
Db 312 AAGCAATTCACAGATGACCTATTGTATGGAATGTTCTGAATCGGAAGAAAGTAACATC 371  
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
Db 372 ATTTGCTCGAGAGAGGTGGACGAGATGCTGTAGAGGGATCATTCACATGATTTTGA 431  
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80  
Db 432 AAGGTTTCAGAGTCTGTAACTCTTCTTAATCCCTTAAAGGAGTGAACATATCTCTTA 491  
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 100  
Db 492 TTTGAGGACTTGAATGGACAAGTCTTTTCATCAGACATCAGAAAGGAGACTTGGACGAT 551  
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPhetyrProL 120  
Db 552 TTGCTCAGGATTTACAAAGGACTGTGACCATACCCATCTTTTCTGAACCTTTTATCCCC 611  
Qy 120 euGlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGlu 136  
Db 612 TTGGTGAAGATATGACATTATTTTAACTTGAAGACACCTTCACAGAA 661

## RESULT 5

AI263294/c 364 bp mRNA linear EST 03-FEB-1999  
LOCUS qx57b01.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',  
DEFINITION mRNA sequence.

ACCESSION AI263294

VERSION AI263294.1 GI:3871497

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 364)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 2146 Std Error: 0.00

Seq primer: -400P from Gbco

High quality sequence stop: 364.

FEATURES  
source

Location/Qualifiers

1..364  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2005417"  
/clone\_lib="NCI\_CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 117 a 84 c 55 g 108 t

## ORIGIN

## Alignment Scores:

Pred. No.: 7.32e-107 Length: 364  
Score: 114.00 Matches: 114  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 11.13% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AI263294 (1-364)

Qy 911 LysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhe 930  
Db 364 AAGCTTGGTGTGAAAACTGGAGACTCAGATACAGATAGATTAGTGCATTT 305  
Qy 931 PheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 950  
Db 304 TTTGGAAGAAGCCCTCTGAAAACTTCAGCAGTGAATTTGGCGGAAATCGTGTGAGC 245  
Qy 951 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePhe 970  
Db 244 AGTATGATGGTGTGCTTCATGGGTGATTTGAGAACTTAAAGCAATAGTGTCTTTT 185  
Qy 971 AspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnVal 990  
Db 184 GACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATAGTCAGAAAACTTAGCCAAGTG 125  
Qy 991 LeuSerLysLeuThrPheLeuGlnGlnAlaArgLeuValGlyTrpGlnPheAspAsp 1010  
Db 124 TTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGAT 65  
Qy 1011 AspLeuSerValIleThrGlyAlaPheLysLeuValThrAla 1024  
Db 64 GATCTCAGTGTATTACAGGTGCTTTTAAACTAGTAACCTGCT 23

## RESULT 6

AW337918/c

LOCUS AW337918

DEFINITION AW337918

VERSION AW337918.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 261)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

AW337918 261 bp mRNA linear EST 31-JAN-2000  
LOCUS AW337918

DEFINITION AW337918

VERSION AW337918.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 261)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center



Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 201.

## FEATURES

source

Location/Qualifiers  
1. .261  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2918853"  
/clone\_lib="NCI\_CGAP\_CML1"  
/tissue\_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"  
/lab\_host="DH10B"  
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."  
BASE COUNT 86 a 54 c 38 g 83 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9,33e-66 Length: 261  
Score: 74.00 Matches: 74  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.23% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x AW337918 (1-261)

QY 951 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePhe 970  
|||||  
Db 260 AGTGATGATGCTTGCCTTCATCGGTGTATTTGAGAACTTAAGCAATTAGCTTTT 201  
QY 971 AspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnVal 990  
|||||  
Db 200 GACTTTAGTACTAAAGAAATTTACTCTGATCAGCAATTAAGCAAACTTAGCCAAAGTG 141  
QY 991 LeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAsp 1010  
|||||  
Db 140 TTATCAAGTTAACTTTCTGCAAGAGCTAGCTGTGTGGTGGCAATTTGATGATGAT 81  
QY 1011 AspLeuSerValIleThrGlyAlaPheLysLeuValThraLa 1024  
|||||  
Db 80 GATCTCAGTGTATTACAGGTGCTTTAAACTAGTAACCTGCT 39

## RESULT 7

AV656315  
LOCUS AV656315 371 bp mRNA linear EST 16-JAN-2002  
DEFINITION AV656315 GLC Homo sapiens cDNA clone GLCEQA10 3', mRNA sequence.  
ACCESSION AV656315  
VERSION AV656315.1 GI:9877329  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 371)

Xu.X., Huang.J., Xu.Z., Qian.B., Zhu.Z., Yan.Q., Cai.T., Zhang.X., Xiao.H., Qu.J., Liu.F., Huang.Q., Cheng.Z., Li.N., Du.J., Hu.W., Shen.K., Lu.G., Fu.G., Zhong.M., Xu.S., Gu.W., Huang.W., Zhao.X., Hu.G., Gu.J., Chen.Z. and Han.Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver  
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
21625106

## JOURNAL

## MEDLINE

COMMENT

Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)

## FEATURES

source

Location/Qualifiers  
1. .371  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GLCEQA10"  
/clone\_lib="GLC"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT 112 a 85 c 91 g 82 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 3,83e-51 Length: 371  
Score: 60.00 Matches: 113  
Percent Similarity: 98.26% Conservative: 0  
Best Local Similarity: 98.26% Mismatches: 1  
Query Match: 5.86% Indels: 2  
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x AV656315 (1-371)

QY 625 GluLysAlaAlaGluAspThrGlyIleHisMetGluGluAlaProGluThrTyrIle 644  
|||||  
Db 1 GAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAGAGGCCCAACCTACATT 60  
QY 645 ProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArgThrLeuGluVal 664  
|||||  
Db 61 CCCAGCAGGCTGTATCTTTGTTCTCACTGGAAGCAGCAATTGAGGACTCTGGAGGTC 120  
QY 665 ThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePh 684  
|||||  
Db 121 ACACCTCCGGGATTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGAAATATT 179  
QY 684 eSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLe 704  
|||||  
Db 180 CAGCTCTGCCAAGCCTCAGGCTGCAATAAAGAGATGCTGTGGTGGGAGGACCT 239  
QY 704 uSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLe 724  
|||||  
Db 240 CAGTTTGGTCTCCAGCACCTGTGAAGACATTTATCTCTCATGTGGGAGGCCAGTCCCT 299  
QY 724 uThrIleGluAspGluArgHisIleThrSerValThrAsnLeu 738  
|||||  
Db 300 CACCATAAGATGAGAGGCACATCACATCTGTGAACAAACCTG 342

## RESULT 8

AQ320928/c  
LOCUS AQ320928 553 bp DNA linear GSS 06-MAY-1999  
DEFINITION RPC111-93C9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-93C9, DNA sequence.

ACCESSION AQ320928

VERSION AQ320928.1 GI:4053662

KEYWORDS GSS.

SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 553)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

Other GSSs: RPC111-93C9.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850



```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2372c1"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT      188 a  126 c  124 g  192 t
ORIGIN

Alignment Scores:
Pred. No.:      1.66e-38      Length:      630
Score:          48.00      Matches:      48
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      4.69%      Indels:      0
DB:              17      Gaps:      0

US-09-697-089-2 (1-1024) x A0112439 (1-630)
QY 784 AlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeuSerAsp 803
|||||
Db 486 GCTGAAGGCTGAAACCTGAGAGAGATGTTTATTTCATTGACCACCTGTCTGAC 545
|||||
QY 804 IleGlyGluGlyMetAspTyrIleValLysSerLeuSerGluProCysAspLeuGlu 823
|||||
Db 546 ATTGGAGAGGATGATACATAGTCAAGTCTCTGTCAGTGAAACCTGTGACCTTGAA 605
|||||
QY 824 GluIleGlnLeuValSerCysCys 831
|||||
Db 606 GAAATTCAAATTAGTCTCCTGCTGC 629
|||||

RESULT 11
AW418826/c      509 bp      mRNA      linear      EST 09-FEB-2000
LOCUS      ha21e11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874380 3',
DEFINITION      mRNA sequence.
ACCESSION      AW418826
VERSION      AW418826.1 GI:6946758
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 461.
Location/Qualifiers
1..509
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2874380"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
```

```
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Patima Bonaldo. "

BASE COUNT      161 a  99 c  80 g  169 t
ORIGIN

Alignment Scores:
Pred. No.:      1.63e-35      Length:      509
Score:          45.00      Matches:      45
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      4.39%      Indels:      0
DB:              10      Gaps:      0

US-09-697-089-2 (1-1024) x AW418826 (1-509)
QY 980 AspProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlu 999
|||||
Db 508 GATCCAGCATAGTACAGAAACTTACCCAGTGTATCCAGTTAACTTTCTGCAAGAA 449
|||||
QY 1000 AlaArgLeuValcIyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPhe 1019
|||||
Db 448 GCTAGGCTTGTGGTGCAATTGTATGATGATGATGATCTCAGTGTATTACAGGTGCTTTT 389
|||||
QY 1020 LysLeuValThrAla 1024
|||||
Db 388 AACTAGTAACCTGCT 374
|||||

RESULT 12
AQ624020      470 bp      DNA      linear      GSS 16-JUN-1999
LOCUS      HS_5378_B2_C12_SP6E RPCI-11 Human Male BAC library Homo sapiens
DEFINITION      genomic clone Plate=954 Col=24 Row=F, DNA sequence.
ACCESSION      AQ624020
VERSION      AQ624020.1 GI:5086412
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 954 row: F column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 470.
Location/Qualifiers
1..470
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
source
```

/clone="Plate=954 Col=24 Row=F"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/sex="male"

/note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRII. Size selected DNA was cloned into the  
pBACE3.6 vector at EcoRI sites"

BASE COUNT 142 a 101 c 107 g 117 t 3 others

ORIGIN

#### Alignment Scores:

Pred. No.: 3.09e-25 Length: 470  
Score: 35.00 Matches: 35  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.42% Indels: 0  
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x AQ624020 (1-470)

QY 679 TyrLeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAla 698

Db 65 TATCTGGGAATATTCAGCTCTGCCAAGCCTCAGGCTGCAATTAAGAGATGTGCT 124

QY 699 GlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsn 713

Db 125 GGTGTGGCTGGAAGCCTCAGTTTGGTCTCTCAGCAGCTGTAGAAC 169

#### RESULT 13

BB627584

LOCUS

DEFINITION BB627584 RIKEN full-length enriched, adult male urinary bladder Mus

musculus cDNA clone 9530011P19 5', mRNA sequence.

ACCESSION BB627584

VERSION BB627584.1 GI:16465218

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### AUTHORS

1 (bases 1 to 650);  
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,  
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,  
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,  
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,  
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,  
Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
Unpublished (2001)

#### TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura  
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara

,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa  
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and  
Hayashizaki,Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.

#### e mouse tissues.

FEATURES  
source

Location/Qualifiers  
1. .650  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="9530011P19"  
/clone\_lib="RIKEN full-length enriched, adult male urinary  
bladder"  
/sex="male"  
/tissue\_type="urinary bladder"  
/dev\_stage="adult"  
/lab\_host="Dh10B"  
/note="Site\_1: SalI; Site\_2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN, Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Not - 20.0 and subtraction to Not - 370.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCGCCCCCCCCCC  
3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
modified pBluescript KS(+) after bulk excision from  
Lambda FLC I."

BASE COUNT 164 a 174 c 173 g 139 t  
ORIGIN

#### Alignment Scores:

Pred. No.: 4.77e-24 Length: 650  
Score: 34.00 Matches: 34  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.32% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x BB627584 (1-650)

QY 255 ProGlnAsnCysProGluIleGluAlaLeuLysGluAsnHisArgPheLysAsnMet 274

Db 380 CCCCAGAACTCCAGAAATTAAGAGGAAACCATCGCTTCAAGAACATG 439

QY 275 ValIleValThrThrThrGluCysLeuArgHisIleArg 288

Db 440 GTCATTGTCCACCACCACCGAGTGCTGAGGCATATCAGA 481

#### RESULT 14

AQ283886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AQ283886 219 bp DNA linear GSS 27-APR-1999  
RPC11-78E13.TV RPCI-11 Homo sapiens genomic clone RPCI-11-78E13,  
DNA sequence.

AQ283886

AQ283886.1 GI:3910204

GSS.

Human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 219)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
Research Genetics (info@resgen.com). BAC end search page:  
http://www.tigr.org/tldb/hungen/bac\_end\_search/bac\_end\_search.html  
Seq primer: T7  
Class: BAC ends.

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 942  
High quality sequence stops: 347  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 942 Std Error: 0.00  
Seq primer: M13Rp1  
High quality sequence stop: 347.

FEATURES  
source  
1..219  
/organism="Homo sapiens"  
/db\_xref="GDB:7529676"  
/db\_xref="taxon:9606"  
/clone="RPCI-11-78E13"  
/clone\_lib="RPCI-11"  
/sex="Male"  
/cell\_type="lymphocytes"  
/note="vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
RPC111 Human Male BAC Library"  
69 a 45 c 46 g 59 t

FEATURES  
source  
1..412  
/organism="Homo sapiens"  
/db\_xref="GDB:576544"  
/db\_xref="taxon:9606"  
/clone="IMAGE:162300"  
/clone\_lib="Soares breast 3NbHBst"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: breast; Vector: p7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of a modified p7T3 vector (Pharmacia).  
Library went through one round of normalization to a Cot =  
20. Library constructed by Bento Soares and M.Fatima  
Bonaldo."

BASE COUNT 69 a 45 c 46 g 59 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.53e-23 Length: 219  
Score: 33.00 Matches: 33  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.22% Indels: 0  
DB: 17 Gaps: 0

BASE COUNT 129 a 84 c 73 g 124 t 2 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.32e-22 Length: 412  
Score: 32.00 Matches: 32  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.12% Indels: 0  
DB: 14 Gaps: 0

US-09-697-089-2 (1-1024) x AQ283886 (1-219)  
Qy 701 AlaGlySerLeuSerLeuValIleuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 3 GCTGGAAGCCTTAGTGTGCTCCTCAGCACCTGTGAAGACATTTATCTCATGTGGAA 62  
Qy 721 AlaSerProLeuThrIleGluAaspGluArgHisIleThr 733  
Db 63 GCCAGTCCCTGACCATAGAGATGAGAGGCACATCACA 101

US-09-697-089-2 (1-1024) x H25984 (1-412)  
Qy 993 LysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrGlnPheAspAspAspLeu 1012  
Db 338 AAGTTAACTTTTCTGCAAGAAGCTAGGCTGTGGGTGGCAATTTGATGATGATCTC 279  
Qy 1013 SerValIleThrGlyAlaPheLysLeuValThrAla 1024  
Db 278 AGTGTTATTACAGGCGCTTTTAAACTAGTAACTGCT 243

RESULT 15  
H25984/c  
LOCUS H25984 412 bp mRNA linear EST 10-JUL-1995  
DEFINITION y156g07.r1 Soares breast 3NbHBst Homo sapiens cDNA clone  
IMAGE:162300 5', mRNA sequence.  
ACCESSION H25984  
VERSION H25984.1 GI:895107  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Search completed: January 31, 2003, 07:10:58  
Job time : 3294 secs

REFERENCE 1 (bases 1 to 412)  
AUTHORS Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
M., Hultman,M., Kucaba,T., Ie,M., Lennon,G., Marra,M., Parsons,J.,  
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston  
R., Williamson,A., Wohlmann,P. and Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 942  
High quality sequence stops: 347  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 942 Std Error: 0.00  
Seq primer: M13Rp1  
High quality sequence stop: 347.



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: January 31, 2003, 04:22:17 ; Search time 85 Seconds  
(without alignments)  
3694.553 Million cell updates/sec

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Perfect score: 1024  
Sequence: 1 MNFIKNSRALIQRMGTVI.....WQFDDDDLSVITGAFKLWTA 1024

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Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 878600

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlh  
-MODE=frame+p2n.model  
-Q=/cgn2\_1/USPTO.spool/US09697089/runat\_29012003\_091154\_13493/app\_query.fasta.1.1223  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09697089 -CGN\_1\_1\_46\_@runat\_29012003\_091154\_13493 -NCPU=6 -ICPU=3  
-NO\_XLIFY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	8	0.8	591	4	US-09-144-367-4
2	8	0.8	1220	4	US-09-227-357-54
3	8	0.8	1225	1	US-08-286-020-1
4	8	0.8	1225	1	US-08-603-919-1
5	8	0.8	1839	1	US-08-272-875-1
6	8	0.8	1839	1	US-08-272-875-2
C 7	8	0.8	1980	1	US-08-350-741-1
C 8	8	0.8	1980	2	US-08-463-875A-1
C 9	8	0.8	2759	4	US-09-144-367-1
C 10	8	0.8	3236	4	US-08-961-527-222
11	8	0.8	3573	4	US-09-353-585-4
C 12	8	0.8	5275	1	US-08-485-588-1

C 13	8	0.8	5275	1	US-08-484-565-1
C 14	8	0.8	5275	2	US-08-480-751-1
C 15	8	0.8	5275	2	US-08-943-986-1
C 16	8	0.8	5275	3	US-08-353-784-1
C 17	8	0.8	5275	3	US-08-484-119B-1
C 18	8	0.8	5275	4	US-08-484-159-1
19	8	0.8	6471	4	US-09-353-585-1
20	8	0.8	11907	4	US-08-061-376-4
21	8	0.8	12752	2	US-08-459-146-1
22	8	0.8	12752	2	US-08-459-065-1
23	8	0.8	14255	1	US-08-320-559-1
24	8	0.8	14255	1	US-08-327-392-1
25	8	0.8	14255	1	US-08-306-691B-55
26	8	0.8	14255	3	US-08-545-860D-1
27	8	0.8	14255	5	PCT-US94-04496-1
28	8	0.8	87350	3	US-08-781-891-79
29	8	0.8	87543	4	US-09-791-211-3
C 30	7	0.7	34	4	US-08-840-767-29
C 31	7	0.7	110	1	US-08-356-790-2
C 32	7	0.7	219	3	US-07-791-931-2
C 33	7	0.7	246	1	US-08-053-131-154
C 34	7	0.7	246	1	US-08-096-762-154
C 35	7	0.7	246	4	US-09-042-353-69
C 36	7	0.7	246	4	US-08-758-417A-333
C 37	7	0.7	282	4	US-09-042-353-94
C 38	7	0.7	282	4	US-09-042-353-111
C 39	7	0.7	282	4	US-09-042-353-113
C 40	7	0.7	282	4	US-08-758-417A-358
C 41	7	0.7	282	4	US-08-758-417A-375
C 42	7	0.7	282	4	US-08-758-417A-377
C 43	7	0.7	284	4	US-09-042-353-78
C 44	7	0.7	284	4	US-08-758-417A-342
C 45	7	0.7	285	4	US-09-042-353-110

ALIGNMENTS

RESULT 1

US-09-144-367-4/c  
; Sequence 4, Application US/09144367  
; Patent No. 6432639  
; GENERAL INFORMATION:  
; APPLICANT: Lichter, Jay  
; APPLICANT: Guido, Marco  
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4  
; FILE REFERENCE: SEQ 12P  
; CURRENT APPLICATION NUMBER: US/09/144,367  
; CURRENT FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 60/058,612  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 591  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: (0)...(0)  
US-09-144-367-4

Alignment Scores:  
Pred. No.: 76.9 Length: 591  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-144-367-4 (1-591)

QY 361 ThrLeuPheHisThrPheTyrAsp 368  
|||||



Db 49 ACACTTTCCATACTTTTATGAC 26

RESULT 2

US-09-227-357-54

; Sequence 54, Application US/09227357

; Patent No. 6342581

; GENERAL INFORMATION:

; APPLICANT: Fischer et al.

; TITLE OF INVENTION: 123 Human Secreted Proteins

; FILE REFERENCE: P2010P1

; CURRENT APPLICATION NUMBER: US/09/227,357

; CURRENT FILING DATE: 1998-01-08

; EARLIER APPLICATION NUMBER: PC7/US98/13684

; EARLIER FILING DATE: 1998-07-07

; EARLIER APPLICATION NUMBER: 60/051,926

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,793

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,925

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,929

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,803

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,732

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,931

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,932

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,916

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,930

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,918

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,920

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,733

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,795

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,919

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,928

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/055,722

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,723

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,948

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,949

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,953

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,950

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,947

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,964

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/056,360

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,684

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,984

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,954

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/058,785

; EARLIER FILING DATE: 1997-09-12

; EARLIER APPLICATION NUMBER: 60/058,664

; EARLIER FILING DATE: 1997-09-12

; EARLIER APPLICATION NUMBER: 60/058,660

; EARLIER FILING DATE: 1997-09-12

; EARLIER APPLICATION NUMBER: 60/058,661

; EARLIER FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 672

; SOFTWARE: Patentin ver. 2.0

; SEQ ID NO 54

; TYPE: DNA

; LENGTH: 1220

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1197)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1208)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1209)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-227-357-54

Alignment Scores:

Pred. No.: 156 Length: 1220

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 0.78% Indels: 0

DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-227-357-54 (1-1220)

Qy 199 PheValPhePheLeuArgLeuSer 206

Db 253 TTTGTTTTTTCTTGAGACTGAGT 276

RESULT 3

US-08-286-020-1

; Sequence 1, Application US/08286020

; Patent No. 5539095

; GENERAL INFORMATION:

; APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela

; TITLE OF INVENTION: A Chitinase cDNA Clone From a

; TITLE OF INVENTION: Disease Resistant American

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ian C. McLeod

; STREET: 2190 Commons Parkway

; CITY: Okemos

; STATE: Michigan

; COUNTRY: USA

; ZIP: 48864

COMPUTER READABLE FORM:

OPERATING SYSTEM: MS-DOS 5.00

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,020

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931

REFERENCE/DOCKET NUMBER: MSU 4.1-207

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5539095e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1225

TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:

ORGANISM: Ulmus Americana  
STRAIN: NPS 3-487  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: N/A  
POSITION IN GENOME: N/A  
FEATURE:

NAME/KEY: chitinase encoding DNA

LOCATION:

IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: DNA needed for chitinase

OTHER INFORMATION: in elm.

PUBLICATION INFORMATION:

US-08-286-020-1

Alignment Scores:  
Pred. No.: 156 Length: 1225  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-286-020-1 (1-1225)

Qy 452 GlyArgLeuSerSerLeuLeu 459

Db 1085 GCGCGTCGTTGTCGTCACCTCTT 1108

RESULT 4

US-08-603-919-1

Sequence 1, Application US/08603919

Patent No. 5728382

GENERAL INFORMATION:

APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela

TITLE OF INVENTION: A Chitinase cDNA Clone From a

TITLE OF INVENTION: Disease Resistant American

TITLE OF INVENTION: Elm Tree

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage

COMPUTER: Acer

OPERATING SYSTEM: MS-DOS 5.00

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/603,919

FILING DATE:

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-207  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5728382e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1225

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: Ulmus Americana

STRAIN: NPS 3-487

INDIVIDUAL ISOLATE: N/A

DEVELOPMENTAL STAGE: N/A

HAPLOTYPE: N/A

TISSUE TYPE: N/A

CELL TYPE: N/A

CELL LINE: N/A

ORGANELLE: N/A

IMMEDIATE SOURCE: N/A

POSITION IN GENOME: N/A

FEATURE:

NAME/KEY: chitinase encoding DNA

LOCATION:

IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: DNA needed for chitinase

OTHER INFORMATION: in elm.

PUBLICATION INFORMATION:

US-08-603-919-1

Alignment Scores:

Pred. No.: 156 Length: 1225  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-603-919-1 (1-1225)

Qy 452 GlyArgLeuSerSerLeuLeu 459

Db 1085 GCGCGTCGTTGTCGTCACCTCTT 1108

RESULT 5

US-08-272-875-1

Sequence 1, Application US/08272875

Patent No. 5487996

GENERAL INFORMATION:

APPLICANT: Takeji SHIBATANI

APPLICANT: Saburo KOMATSUBARA

APPLICANT: Kenji OMORI

APPLICANT: Hiroyuki AKATSUKA

TITLE OF INVENTION: GENE CODING FOR ESTERASE AND NOVEL

TITLE OF INVENTION: MICROORGANISM CONTAINING SAID GENE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/272,875  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/980,516A  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA: JP 355440/1991  
FILING DATE: 25-NOV-1991  
APPLICATION NUMBER: JP 137502/1992  
FILING DATE: 13-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3175P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 241 1300  
TELEFAX: 703 241 2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1839 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL:  
ANTI-SENSE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN: Serratia marcescens Sr41  
US-08-272-875-1

Alignment Scores:  
Pred. No.: 232 Length: 1839  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-272-875-1 (1-1839)

QY 450 ThrAlaGlyArgLeuSerSer 457  
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Db 1094 ACAGCGGCGCGAGTTTATCATCG 1117

RESULT 6

US-08-272-875-2  
Sequence 2: Application US/08272875  
Patent No. 5487996  
GENERAL INFORMATION:  
APPLICANT: Takeji SHIBATANI  
APPLICANT: Saburo KOMATSUBARA  
APPLICANT: Kenji OMORI  
APPLICANT: Hiroyuki AKATSUKA  
TITLE OF INVENTION: GENE CODING FOR ESTERASE AND NOVEL  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
STREET: P.O. Box 747  
CITY: Falls Church

STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/272,875  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/980,516A  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA: JP 355440/1991  
FILING DATE: 25-NOV-1991  
APPLICATION NUMBER: JP 137502/1992  
FILING DATE: 13-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3175P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 241 1300  
TELEFAX: 703 241 2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1839 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL:  
ANTI-SENSE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN: Serratia marcescens M-1  
US-08-272-875-2

Alignment Scores:  
Pred. No.: 232 Length: 1839  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-272-875-2 (1-1839)

QY 450 ThrAlaGlyArgLeuSerSer 457  
|||||  
Db 1094 ACAGCGGCGCGAGTTTATCATCG 1117

RESULT 7

US-08-350-741-1/c  
Sequence 1: Application US/08350741  
Patent No. 5804194  
GENERAL INFORMATION:  
APPLICANT: DOUGAN G.,  
APPLICANT: CHARLES I.G.,  
APPLICANT: HORMAECH C.E.,  
APPLICANT: JOHNSON K.S.,  
APPLICANT: CHATFIELD S.N.  
TITLE OF INVENTION: LIVE VACCINES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON and VANDERHVE PC  
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON

```
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,741
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/340,741
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 07/952,737
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: GB 9007194.5
; FILING DATE: 30-MAR-1990
; APPLICATION NUMBER: PCT/GB91/00484
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 395..1822
; US-08-350-741-1

Alignment Scores:
Pred. No.: 249 Length: 1980
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-350-741-1 (1-1980)
QY 451 AlaglyArgLeuSerLeu 458
Db 1331 GCTGGCGTCGACTTTCATCGCTT 1308

RESULT 8
US-08-463-875A-1/c
; Sequence 1, Application US/08463875A
; Patent No. 5980907
; GENERAL INFORMATION:
; APPLICANT: DOUGAN, Gordon
; APPLICANT: CHARLES, Ian G.
; APPLICANT: HORMAECH, Carlos E.
; APPLICANT: JOHNSON, Kevin S.
; APPLICANT: CHATFIELD, Steven N.
; TITLE OF INVENTION: LIVE VACCINES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
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; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,875A
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/340,741
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 07/952,737
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: GB 9007194.5
; FILING DATE: 30-MAR-1990
; APPLICATION NUMBER: PCT/GB91/00484
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 395..1822
; US-08-463-875A-1

Alignment Scores:
Pred. No.: 249 Length: 1980
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 2 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-463-875A-1 (1-1980)
QY 451 AlaglyArgLeuSerLeu 458
Db 1331 GCTGGCGTCGACTTTCATCGCTT 1308

RESULT 9
US-09-144-367-1/c
; Sequence 1, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2759
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (70)...(1581)  
; OTHER INFORMATION: Human CYP3A4 cDNA reference sequence  
US-09-144-367-1

Alignment Scores: 344 Length: 2759  
Pred. No.: 8.00 Matches: 8  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 0.78% Gaps: 0  
DB: 4

US-09-697-089-2 (1-1024) x US-09-144-367-1 (1-2759)

Qy 361 ThrLeuPheHisThrPheTyraSp 368

Db 283 ACACCTTCCATACCTTTTATGAC 260

RESULT 10

US-08-961-527-222/c  
; Sequence 222, Application US/08961527  
; Patent No. 6420135

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 391

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/961,527

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Brookes, A. Anders

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PB340P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 222:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3236 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-961-527-222

Alignment Scores: 402 Length: 3236  
Pred. No.: 8.00 Matches: 8  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 0.78% Gaps: 0  
DB: 4

US-09-697-089-2 (1-1024) x US-08-961-527-222 (1-3236)

Qy 688 ThrSerLeuArgLeuGlnIleLys 695

Db 2083 ACATCTTGAGGTGCAGATAAAA 2060

RESULT 11

US-09-353-585-4

; Sequence 4, Application US/09353585

; Patent No. 6287865

; GENERAL INFORMATION:

; APPLICANT: Dixon, Mark S

; Jones, David A

; Jones, Jonathan DG

; TITLE OF INVENTION: Plant pathogen resistance genes and uses

; thereof

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon & Vanderhye PC

; STREET: 8th Floor, 1100 No. 6287865th Glebe Road

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/353,585

; FILING DATE: 15-Jul-1999

; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q

; 1/68

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/930,277

; FILING DATE: 27-OCT-1997

; APPLICATION NUMBER: PCT/GB96/00785

; FILING DATE: 01-APR-1996

; APPLICATION NUMBER: GB 9506658.5

; FILING DATE: 31-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Ms Mary J Wilson

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 620-69

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3573 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Tomato

; STRAIN: Cf2

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-353-585-4  
Alignment Scores: 443 Length: 3573  
Pred. No.: 8.00 Matches: 8  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 0.78% Gaps: 0  
DB: 4

US-09-697-089-2 (1-1024) x US-09-353-585-4 (1-3573)

Qy 758 SerLeuGlyAsnLeuLysAsnLeu 765

Db 980 TCATTGGGAATCTGAAAACTTG 1003

RESULT 12

US-08-485-588-1/c  
; Sequence 1, Application US/08485588  
; Patent No. 5688938  
; GENERAL INFORMATION:  
; APPLICANT: Edward M. Brown  
; APPLICANT: Steven C. Hebert  
; APPLICANT: Forrest H. Fuller  
; APPLICANT: James E. Garrett, Jr.  
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
; MOLECULES  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: First Interstate World Center  
; STREET: Suite 4700  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FASTSEQ  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,588  
; FILING DATE: 7 June, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below: 9  
; APPLICATION NUMBER: 08/353,784  
; FILING DATE: 9 December, 1994  
; APPLICATION NUMBER: PCT/US/94/12117  
; FILING DATE: 21 October, 1994  
; APPLICATION NUMBER: U.S. 08/292,827  
; FILING DATE: 23 August, 1994  
; APPLICATION NUMBER: U.S. 08/141,248  
; FILING DATE: 22 October, 1993  
; APPLICATION NUMBER: U.S. 08/009,389  
; FILING DATE: 23 February, 1993  
; APPLICATION NUMBER: U.S. 08/017,127  
; FILING DATE: 12 February, 1993  
; APPLICATION NUMBER: U.S. 07/934,161  
; FILING DATE: 21 August, 1992  
; APPLICATION NUMBER: U.S. 07/834,044  
; FILING DATE: 11 February, 1992  
; APPLICATION NUMBER: U.S. 07/749,451  
; FILING DATE: 23 August, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 213/005  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5275 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 515..3769  
; OTHER INFORMATION:  
US-08-485-588-1

Alignment Scores: 646 Length: 5275  
Pred. No.:

Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 1 Gaps: 0  
US-09-697-089-2 (1-1024) x US-08-485-588-1 (1-5275)  
QY 331 LeuAIGAsnLeuMetLysThrPro 338  
|||||  
Db 2433 TTGCGGAACCTTGATGAAGAGCC 2410  
RESULT 13  
US-08-484-565-1/c  
; Sequence 1, Application US/08484565  
; Patent No. 5763569  
; GENERAL INFORMATION:  
; APPLICANT: Edward M. Brown  
; APPLICANT: Steven C. Hebert  
; APPLICANT: James E. Garrett, Jr.  
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
; MOLECULES  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: First Interstate World Center  
; STREET: Suite 4700  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FASTSEQ  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,565  
; FILING DATE: 7 June, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below: 9  
; APPLICATION NUMBER: 08/353,784  
; FILING DATE: 9 December, 1994  
; APPLICATION NUMBER: PCT/US/94/12117  
; FILING DATE: 21 October, 1994  
; APPLICATION NUMBER: U.S. 08/292,827  
; FILING DATE: 23 August, 1994  
; APPLICATION NUMBER: U.S. 08/141,248  
; FILING DATE: 22 October, 1993  
; APPLICATION NUMBER: U.S. 08/009,389  
; FILING DATE: 23 February, 1993  
; APPLICATION NUMBER: U.S. 08/017,127  
; FILING DATE: 12 February, 1993  
; APPLICATION NUMBER: U.S. 07/934,161  
; FILING DATE: 21 August, 1992  
; APPLICATION NUMBER: U.S. 07/834,044  
; FILING DATE: 11 February, 1992  
; APPLICATION NUMBER: U.S. 07/749,451  
; FILING DATE: 23 August, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 213/006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5275 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-484-565-1

Alignment Scores:
Pred. No.: 646 Length: 5275
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-484-565-1 (1-5275)
QY 331 LeuArgAsnLeuMetLysThrPro 338
Db 2433 TTGCGGAACCTGTGATGAAGACGCC 2410

RESULT 14
US-08-480-751-1/c
; Sequence 1, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,751
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
```

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; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-480-751-1

Alignment Scores:
Pred. No.: 646 Length: 5275
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 2 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-480-751-1 (1-5275)
QY 331 LeuArgAsnLeuMetLysThrPro 338
Db 2433 TTGCGGAACCTGTGATGAAGACGCC 2410

RESULT 15
US-08-943-986-1/c
; Sequence 1, Application US/08943986
; Patent No. 5962314
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,986
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,565
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
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Mon Feb 3 14:11:33 2003

FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 515..3769  
OTHER INFORMATION:  
US-08-943-986-1

Alignment Scores:  
Pred. No.: 646 Length: 5275  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 2 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-943-986-1 (1-5275)

QY 331 LeuArgAsnLeuMetLysThrPro 338  
|  
DB 2433 TTCGGAAGTTGATGAAGAGCGCC 2410

Search completed: January 31, 2003, 07:12:50  
Job time : 106 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 06:19:11 ; Search time 110 Seconds

(without alignments)  
4182.247 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 1024

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 396772 seqs, 224632407 residues

Word size: 1

Total number of hits satisfying chosen parameters: 792425

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	827	80.8	3615	10	US-09-841-739-4

c	5	827	80.8	3615	10	US-09-841-739-12	Sequence 12, Appl
	6	721	70.4	3396	9	US-09-864-921-96	Sequence 96, Appl
	7	271	26.5	1395	9	US-09-864-921-98	Sequence 98, Appl
	8	232	22.7	891	9	US-09-864-921-179	Sequence 179, Appl
	9	206	20.1	618	9	US-09-864-921-181	Sequence 181, Appl
	10	154	15.0	768	9	US-09-864-921-102	Sequence 102, Appl
	11	150	14.6	608	10	US-09-764-864-339	Sequence 339, Appl
	12	97	9.5	522	10	US-09-764-864-754	Sequence 754, Appl
	13	89	8.7	578	9	US-09-864-921-100	Sequence 100, Appl
	14	87	8.5	261	9	US-09-864-921-177	Sequence 177, Appl
	15	87	8.5	421	10	US-09-864-761-4236	Sequence 4236, Ap
	16	73	7.1	220	10	US-09-864-761-20988	Sequence 20988, A
	17	36	3.5	165	9	US-09-864-921-183	Sequence 183, App
	18	15	1.5	483	10	US-09-728-445-337	Sequence 337, App
c	19	9	0.9	29	9	US-09-864-921-160	Sequence 160, App
	20	9	0.9	331	10	US-09-878-574-2550	Sequence 2550, Ap
	21	9	0.9	350	10	US-09-924-035A-517	Sequence 517, App
	22	9	0.9	376	9	US-09-796-692-7456	Sequence 7456, Ap
	23	9	0.9	2631	10	US-09-815-242-3821	Sequence 3821, Ap
	24	9	0.9	2643	10	US-09-815-242-6578	Sequence 6578, Ap
	25	9	0.9	3166	9	US-09-895-913A-339	Sequence 339, App
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	27	8	0.8	25	9	US-09-864-921-161	Sequence 161, App
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	29	8	0.8	25	9	US-09-864-921-165	Sequence 165, App
	30	8	0.8	33	9	US-09-864-921-157	Sequence 157, App
	31	8	0.8	347	10	US-09-864-761-24774	Sequence 24774, A
	32	8	0.8	348	10	US-09-783-590-1258	Sequence 1258, Ap
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	36	8	0.8	423	10	US-09-983-965-2718	Sequence 2718, Ap
	37	8	0.8	426	10	US-09-969-347-37	Sequence 37, Appl
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	39	8	0.8	509	10	US-09-864-761-8028	Sequence 8028, Ap
	40	8	0.8	519	9	US-09-954-531-111	Sequence 111, App
	41	8	0.8	519	9	US-09-954-531-325	Sequence 325, App
c	42	8	0.8	585	10	US-09-764-869-2094	Sequence 2094, Ap
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c	44	8	0.8	585	10	US-09-764-869-2096	Sequence 2096, Ap
c	45	8	0.8	606	10	US-09-951-470-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-841-739-3  
; Sequence 3, Application US/09841739  
; Patent No. US20020034784A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3072  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-3

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Score:	1024.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
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Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrrpAsnTyrProLeu 80  
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Db 1081 ACGCTGTTCCTACATCTTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT 1140  
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RESULT 2

US-09-841-739-1  
; Sequence 1, Application US/09841739  
; Patent No. US20020034784A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/597,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)....(3107)  
US-09-841-739-1  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Qy ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
Db 936 ACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTGGAAGC 995  
Qy LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
Db 996 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT 1055  
Qy ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
Db 1056 GTGGTCATCACTTGTGCAATCCAGATGGTGAAAGTGAGTTCCACTCTCACACAAACA 1115  
Qy ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380  
Db 1116 ACGCTGTTCATACCTTCTATGATCTGTTGATACAGAAAACAACACAAACATAAAGT 1175  
Qy ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
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Qy ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Db 1236 GTGTTCTCCCAAGTTTGATTTCCGACTGCAGGATGTGTCACGCGTGAATGAGGATGTC 1295  
Qy LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db 1296 CTGCTGACAACTGGGCTCCTCTGTAATATACACCTCAAGGTTCAAGCCAAAGATATAA 1355  
Qy PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460  
Db 1356 TTCCTTTCACAGTCAATTCAGAGGATACACAGCAGGAGGAGACTCAGCAGTTTATTGACG 1415  
Qy SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
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Db 1476 TCGGACATTACATCCATTATAGCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGGAA 1535  
Qy AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520  
Db 1536 GCCACAGGGGTGTATCAAGACCTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGA 1595  
Qy LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540  
Db 1596 CTTTCCATCGCAAGAGCCCTCTGAGACAGGAAATCTTTGCAAGTGTGAAAGACACC 1655  
Qy ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1656 ACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715  
Qy LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
Db 1716 TTATATCAAGAGAGTACATCAATCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA 1775  
Qy GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAppPheGlu 600  
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Db 1776 GGTAAAAAGCTTATATATCAACTCAGGGAACATCCCGATTACTTATTATTGACTTCTTTGAA 1835  
Qy HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620  
Db 1836 CATTTGCCCAATTTGCAAGTGTCTGTGACTTCATTAACCTGGACTTTTATGGGGAGCT 1895  
Qy MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640  
Db 1896 ATGCTTCATGGGAAAAAGGCTGCAGAGACACACAGTGAATCCACATGGAAGAGGCCCA 1955  
Qy GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660  
Db 1956 GAAACCTACATTTCCAGCAGGGCTGTATCTTTGTCTTCACTGAAGCAGAAATTCAGG 2015  
Qy ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db 2016 ACTCTGAGGTCACACTCCGGGATTTGAGCAAGTTGAATAGCAAGATATCACATATCTG 2075  
Qy GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Db 2076 GGGAAATATTCAGCTCTGCCACAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2135  
Qy AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 2136 GCTGGAAGCCTCAGTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCATGGTGGAA 2195  
Qy AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Db 2196 GCCAGTCCCTCACCATTAGAAGATGAGAGGCACATCATCTGTAAACAACCTGAAACCC 2255  
Qy LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2256 TTGAGTATTTCATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2315  
Qy AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
Db 2316 AACTTGAAGAACCTTACAAAGCTCATATGGATAACTAAAGATGAATGAAGAAGATGCT 2375  
Qy IleLysLeuAlaGluGlyLeuLysAsnLysLysMetCysLeuPheHisLeuThrHis 800  
Db 2376 ATAAACTAGCTGAAGCCTGAAACACCTGAAGAAGATGTGTTTATTTTCATTGACCCAC 2435  
Qy LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Db 2436 TTGTCTCACATTTGGAGAGGAAATGGATTACATAGTCAAGTCTCTGCTCAAGTGAACCTGT 2495  
Qy AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2496 GACCTTGAAGAAATTCATATTAGTCTCTGCTGCTGTGCTGCAAAATGCAGTGAATCTCTA 2555  
Qy AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db 2556 GCTCAGAATCTTCAATTTGGTCAAACTGAGCATCTTGTGATTTATCAGAAATTAACCTG 2615  
Qy GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Db 2616 GAAAAAGATGGAATGAAGCTCTTCATGAACTGATCGACAGGATGAAGCTGCTAGAAGAC 2675  
Qy LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2676 CTCACCCACTGATGTGCTCGGGCTGTGACGTGCAAGCCCTGAGCAGCTGTGTG 2735  
Qy LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
Db 2736 AAACATTTGGAGGAGGTCACACAACTCGTCAAGCTTGGTGTGAAACTGGAGACTCACA 2795  
Qy AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
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Qy GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrTrpLeuAlaPheMetGlyVal 960  
Db 2856 CAGTTGAATTTGGCGGGAAATCGGTGTGAGCAGTGAATGGCTTGCTTTCATGGGTGTA 2915









Db	3195	ACTCGTCAGCCTTGGGTGCAAAACCTGGAGACTCACAGATACAGAGATTAGAATTTTAGG	3254
Qy	928	YAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr	948
Db	3255	TGCATTTTTTGGAAAGAACCCCTCTGAAAACCTCCAGCAGTTGAATTTGGCGGCAATCG	3314
Qy	948	qValSerSerAspGlyTrpLeuAlaPheMetcllyValPheGluAsnLeuLysGlnLeuVa	968
Db	3315	TGTGACGAGTGATGGATGGCTTCGCTTCATGGGTGTATTTCAGAACTCTTAAGCAATTAGT	3374
Qy	968	lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArLgysLeuSe	988
Db	3375	GTTTTTTGACTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG	3434
Qy	988	rGlnValLeuSerLysLeuThrPheLeuClncLuAlaArLeuValGlyTrpGlnPheAs	1008
Db	3435	CCAAGTGTTATCCAGGTAACTTTTCTGCAGAAAGCTAGGCTTGTGTGGGTGGCAATTTGA	3494
Qy	1008	pAspAspLeuSerValIleThr	1016
Db	3495	TGATGATGATCTCAGTGTTATTACA	3519

## RESULT 5

RESULTS 3  
US-09-841-739-12/c

: Sequence 12. Application US/09841739

: Patent No. US20020034784A1

GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREFOR

; FILE REFERENCE: 07334-329001

; CURRENT APPLICATION NUMBER: US/09/841,739

; CURRENT FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: US 09/697,089

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: US 60/161,822

;  
; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 12

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; LENGTH: 3615
TYPE: 0000

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; TYPE: DNA  
ORNTCM:; ORGANISM: Homo sapiens  
 FIS-00-841-730-12

US-09-041-139-12

Alignment scores:

Pred. No.:	0	Length:	3615
Score:	827.00	Matches:	927
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	80.76%	Indels:	2
DB:	10	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-841-739-12 (1-3615)

Qy	89	LeuPheHisGlnThrSerClyAspLeuaspLeuAlaGlnAspLeuLysAspLeu	108
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Qy	109	TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIleIlePhe	128
Db	2820	TACCATACCCCATCTTTCTCGAACTTTATCCCTTGGTGAAGATATTGACATATTATTTT	2761
Qy	129	AsnLeuLysSerThrPheThrGluProValLeuThrPArgLysAspGlnHisHisHisArg	148
Db	2760	AACCTTGAAGAAGCACCCTTCACAGACCTCTCCTGTGGAGGAGGACCACACCATCATCCCGC	2701
Qy	149	ValcIuGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu	168
Db	2700	GTGGACGCTGACCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTTCATCATTTGAA	2641
Qy	169	GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer	188
Db	2640	GGGGAATCTGGAAAGGCAAGTCCACTCTGTGTGACGCAATGGCATGCTCTGGGGCTCC	2581

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QY 549 ileAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568
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Db 1500 ATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGTAGTACATCCAA 1441

QY 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer 588
|||||
Db 1440 TCAGCCCTGAGCCAGCAAAATTTGAAGCTTCTCTTCAAGGTAAGAGCTTATATATCAACTCA 1381

QY 589 GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla 608
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Db 1380 GGAACATCCCCGATTACATTATTGACTTCTTTGAACATTTGCCCAATTTGTGCAAGTGCC 1321

QY 609 LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTyrGluLysAlaAla 628
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QY 629 GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla 648
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Db 1260 GAAGACACAGGTGGAATCCACATGGAAGAGGCCCAACCTTACATTTCCAGCAGGGCT 1201

QY 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp 668
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Db 1200 GTATCTTTGTTCTTCAACTGGGAAGAGGAATTCAGGACTCTGGAGGTCACATCCCGGAT 1141

QY 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh 688
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QY 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaLaglySerLeuSerLeuValle 708
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Db 1081 AAGCCCTCAGGCTGCAAAATAAGAGATGTGCTGTGTGGTGGAGGCTCAGTTTGGTCTCT 1022

QY 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728
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Db 1021 CAGCAGCTGTAGAACAATTATCTCTCATGTGTGAAGCAGTCCCTCACCATAGAAGA 962

QY 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs 748
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Db 961 TGAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAGTATTTCATGACCTACAGAA 902

QY 748 nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768
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Db 901 TCACCGGCTGCCGGGTGGTGTGACTCACAGCTTGGGTAACTTGAAGAACTTACAAAGCT 842

QY 768 ulleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys 788
|||||
Db 841 CATATGGATACATAAAGATGAATCAAGAGATGCTATAAACTAGCTGAAGGCTGAA 782

QY 788 sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyMe 808
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Db 781 AAACCTGAAGAAGATGTGTTATTTTCACTTGACCCACTTGTCTGACATTTGGAGAGGGAAT 722

QY 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828
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Db 721 GGATTACATAGTCAAGCTCTCTCTCAAGTGAACCTGTGACCTTGAAGAAATTCAAATTAGT 662

QY 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
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Db 661 CTCCTGCTGCTGTCTGCAAAATGCAGTGAAATCTCTAGCTCAGATCTTCACAAATTTGGT 602

QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868
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Db 601 CAAACTGAGCATTTCTTGATTTATCAGAAAAATACCTGGAAAAAGATGGAATCAACTCT 542

QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProThr 888
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Db 541 TCATGAACCTGATCGACAGATGAACGTGTAGAACAGCTCACCGCACTGATGCTGCCCTG 482

QY 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGl 908
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Db 481 GGCTGTGACGTGCAAGGAGGCTGTGAGCAGCTGTGTGAACAATTTGGAGGAGGTCCCA 422

QY 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928
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Db 421 ACTCGTCAAGCTGGGTGGAAACCTGGAGACTCACAGATACAGATAGAAATTTAGG 362

QY 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
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Db 361 TGCATTTTGGAAAGAACCTCTGAAAAAATTTCCAGCAGTTGAATTTGGCGGGAATCG 302

QY 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
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Db 301 TGGAGCAGTGATGGATGGCTTGCCTTCATGGGTGATTGTGAGAACTTAAAGCAATTAGT 242

QY 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988
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Db 241 GTTTTGTAGCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 182

QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
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Db 181 CCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAAGTAGGCTTGTGGGTGGCAATTTGA 122

QY 1008 pAspAspAspLeuSerValIleThr 1016
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Db 121 TGATGATGATCTCAGTGTATTACA 97

RESULT 6
US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/379,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96

Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 721.00 Matches: 1021
Percent Similarity: 99.42% Conservativeness: 0
Best local Similarity: 99.42% Mismatches: 3
Query Match: 70.41% Indels: 6
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-96 (1-3396)

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Qy 41 IleCysCysGluLysValGluClnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
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Db 397 ATTTGCTCGGAGAGGTGGAGCAGGATGCTCTGAGGGATCATTCACATGATTTTGAAA 456  
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80  
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Db 457 AAGGTTGAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGAACATCTCCTCTA 516  
Qy 81 PheGlnAspLeuAsnGlyClnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
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Db 517 TTTCAGGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAAGGAGACTTGSACGAT 576  
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
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Db 577 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT 636  
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Db 936 CTGTGATATCTGCAACATCAGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGG 995  
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Qy 260 uIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrTh 280  
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Db 1116 CACTGAGTGCTGAGGCACATACGCGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATAT 1175  
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Db 1715 TTTTCGACATTTACATCCACTTATAGCAGCTGCTCCGCTACACCTGTGGTCACTGTGG 1774  
Qy 500 luAlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuG 520  
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Db 1775 AAGCCACCAGGCGTGTATGAAGCACCTCGCAGCAGTGTATCAACACGCGTCCCTTCG 1834  
Qy 520 lyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnT 540  
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Db 1835 GACTTTCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTGCAAAAGTGTGAAAAACA 1894  
Qy 540 hrThrGluGlnGluLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH 560  
|||||  
Db 1895 CCCTGAGCAAGAAATCTGAAGCCATAAATCAATTCCTTTGTAGAGTGTGGCATCC 1954  
Qy 560 isLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheG 580  
|||||  
Db 1955 ATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTC 2014  
Qy 580 lngLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheG 600  
|||||  
Db 2015 AAGTAAAGGCTTATATATCAACTCAGGAAACATCCCGATTTACTATTGACTTCTTTG 2074  
Qy 600 luHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyA 620  
|||||  
Db 2075 AACATTTGCCCAATTTGTCAAGTGCCTGGACTTCATTTAAACTGGACTTTTATGGGGAG 2134  
Qy 620 laMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlap 640  
|||||  
Db 2135 CTATGGCTTTCATGGGAAAGGCTGCAGAAAGCACAGGTGGAAATCCACATGGAAGAGGCC 2194  
Qy 640 roGluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheA 660  
|||||  
Db 2195 CAGAAACCTACATTTCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAAATCA 2254  
Qy 660 rgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr -Tyr 679  
|||||  
Db 2255 GGACTCTGGAGGTCAACATCCGGGATTTCAAGAGTTGAATAAGCAAGATATCAG -ATAT 2313  
Qy 680 LeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGly 699  
|||||  
Db 2314 CTGGGGAAAATTTATTCAGCTCTGCCAAGCCTCAGGCTGCAAAATAAAGAGATGTCTCGT 2373  
Qy 700 ValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetVal 719  
|||||  
Db 2374 GTGCTGGAGCCCTCAGTTTGTCTCTCAGCACCTGTGAAGAACATTTATCTCTCATGTG 2433  
Qy 720 GluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLys 739  
|||||  
Db 2434 GAAGCCAGTCCCTTCAACATAGAGATGAGAGGCACATCATCTGTAAACAAACCTGAAA 2493  
Qy 740 ThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeu 759  
|||||

Db 2494 ACCTTGAGTATTATCATGACCTACAGANTCAACGGCTGCCGGTGGCTGACTGACACCTTG 2553  
QY 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAsp 779  
|||||  
Db 2554 GGTAACTTGAAGAACCCTTCAAAAGCTCAATAAGTAAACATAAGATGAAGAAGAT 2613  
QY 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799  
|||||  
Db 2614 GCTATAAAACTAGCTGAAGCCCTGAAAAACCTGAAGAAGATGCTTATTTTCAATTTGACC 2673  
QY 800 HisLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerGluPro 819  
|||||  
Db 2674 CACTTCTCTGACATTGGAGAGGAATGGATTACATAGTCAAGTCTCTCAAGTGAACCC 2733  
QY 820 CysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIle 839  
|||||  
Db 2734 TGTGACCTTGAAGAAATTCATATAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2793  
QY 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859  
|||||  
Db 2794 CTAGCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAAATAC 2853  
QY 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879  
|||||  
Db 2854 CTGGAAAAAGATGGAATCAAGCTCTTCATGAACCTGACAGGATGAACGTGCTAGAA 2913  
QY 880 GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeu 899  
|||||  
Db 2914 CAGCTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTG 2973  
QY 900 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu 919  
|||||  
Db 2974 TTGAACATTTGGAGAGGTCCCAACCTCGTCAAGCTTGGGTGGAAGAACCTGGAGACTC 3033  
QY 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939  
|||||  
Db 3034 ACAGATACAGATTAAGATTTTAGTGCTATTTTGGAAAGAACCCCTCTGAAAAACTTC 3093  
QY 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 959  
|||||  
Db 3094 CAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGATGGATGGCTTGCCTTCATGGGT 3153  
QY 960 ValPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuPro 979  
|||||  
Db 3154 GTATTGAGAACTTAAAGCAATTAAGTCTTTTGTGACTTTAGTAAAGAAATTTCTACCT 3213  
QY 980 AspProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlu 999  
|||||  
Db 3214 GATCCAGCATTAAGTCAAGAAACTTAGCCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAA 3273  
QY 1000 AlaArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPhe 1019  
|||||  
Db 3274 GCTAGGCTTGTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3333  
QY 1020 LysLeuValThrAla 1024  
|||||  
Db 3334 AAACCTAGTAACCTGCT 3348

RESULT 7

US-09-864-921-98  
; Sequence 98, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sug-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Hayashi, Hideki  
; APPLICANT: Pawlowski, Krzysztof  
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
  
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
; FILE REFERENCE: P-LJ 4752  
; CURRENT APPLICATION NUMBER: US/09/864,921  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 09/579,240  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/686,347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/275,980  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 1395  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (277)...(1353)  
US-09-864-921-98  
  
Alignment Scores:  
Pred. No.: 2,55e-277 Length: 1395  
Score: 271.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 26.46% Indels: 0  
DB: Gaps: 0  
  
US-09-697-089-2 (1-1024) x US-09-864-921-98 (1-1395)  
QY 754 GlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIle 773  
Db 541 GGTCTGACTGACGAGCTTGGTAACTTGAAGAACCTTACAAGCTCATAATGGATAACATA 600  
QY 774 LysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysMet 793  
|||||  
Db 601 AAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCCTGAAAAACCTGAAGAAGATG 660  
QY 794 CysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleValLys 813  
|||||  
Db 661 TGTATTATTTTCAATTTGACCCACTTGTCTGACATTTGGAGAGGAATGGATTACATAGTCAAG 720  
QY 814 SerLeuSerSerGluProCysAspLeuGluIleGlnLeuValSerCysCysLeuSer 833  
Db 721 TCTCTGCTCAAGTGAACCCCTGTGACCTTGAAGAAATTCATATTAGTCTCTCTGCTTGTCT 780  
QY 834 AlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeu 853  
Db 781 GCAAAATGCAAGTGAATAATCTAGCTCAGAAATCTTCACAATTTGGTCAAACTGAGCATCTT 840  
QY 854 AspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAsp 873  
Db 841 GATTTATCAGAAAAATTTACCTGGAAAAAAGATGGAATGAAGCTTTCATGAACCTGATCGAC 900  
QY 874 ArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGln 893  
Db 901 AGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAA 960  
QY 894 GlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLysLeuGly 913  
Db 961 GGCAGCCTGAGCAGCCTGTTGAACATTTTGGAGGAGGTGCCCAACTCCTCAAGCTTGGG 1020  
QY 914 LeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLys 933  
Db 1021 TTGAAAACTGGAGACTCAGATACAGAGATTTAGATTTTGGTGCATTTTGGGAAG 1080  
QY 934 AsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 953  
Db 1081 AACCCCTCTGAAAAACTTCCAGCAGTTGAATTTGGCGGGAATCTGCTGAGCAGTGTATGA 1140  
QY 954 TrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPheSer 973  
|||||

Db 1141 TGGCTTGCTTCATCGGTGTATTTCAGAAATCTTAAGCAATAGTGTCTTTTTCAGCTTAGT 1200

Qy 974 ThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuSerLys 993

Db 1201 ACTAAGAATTCACCTGATCCAGCATTAGTCAGAAACTTAGCCAAAGTGTATCCAAAG 1260

Qy 994 LeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspAspLeuSer 1013

Db 1261 TTAACCTTCTCGAAGAGCTAGCTGTCTGGGTGGCAATTTGATGATGATGATCTCAGT 1320

Qy 1014 ValLeuThrGlyAlaPheLysLeuValThrAla 1024

Db 1321 GTTATTACAGGTGCTTTTAAACTAGTAACCTGCT 1353

RESULT 8

US-09-864-921-179

; Sequence 179, Application US/09864921

; Patent No. US20020176853A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; APPLICANT: Pio, Frederick F.

; APPLICANT: Godzik, Adam

; APPLICANT: Stehlik, Christian

; APPLICANT: Damiano, Jason S.

; APPLICANT: Lee, Sug-Hyung

; APPLICANT: Oliveira, Vasco A.

; APPLICANT: Hayashi, Hideki

; APPLICANT: Pawlowski, Krzysztof

; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing

; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use

; FILE REFERENCE: P-LJ 4752

; CURRENT APPLICATION NUMBER: US/09/864, 921

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 09/579,240

; PRIOR FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/686,347

; PRIOR FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: US 60/275,980

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 179

; LENGTH: 891

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(891)

US-09-864-921-179

Alignment Scores:

Pred. No.: 3,43e-236 Length: 891

Score: 232.00 Matches: 296

Percent Similarity: 99.33% Conservative: 0

Best Local Similarity: 99.33% Mismatches: 1

Query Match: 22.66% Indels: 2

DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-179 (1-891)

Qy 161 LeuGlnSerProCysIleIleGluGlyCysGlyLysSerThrLeuLeuGln 180

Db 1 CTTTCAGAGCCCTCATTCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 60

Qy 181 ArgIleAlaMetLeuTppGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200

Db 61 CGCATTCGATGCTGGGGCTCGGAAGGTGCAAGGCTCTGCAAGTTCAAATTCGTC 120

Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220

Db 121 TTCCTCTCGCTCAGCAGGCGCCAGGGTGAGCTTTTGAACCCCTCTGTGATCACTC 180

Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240

Db 181 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTTCATGGCCATGCTGCTCAAGCTCGG 240

Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260

Db 241 CAGAGGGTCTCTTTTCCCTTCTTGATGGGTACAATGAATTCAGCCCAAGAACTGCCCAAA 300

Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280

Db 301 ATCGAAGCCCTGTATAAGGAACACCCGCTTCAAGAACATGGTCACTGCTCACCACATACC 360

Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300

Db 361 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATG 420

Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320

Db 421 ACAGAAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTTCCTGAAGGC 480

Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340

Db 481 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGATCTCATGAAGACCCCTCTCTTT 540

Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360

Db 541 GTGGTCATCACTTGTGCAATCCAGATGGTGAAAGTGAGTTCCACTCTCACACACAAACA 600

Qy 361 ThrLeuPheHisThrPheTyrAspLeuIleGlnLysAsnLysHisLysHisLysGly 380

Db 601 ACGTGTTCATACCTCTTATGATCTGTGATACAGAAAAACAACAACATATAAGGT 660

Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCys-GlyAspLeuAlaLeuGluGly 400

Db 661 GTGGCTGCAAGTGACTTCATTCGGAGCGCTGGACCACCG-TGGAGACCTAGCTCTGGAGG 719

Qy 400 yValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420

Db 720 TGTGTTCTCCCAAGTTTGAATTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGT 779

Qy 420 LLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLy 440

Db 780 CTGCTCACAACTGGGCTCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 839

Qy 440 sPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457

Db 840 ATCTCTTTCACAAAGTCATTCCAGGAGTACACAGCAGGACGAGAGACTCAGCACT 891

RESULT 9

US-09-864-921-181

; Sequence 181, Application US/09864921

; Patent No. US20020176853A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; APPLICANT: Pio, Frederick F.

; APPLICANT: Godzik, Adam

; APPLICANT: Stehlik, Christian

; APPLICANT: Damiano, Jason S.

; APPLICANT: Lee, Sug-Hyung

; APPLICANT: Oliveira, Vasco A.

; APPLICANT: Hayashi, Hideki

; APPLICANT: Pawlowski, Krzysztof

; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing

; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use

; FILE REFERENCE: P-LJ 4752

; CURRENT APPLICATION NUMBER: US/09/864, 921

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 09/579,240

; PRIOR FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/686,347

; PRIOR FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: US 60/275,980

; PRIOR FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 195

; APPLICANT: Reed, John C.  
 ; APPLICANT: Pio, Frederick F.  
 ; APPLICANT: Godzik, Adam  
 ; APPLICANT: Stehlik, Christian





```

; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100

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Alignment Scores:		
Pred. No.:	4,448-83	261
Score:	87.00	87
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	8.50%	Indels: 0
DB:	9	Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-177 (1-261)

20	Qy	1	MetAspPhelIcysAspAsnSerArgAlaLeuilecGlnArgMetGlyMetThrValIle	20
21	Qy	1	ATGAATTTCTAAAGACAAATAGCGAGCCCTTATTCAAAGATGGGAATGACTGTTATA	60
22	Qy	21	LysGlnIleThrAspAspLeupheValTrpAsnValLeuAsnArgGluGluValAsnIle	40
23	Db	61	AAGCAAAATCACAGATGACCTATTTGTATGGAAATGCTTGAATCGCAAGAAGTAAACATC	12
24	Qy	41	IleCysCysGlnLysValcIcGlnAspAlaalaArgGlyIleIleHisMetIleLeuLys	60
25	Db	121	ATTTGCTGCGAAGAGTGGAGCAGGATGCTCTAGAGAGGATCATTCACATGATTTTGAAT	18

Qy 81 PheGlnAspLeuAsnGlyGln 87  
 Dd 241 TTT CAGGACTTG AATGGACAA 26

RESULT 15  
US-09-864-761-4236  
; Sequence 4236, Application US/09864761  
; Patent No. US20020048763A1

```

: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED
: TITLE OF INVENTION: GENE EXPRESSION ANAL
: FILE REFERENCE: Aemica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24363.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 4236  
; LENGTH: 421  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC011232.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 16  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
US-09-864-761-4236

Alignment Scores:  
Pred. No.: 1.9e-75 Length: 421  
Score: 80.00 Matches: 80  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.81% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-761-4236 (1-421)

QY	928	GlyAlaPheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsn	947
Db	181	GGTCATTTTTGGAAAGAACCCCTCTGAAAACACTCCAGCAGTTGAATTTGGCGGGAAT	240
QY	948	ArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeu	967
Db	241	CGTGTGACGAGTGTATGGCTGCCCTTCATGGGTGTTATTTGAGAATCTTAAGCAATTA	300
QY	968	ValPhePheAspPheSerThrLysGluPheLeuProAlaLeuValArgLysLeu	987
Db	301	GTGTTTTTTGACTTTAGTACTAAAGAATTTCTACCTCATCCAGCATTTAGTCAGAAAACCTT	360
QY	988	SerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrGlnPhe	1007
Db	361	AGCCAAGTGTTATCCAAAGTTAACTTTCTTCAAGAAGCTAGGCTTTGTTGGTGGCAATTT	420

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Job time : 151 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 04:27:08 ; Search time 5176 Seconds  
(without alignments)  
4974.093 Million cell updates/sec

Title: US-09-697-089-2  
Perfect score: 1024  
Sequence: 1 MNFTKNSRALIQMGMTVI.....WQFDDDLSVITGAFKLVT 1024

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Word size: 1

Total number of hits satisfying chosen parameters: 49569006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-Q=/cgn2\_1/USPTO\_spool/US09697089/runat\_29012003\_091155\_13509/app\_query.fasta\_1.1223  
-DB=Pending\_Patents\_NA\_Main -QMT=fastcap -SUFFIX=olip2n.rnpnm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1024	100.0	3072	27	US-09-697-089-3
3	1024	100.0	3072	32	US-09-841-739-3
4	1024	100.0	3133	1	PCT-US00-29643-1
5	1024	100.0	3133	27	US-09-697-089-1
6	1024	100.0	3133	32	US-09-841-739-1
					Sequence 3, Appli
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 1, Appli

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7 923 90.1 3075 41 US-10-156-733-1
8 923 90.1 3219 41 US-10-156-733-14
9 922 90.0 3213 41 PCT-US01-07143-23
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11 827 80.8 3612 27 US-09-697-089-6
12 827 80.8 3612 32 US-09-841-739-6
13 827 80.8 3615 1 PCT-US00-29643-4
14 827 80.8 3615 1 PCT-US00-29643-6
15 827 80.8 3615 27 US-09-697-089-4
16 827 80.8 3615 27 US-09-697-089-12
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## ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-3
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QY 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
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QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
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; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
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; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-697-089-3

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QY 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
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QY 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
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QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220
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QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrlleSerLeuMetValGlu 720  
Db 2101 GCTGGAGCCTCAGTTTGGTCTCAGCACCCTGTAAAGAACATTATCTCTCATGTGGAA 2160  
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Db 2161 GCCAGTCCCTCACCATAGAAGATGAGGCGACATCACATCTCTAAACAACCTGAAACCC 2220  
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2221 TTGAGTATTTCATGACCTACAGATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGT 2280  
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780  
Db 2281 AACTTCAGAACCTTCAAAAGCTCATTAATGGATAACATAAGATGAATGAAGAAGTCT 2340  
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Db 2341 ATAAACTAGCTGAAGCCTGAAAAACCTGAAGAAGATGTGTTATTTTCATTGTACCCAC 2400  
QY 801 LeuSerAspIleGlyGluGlyMetAspTyrlleValLysSerLeuSerSerGluProCys 820  
Db 2401 TTGTCTGACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGT 2460  
QY 821 AspLeuGluGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2461 GACCTTGAAGAAATTCANATTAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520  
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrlle 860  
Db 2521 GCTCAGAATCTTCACAAATTTGGTCAAACTGAGCATCTCTTGAATTCACAGAAATTAACCTG 2580  
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Db 2581 GAAAAAGATGGAAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACGTGTAGAACAG 2640  
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2641 CTCACCGCACTGATGCTGCCCTGGGCTGTGAGTGCAGGAGCCTGAGCAGCCTGTGTG 2700  
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
Db 2701 AAACATTTGGAGGAGGTCCCAACATCTCAAGCTTGGCTTGGAAACCTGGAGACTCACA 2760  
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 2761 GATACAGAGATTAGAAATTTAGTGCATTTTGGTGAAGAACCCTCTGAAAACTTCCAG 2820  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960  
Db 2821 CAGTTGAATTTGGGGGAATCGTGTGACAGCTGATGGATGGCTTCCCTTCATGGGTGTA 2880  
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
Db 2881 TTTGAGAACTTAAGCAATTAGTGTTTTGTACTTTTAGTACTAAAGAAATTTCTACCTGAT 2940  
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
Db 2941 CCAGCATTAGTCAGAAAACTTAGCCCAAGTGTATTCAAGTTAACTTTTCTGCAAGAAGCT 3000

QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
Db 3001 AGGCTGTTGGTGGCAATTTGATGATGATGATCTCAGTGTATTATTACAGGTGCTTTTAAA 3060  
QY 1021 LeuValThrAla 1024  
Db 3061 CTAGTAACGTCT 3072  
RESULT 3  
US-09-841-739-3  
; Sequence 3, Application US/09841739  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3072  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-3  
Alignment Scores:  
Pred. No.: 0 Length: 3072  
Score: 1024.00 Matches: 1024  
Percent Similarity: 100.00% Conservative: 0  
Best local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 32 Gaps: 0  
US-09-697-089-2 (1-1024) x US-09-841-739-3 (1-3072)

QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
Db 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTATTCAAAGAATGGGAATGACTGTATATA 60  
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40  
Db 61 AGCAAAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120  
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
Db 121 ATTTGCTGCGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrlleProLeu 80  
Db 181 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTA 240  
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
Db 241 TTTTCCAGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAGAGACACTGGACGAT 300  
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrlleHisThrProSerPheLeuAsnPheTyrlleProLeu 120  
Db 301 TTGGCTCAGGATTTAAAGGACTTTGATACCATACCCCATCTTTCTGAACCTTTTATCCCTT 360  
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140  
Db 361 GGTGAGATATTGACATATTATTTTAACTTCAAAAGCACCTTCACAGAACTGTCTGTGG 420  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
Db 421 AGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGNATGCCCTCTCTGCAGGCT 480  
QY 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180

Db 481 CTTTCAGACCCCTGCATCATTTGAAGGGAATCTGGCAAGCAAGTCCACTCTGCTGCAG 540  
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheIysPheVal 200  
Db 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAGGTGCAAGGCTCTGCACCAAGTTCAAAATTCGTC 600  
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220  
Db 601 TTCCTTCCCTCCGCTCAGCAGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660  
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240  
Db 661 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGTGGCATGCTGCTGAAGCTGGG 720  
Qy 241 GlnArgValLeuPheLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
Db 721 CAGAGGGTCTTTCCTTCTTGATGGCTCAATGAATCAAGCCCGCCAGCAATGCCAGAA 780  
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280  
Db 781 ATCGAAGCCCTGATAAAGGAACACACCGCTTCAAGACATGGTCATCGTCACCACCTACC 840  
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
Db 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATG 900  
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
Db 901 ACAGAAGACAGCCCGCCAGCTCTCATCCGAGAGTGTGATCAGGAGCTTGTCTGAAGGC 960  
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
Db 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
Db 1021 GTGGTTCATCATTGTGCAATCCAGATGGGTGAAAGTAGTGTCCACTCTCACACACAACA 1080  
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380  
Db 1081 ACGCTGTTCATACCTCTTATGATCTGTGATACAGAAAAACAACAACATAAAGGT 1140  
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
Db 1141 GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACCTGTGAGACCTAGCTCTGAGGGT 1200  
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Db 1201 GTGTTCTCCCAAGTTTGTATTCGAACTGCAGGATGTCTCCAGCGTGAATGAGGATGTC 1260  
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db 1261 CTGCTGACAACTGGGCTCTCTGAATATATACGCTCAAGAGTTCAAGCCAAAGTATANA 1320  
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460  
Db 1321 TTCCTTCAAGTCAATCCAGGAGTACACAGCAGGACGAGACATCAGCAGTTTATTGAGC 1380  
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
Db 1381 TCTCATGAGCCAGAGGAGTGACCAAGGGGAATGTTACTTTGCAGAAAAATGGTTTCCATT 1440  
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db 1441 TCGGCATTTACATCCATTTAGCAGCCTGCTCCGGTACACTGTGGGTCACTGTGGAA 1500  
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520  
Db 1501 GCCACGAGGGCTGTATGAAGCACCCTCCGACAGTGTATCAACAGGGCTGCTTCTCGGA 1560  
Qy 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540  
|||||

Db 1561 CTTTCCATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1621 ACTGAGCAGAAATTTCTGAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680  
Qy 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
Db 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 1740  
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600  
Db 1741 GGTAAAAGCTTATATATCACTCAGGGAAACATCCCGCATTAATTTACTTTATTTGACTTCTTTGAA 1800  
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620  
Db 1801 CATTTGGCCCAATTTGCAAGTGTCTGGACHTTCATTAACCTGGACHTTTTATGGGGAGCT 1860  
Qy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640  
Db 1861 ATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660  
Db 1921 GAAACCTACATTCACAGCAGGGCTGTATCTTTGTCTTCAACTGGAAGCAGGAATTCAGG 1980  
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db 1981 ACTCTGAGGGTCACACTCCGGGATTTCAGCAAGTTGAATAGCAAGATATCACATATCTG 2040  
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgIleGlnIleLysArgCysAlaGlyVal 700  
Db 2041 GGGAAAAATATTCAGCTCTGCCACAAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2100  
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 2101 GCTGGAGCCCTCAGTTGGTCTCTCAGCACCTGTGAAGACATTTATCTCTCATGGTGAA 2160  
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAspLeuLysThr 740  
Db 2161 GCCAGTCCCCTCACCATAGAAGATGAGAGGCACATCATCTGTAAACAACCTGNAACACC 2220  
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTCGCGGTGCTGTCTGACTCAGACGTGGGT 2280  
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780  
Db 2281 AACTTGAAGAACCTTACAAAGCTCATATGGATAACATAAAGATGAATGAAGAAGATGCT 2340  
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis 800  
Db 2341 ATAAACTAGCTGAGGCCCTGAAAAACCTGAAGAAGATGTGTGTTTATTTTCATTTGACCAC 2400  
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Db 2401 TTGCTGCATTTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGT 2460  
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2461 GACCTTGAAGAAATTCAAATTAGTCTCTGCTGTGTGTGTGCAAAATGCAAGTGAATTCCTA 2520  
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db 2521 GCTCAGAAATCTTCAAAATTTGGTCAAACCTGAGCAATCTTGAATTTATCAGAAAAATACCTG 2580  
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGluGln 880  
Db 2581 GAAAAAGATGGAATGAAGCTTTCATGAACTGATCGACAGATGAAGCTCTAGACAG 2640  
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2641 CTCACCGACTGATGCTGCCCTGGGGCTGTGACGTGAAGCAGCCTGAGCAGCTGTGTG 2700



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QY 901 LysHisLeuGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
|||||
Db 2701 AAACATTGGAGAGTCCCAACACTCGTCAAGCTTGGGTGAAACATGGAGACTACA 2760

QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
|||||
Db 2761 GATACAGAGATTAGAATTTTAGGTGCATTTTGGGAAGAACCTCTGAAAAATCTCCAG 2820

QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
|||||
Db 2821 CAGTTGAATTTGGCGGAATCGTGAGCAGTGATGGATGGCTTGCCCTCATGGGTGTA 2880

QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
|||||
Db 2881 TTTGACAATCTAAGCAATAGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGAT 2940

QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
|||||
Db 2941 CCAGCATTAGTCAGAAACTTAGCCAAGTGTATCCAAGTTAACTTTTCTGCAAGAAGCT 3000

QY 1001 ArgLeuValClyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
|||||
Db 3001 AGCCTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTACAGGTGCTTTTAA 3060

QY 1021 LeuValThrAla 1024
|||||
Db 3061 CTAGTAACGTCT 3072

RESULT 4
PCT-US00-29643-1
; Sequence 1, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
PCT-US00-29643-1

Alignment Scores:
Pred. No.: 0 Length: 3133
Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US00-29643-1 (1-3133)

QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
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Db 36 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA 95

QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
|||||
Db 96 AAGCAATCACAGATCACCTATTGTTGTAATGGAATGTTCTCAATCGCGAAGAAAGTAAACATC 155

QY 41 IleCysCysLysValGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
Db 156 ATTTGCTCGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 215
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QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
|||||
Db 216 AAGGGTTAGAGTCTCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGAACACTATCTCTA 275

QY 81 PheGluAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
|||||
Db 276 TTTTCAGGACTTGAATGCACAAAGCTTTTTCATCAGACATCAGAAGGAGACTTGGAGCAT 335

QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTrpProLeu 120
|||||
Db 336 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATCCCTT 395

QY 121 GlyGluAspIleAspIleLeuPheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
|||||
Db 396 GGTGAAGATATTGACATATTATTTTAAGTGAAGAACACCTTCACAGAACCTGTCTGTGG 455

QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
|||||
Db 456 AGAAGGACCAACACCATCATCCCGCTGGAGCAGTGAACCTGAATGGCTCTCTGCAGGCT 515

QY 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
|||||
Db 516 CTTTCAGAGCCCTCGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCAG 575

QY 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
|||||
Db 576 CGCATTTGCCATGCTCTGGGCTCCGGNAAGTGAAGGCTCTGACCAAGTTCAATTCGTC 635

QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
|||||
Db 636 TTCTTCTCGCTCTCAGCAGGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 695

QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
|||||
Db 696 CTGGATATACCTGGCACAATTCAGGAAGCAGACATTCATGGCCATGCTGTGGAAGCTCGG 755

QY 241 GlnArgValLeuPheLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
|||||
Db 756 CAGAGGGTCTCTTTCTCTTGTGCTACAATGAATTCAGCCGCCAGAGACTGCCAGAA 815

QY 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
|||||
Db 816 ATCGAAGCCCTGTATAAAGGAAAAACCCCGCTTCAAGAACAATGCTCATCGTCACACTACC 875

QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
|||||
Db 876 ACTGAGTGCTTGAGGCACATACCGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATG 935

QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
|||||
Db 936 ACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTGGAAGGC 995

QY 321 LeuLeuGlnGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
|||||
Db 996 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCTCATGAGACCCCTCTCTTT 1055

QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
|||||
Db 1056 GTGGTCATCATTGTGCAATCCAGATGGGTGAAGTGAAGTGATGCCACTCTCACACAAACA 1115

QY 361 ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysGly 380
|||||
Db 1116 ACCTGTTCCATACCTTCTATGATCTGTGATACAGAAAAACAAACACAAATAAAGGT 1175

QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
|||||
Db 1176 GTGGCTGCAAGTGACTTCATTCGAGGCCTGGACCACTGTGGAGACCTAGTCTGTGGGGT 1235

QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
|||||
Db 1236 GTGTTCTCCACAAGTTTGTATTTCGAACCTGCAGGATGTGTCAGCGTGAATGAGGATGTC 1295
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Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db 1296 CTGCTGACAACTGGGCTCCTCTGTAATATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1355  
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460  
Db 1356 TTCCTTCAACAGTCATCCAGGAGTACACAGGAGCAAGACTCAGCAGGTTTATTGACG 1415  
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
Db 1416 TCTCATGAGCCAGAGGAGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTCCATT 1475  
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db 1476 TCGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTATCTGTGGA 1535  
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520  
Db 1536 GCCACCAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGA 1595  
Qy 521 LeuSerIleAlaLysArgProLeuTriArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
Db 1596 CTTTCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACC 1655  
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1656 ACTGAGCAAGAATAATCTGAAAGCCATAAATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715  
Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGln 580  
Db 1716 TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTTCTTTCAA 1775  
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600  
Db 1776 GGTAAAGCTTATATATCACTCAGGAAATCCCGGATTAATTTGACTTCTTTGAA 1835  
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
Db 1836 CATTTGCCCAATTTGTCAAGTGCTCTGGACTTCATTAACATGGACTTTTATGGGGAGCT 1895  
Qy 621 MetAlaSerTriPGLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640  
Db 1896 ATGGCTTCATCGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1955  
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTriPGLysGlnGluPheArg 660  
Db 1956 GAAACCTACATCCAGCAGGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 2015  
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db 2016 ACTCTGGAGGTACACTCCGGGATTTGAGCAAGTTGAATAAGCAAGATATCACATATCTG 2075  
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Db 2076 GGGAAAATATTACGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2135  
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 2136 GCTGGAGCCTCAGTTGGTCTCAGCACCTGTAGAACATTTATCTCTCATGGTGGAA 2195  
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Db 2196 GCCAGTCCCTCCACATAGAAGATGAGAGGCACATCATCTGTAACAAACCTGAAAACC 2255  
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2256 TTGAGTATTACATACCTACAGAAATCAACGGCTGCGGGGTGCTGACTGACAGCTTGGGT 2315  
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780  
Db 2316 AACTTGAGAACCTTACAAAGCTCATATGGATACATAAAGATGAATGAAGAAGATGCT 2375  
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800

Db 2376 ATAAACCTAGCTGAGGCGCTGAAAAACCTGAAGAAGATGTGTATTATTCATTGTGCCAC 2435  
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Db 2436 TTGTCTGACATTTGAGAGGGAATGATATACATAGTCAAGTCTCTGTCAGGTGAACCCCTGT 2495  
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2496 GACCTTGAAGAAATCAATTAGTCTCCTGCTGTCTGCAATGCAATGCAATGCAATCCTA 2555  
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db 2556 GCTCAGAATCTTCAAAATTTGGTCAAACTGAGCATCTCTGATTTATCAGAAAAATACCTG 2615  
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Db 2616 GAAAAAGATGGAATGAAGCTCTTCATGAATGTCGACAGGATGAAGCTGCTAGAACAG 2675  
Qy 881 LeuThrAlaLeuMetLeuProTriPGLysCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2676 CTCACCGACTGATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCTCAGCAGCCTGTG 2735  
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTriPArgLeuThr 920  
Db 2736 AAACATTTGGAGGAGTCCCAACCTCGTCAAGCTTGGGTGAAAAAAGCTGGAGACTCACA 2795  
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 2796 GATACAGAGATTAGAAATTTTAGGTGCATTTTGGAAAAAGACCCCTCTGAAAAACTCCAG 2855  
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960  
Db 2856 CAGTTGAATTTGGCGGGAATCGGTGAGCAGTGTATGATGCTTGCCTTCATGGGTGTA 2915  
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
Db 2916 TTTGAGAATCTTAAGCAATTAGTGTTTTTCATTTAGTACTAAAGAAATTTCTACCTGAT 2975  
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAla 1000  
Db 2976 CCAGCATTTAGTCAGAAAAACTTAGCCAGTGTATCCAAAGTTAACTTTTCTGCAAGAGCT 3035  
Qy 1001 ArgLeuValGlyTyrGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
Db 3036 AGGCTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTTACAGAGTCTTTTAAA 3095  
Qy 1021 LeuValThrAla 1024  
Db 3096 CTAGTAACCTGCT 3107

## RESULT 5

US-09-697-089-1

; Sequence 1, Application US/09697089

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-136001

; CURRENT APPLICATION NUMBER: US/09/697.089

; PRIOR FILING DATE: 2000-10-26

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3133

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (36)...(3107)

## US-09-697-089-1

## Alignment Scores:

Pred. No.:	0	Length:	3133
Score:	1024.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

## US-09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133)

Qy	1	MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle	20
Db	36	ATGAATTCATAAAGAGCAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTGTATA	95
Qy	21	LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle	40
Db	96	AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGGGAAGTAACAATC	155
Qy	41	IleCysCysGluLysValGluGlnAspAlaAaArgGlyIleIleHisMetIleLeuLys	60
Db	156	ATTTCGCGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA	215
Qy	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu	80
Db	216	AAGGFTTCAGAGTCTGTAAACCTCTTCTTAATCCCTTAAGAGTGGAACTATCCTCTA	275
Qy	81	PheGlnAspLeuAsnGlyClnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp	100
Db	276	TTTCAGGACTTGAATGGCAAAAGTCTTTTCATCAGACATCAGAGGAGCTTGGACGAT	335
Qy	101	LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu	120
Db	336	TTGGCTCAGGATTTAAAGACTTGTACCATACCCACTCTTTCTGAACCTTTATCCCTT	395
Qy	121	GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
Db	396	GGTGAAGATATTGACATATTATTTAACTTTGAAAGCACCTTCACAGAACCTGTCTGTGG	455
Qy	141	ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla	160
Db	456	AGGAAGGACCAACACCATACCGCTGGAGCAGCTGACCTGAATGGCCCTCTGACGCT	515
Qy	161	LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln	180
Db	516	CTTCAGAGCCCTGCATCATTAAGGGGAACTCTGCAAGGCAAGTCCACTCTGTGCAAG	575
Qy	181	ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Db	576	CGCATTTGCCATCTCTGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC	635
Qy	201	PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu	220
Db	636	TTCTTCCTCCGCTCAGCAGGGCCAGGGTGGACATTTTGAACCCCTCTGTGATCAACATC	695
Qy	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
Db	696	CTGGATATACCTGGCAATCAGGAAGCAGACATTCATGGCCATGCTGTGAGCTGCGG	755
Qy	241	GlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLysProGlnAsnCysProGlu	260
Db	756	CAGAGGTTCTTTCTCTTCATGGCTACATGAATTCAGCCCCAGAACTGCCAGAA	815
Qy	261	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	280
Db	816	ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCTATCCACTACC	875
Qy	281	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
Db	876	ACTGAGTCCCTGAGGCACATACGGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATG	935
Qy	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly	320

Db	936	ACAGAAGACAGCCCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTGCTGAAGC	995
Qy	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
Db	996	TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT	1055
Qy	341	ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr	360
Db	1056	GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTCCACTCTCACACAAACA	1115
Qy	361	ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysLysGly	380
Db	1116	ACGCTGTTCCATPACCTTCTATGATCTGTTGATACAGAAAAACACACATAAAGGT	1175
Qy	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly	400
Db	1176	GTGGCTGCAAGTGACTTCATTGCGAGCCTGGACCTGTGGAGACTAGCTCTGGAGGT	1235
Qy	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal	420
Db	1236	GTGTTCTCCCAAGTTTGTATTCGAACTGCAAGATGTCAGCGTGAATGAGGATGTC	1295
Qy	421	LeuLeuThrThrGlyLeuLeuCysLysTrpThrAlaGlnArgPheLysProLysTrpLys	440
Db	1296	CTGCTGACAACCTGGGCTCCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGTATAA	1355
Qy	441	PhePheHisLysSerPheGlnGluTrpThrAlaGlyArgArgLeuSerSerLeuLeuThr	460
Db	1356	TTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGAGCAAGACTCAGCAGTTTATTGAGC	1415
Qy	461	SerHisGluProGluGluValThrLysGlyAsnGlyTrpLeuGlnLysMetValSerIle	480
Db	1416	TCTCATGCCAGAGAGGAGTGACCAAGGGGAATGGTTACTTCAGAAAAATGGTTCCATT	1475
Qy	481	SerAspIleThrSerThrTrpSerSerLeuLeuArgTrpThrCysGlySerSerValGlu	500
Db	1476	TCGGACATTACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGTGCATCTGTGAA	1535
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaValTrpGlnHisCysLeuLeuGly	520
Db	1536	GCCACAGGGCTGTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA	1595
Qy	521	LeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1596	CTTTCCATCGCCAAAGAGGCTCTCTCGAGACAGGAATCTTTGCAAGTGTGAAAAACAC	1655
Qy	541	ThrGluGlnGluLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1656	ACTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGCAATCCAT	1715
Qy	561	LeuTrpGlnGluSerThrSerLysSerAlaLeuSerGlnPheGluAlaPhePheGln	580
Db	1716	TTATATCAAGAGATACATCCAAATCAGCCCTGAGCAGAAATTTGAAGCTTTCTTTCAA	1775
Qy	581	GlyLysSerLeuTrpIleAsnSerGlyAsnIleProAspTrpLeuPheAspPhePheGlu	600
Db	1776	GGTAAAGCTTATATATCAACTCAGGGAACATCCCGATTAATTTGACTTCTTTGAA	1835
Qy	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTrpGlyAla	620
Db	1836	CATTTGCCCAATTTGCAAGTGTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT	1895
Qy	621	MetAlaSerTrpGluLysAlaAlaGluAspThrGlyIleHisMetGluGluAlaPro	640
Db	1896	ATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA	1955
Qy	641	GluThrTrpIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg	660
Db	1956	GAAACCTACATCCCGAGCAGGCTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGG	2015
Qy	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTrpLeu	680

Db	2016	ACTCTGAGGTCACACTCCGGGATTTCCACCAAGTTGAATAAGCAAGATATCACATATCTG	2075
Qy	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArCysAlaGlyVal	700
Db	2076	GGGAAATATTCAGCTCTGCCAAGCCCTCAGCGTCAAATAAGAGATGTGCTGGTGTG	2135
Qy	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2136	GCTGGAAAGCCTCAGTTTGGTCTCTACAGCCTCTAAGAACATTTATTCTCATGTGGAA	2195
Qy	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2196	GCCAGTCCCTCACCATAGAGATGAGAGGCACATCACATCTGTAAACAAACCTGAAAC	2255
Qy	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2256	TTGAGTATTATCATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTCACAGCTTGGT	2315
Qy	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla	780
Db	2316	AACTTGAAGAACCTTACAAAGCTCATATGGGATACATAAGATGAATGAAGAAGATGCT	2375
Qy	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2376	ATAAACCTAGCTCAAGGCCCTGAAAACCTGAAGAAGATGTGTATTATTCATTTCAGCCAC	2435
Qy	801	LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys	820
Db	2436	TTGTCTGACATTCGAGAGGAATGGATTCATAGTCAAGTCTCTGTCAAGTGAACCCCTGT	2495
Qy	821	AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu	840
Db	2496	GACCTTGAAGAAATTCATATTAGTCTCCTGCTGCTGTCTGCAATGCAGTGAAATCCTA	2555
Qy	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2556	GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATCTCTGTATTTATCAGAAAATTA	2615
Qy	861	GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln	880
Db	2616	GAAGAAGATGGAATGAAGCTCTTCATGAACATGATCGACAGATGAACGCTGTAGAACAG	2675
Qy	881	LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2676	CTCACCCAGCTGATGCTGCCCTGGGCTGTGAGTGTGAAGCGACCTTGAGCAGCCTTGT	2735
Qy	901	LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr	920
Db	2736	AAACATTTGGAGAGAGTCCCAACATCGCTCAAGCTTGGGTTTGA AAAACTGGAGACTCACA	2795
Qy	921	AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln	940
Db	2796	GATACAGATTTAGAATTTTAGTGCAATTTTGGAAAGAACCCCTCTGAAAACATCTCCAG	2855
Qy	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrTrpLeuAlaPheMetGlyVal	960
Db	2856	CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGATGGATGGCTTGCTTCATGGGTGTA	2915
Qy	961	PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp	980
Db	2916	TTTGAGAAATCTTAAGCAATTTAGTGTGTGTGTACCTTTAGTACTAAGAAGAAATTTAC	2975
Qy	981	ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla	1000
Db	2976	CCAGCATTTAGTCAGAAACCTTAGCCAGGTGTTATCCAAAGTTTAACCTTTCTCGAAGAAG	3035
Qy	1001	ArgLeuValGlyTyrGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3036	AGGCTGTTGGGTGGCAATTTGATGATGATCATCTCAGTGTATTACAGGTGCTTTTAA	3095
Qy	1021	LeuValThrAla 1024	
Db	3096	CTAGTAACCTGCT 3107	

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RESULT 6
US-09-841-739-1
; Sequence 1, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred No.: 0 Length: 3133
Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0

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Dib

Db 576 CGCATTCGCATCTCTGGGGCTCCGAAAGTGCAGGCTCTGACCAAGTTCAAAATTCGTC 635  
Qy PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220  
Db TTTCTTCTCCGCTCTCAGCAGGCCCCAGGGTGAGCTTTTGAACCCCTCTGTGATCAACTC 695  
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240  
Db CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 755  
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
Db CAGAGGGTCTTTTCCCTCTCTGATGGCTACAAATGAATTCAGGCCCCAGAACTGCCCAAG 815  
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280  
Db ATCGNAGCCCTGATAAAGGAACCCACCGCTTCAGAACATGGTCATCTCACCACCTACC 875  
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
Db ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG 935  
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
Db ACAGAGACAGCGCCCGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGC 995  
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
Db TTGTGCTCCAAATTCAGAAATCCAGTGCTTGGAGAAATCATGAAGACCCCTCTCTTT 1055  
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
Db GTGGTCATCACTTGTGCAATCCAGATGGTGAAGTGAGTTCACACTCTCACACACAACA 1115  
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGly 380  
Db ACGTGTTCCTACATCTTATGATCTGTGTATACAGAAAAACAACACAAAAATAAAGGT 1175  
Qy 381 ValAlaLaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
Db GTGGCTGCAGTGACTTCATTCGGAGCCTGGACCCTGTGGAGACCTAGCTGAGGAGGT 1235  
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Db GTGTCTCCCAAGTTTGAATTCGAACCTGCAGGATGTGCCAGCGTGAATGAGGATGTC 1295  
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db CTGCTGACAACTGGGCTCCTCTGTAAATATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA 1355  
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460  
Db TTCCTTCAAGTCAATTCAGAGGTACACAGCAGCAAGCACTCAGCAGGTTATFTGAGC 1415  
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
Db TCTCATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTCCATT 1475  
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db TCGGACATTTACATCCACTTATAGCAGCCTGCTCGGGTACACCTGTGGGTCTCTGTGAA 1535  
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520  
Db GCCACAGGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1595  
Qy 521 LeuSerIleAlaLysArgProLeuTriArgGlnGluSerLeuGlnSerValLysAsnThr 540  
Db CTTTCCATCGCAGAGGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC 1655  
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db ACTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715

Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
Db TTATATCAAGAGATGACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAA 1775  
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600  
Db GGTAAAGCTTATATATCAACTCAGGAACATCCCGGATTAATTTGACTTCTTTGAA 1835  
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620  
Db CATTTGCCCAATTTGCAAGTGTCTGACTTCATTAACCTGGAGCTTTATGGGGAGCT 1895  
Qy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640  
Db ATGGCTTCATGGGAAAGGCTCGAGAACACAGGTGGAATCCACATGGAAGAGGCCCA 1955  
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660  
Db GAAACCTACATTCCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 2015  
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db ACTCTGGAGGTCACTCCGGATTTCAAGAGTTGAATAAGCAAGATATCACATATCTG 2075  
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Db GGGAAATATTCAGCTCTGCCACAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2135  
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db GCTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCTCATGTGAA 2195  
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Db GCCAGTCCCTCCACCATAGAAGATGAGAGGCACATCACATCTGTAAACAAACCTGAAACC 2255  
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db TTGAGTATTCATGACCTACAGNATCACGGCTGCCGGGTGGTCTGCTGACGACAGCTTGGT 2315  
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
Db AACTTGAAGAACCTTACAAAGCTCATATGGATAACATAAAGATCAATGAAGAAATGCT 2375  
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Db ATAAACCTAGCTGAAGGCTGAAAAACCTGAAGAAAGATGTGTTTATTTTCATTTGACCCAC 2435  
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Db TTGCTGTACATTTGGAGAGGAAATGGATTCATAGTCAAGTCTCTGTCGAAGTGAACCCCTGT 2495  
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db GACCTTGAAGAAATTCATTTAGTCTCCTGCTGCTGTGCTGCAAAATGCAGTGAATAATCCTA 2555  
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCAATTCCTGATTTATCAAAAAATTTACCTG 2615  
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Db GAAAAAGATGAAATGAAGCTCTTCATGAATGATCGACAGATGAACGTGTAGAACAG 2675  
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db CTCACCGACTGTATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTG 2735  
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
Db AAACATTTGGAGGAGGTCCCAACACTCGTCAAGCTTGGTTGGTTGAAAAACTGGAGACTACA 2795



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QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
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Db 1381 TCTCATGAGCAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTTCATT 1440

QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
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Db 1441 TCGACATATTACATCCACTTATAGCAGCGCTGCTCCGGTACACCTGTGGGTGTCATCTGTGGAA 1500

QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
|||||
Db 1501 GCCACCAAGGCGTGTATGAGACACCTCGCAGCAGTGTATCAACACGCGTGCCTTCTCGGA 1560

QY 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540
|||||
Db 1561 CTTTCCATCCCAAGAGCGCTCTCTGGAGACAGGAATCTTGCACAACTGTGAAAAACACC 1620

QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
|||||
Db 1621 ACTGAGCAAGAAATCTTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680

QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
|||||
Db 1681 TTATATCAAGAGAGTATCATCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 1740

QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
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Db 1741 GGTAAGAGCTATATATCACTCAGGGAACATCCCCGATTAATTTATTTGACTCTTTGAA 1800

QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620
|||||
Db 1801 CATTTGCCAATTTGCAAGTGCCTGGACTTCATTAACCTGGACTTTTATGGGGGAGCT 1860

QY 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
|||||
Db 1861 ATGCTCTCATGGGAAAAGGCTGCAAGACACAGTGGAAATCCACATGGAAGAGGCCCA 1920

QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
|||||
Db 1921 GAACCTACATTTCCAGCAGGGCTGTATCTTTGTTCTCACTGGAAGAGGAATTCAGG 1980

QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLe 680
|||||
Db 1981 ACTCTGGAGGTCACACTCCGGGATTTCCAGAAAGTTGAATAAGCAAGATATCAG-ATATCT 2039

QY 680 uGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVa 700
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Db 2040 GGGGAAAATATTCAGCTCTGCCAAGCCTCAGGCTGCAATAAAGAGATGTGCTGGTGT 2099

QY 700 lAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGl 720
|||||
Db 2100 GGCTTGGAGGCTCAGTTTGGTCTCAGCACCCTGTAAGAACATTTATTTCTCTCATGGTGA 2159

QY 720 uAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysTh 740
|||||
Db 2160 AGCCAGTCCCCTCACCATAGAAGATGAGAGGCACATCACATCTCTAACAACCTGAAAAAC 2219

QY 740 rLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGl 760
|||||
Db 2220 CTTGAGTATTATGACCTACAGAAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGG 2279

QY 760 yAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAl 780
|||||
Db 2280 TAACCTGAAGNACCTTACAAGCTCATATGGATAACATAAAGATGAATGAGAGATGC 2339

QY 780 aIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi 800
|||||
Db 2340 TATAAACTAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTATTATTTGACCCCA 2399

QY 800 sLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCy 820
|||||
Db 2400 CTTGCTGACATTTGGAGGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCGTG 2459
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QY 820 sAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLe 840
|||||
Db 2460 TGACCTTTGAAGAAATTCATATTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2519

QY 840 uAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLe 860
|||||
Db 2520 AGCTCAGAAATCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATTACCT 2579

QY 860 uGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGl 880
|||||
Db 2580 GGAAAAACATGGAAATGAAAGCTCTTCATGAACTGATCGACAGATGAACGTGTAGAACAC 2639

QY 880 nLeuThrAlaLeuMetLeuProTrpGlyCysAspValIcInGlySerLeuSerSerLeuLe 900
|||||
Db 2640 GCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTT 2699

QY 900 uLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuTh 920
|||||
Db 2700 GAAACATTTTGGAGAGGTCCCAACTCGTCAAGCTTTGGGTTGAAAACTGGAGACTCAC 2759

QY 920 rAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGl 940
|||||
Db 2760 AGATACAGAGATTAGAATTTTAGTGTGATTTTGGAAAGAACCCCTCTGAAAAACTTCCA 2819

QY 940 nGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVa 960
|||||
Db 2820 GCAGTTCAATTTGGCGGAAATCGTGTGACAGTGTGATGGCTTGCCTTCATGGGTGT 2879

QY 960 lPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAs 980
|||||
Db 2880 ATTTGAGAATCTTAAGCAATTAGTGTGTTTTTGTAGTACTAAGAAATTTCTTACCTGA 2939

QY 980 pProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAl 1000
|||||
Db 2940 TCCAGCATTAGTCAGAAAACTTAGCCAAGTGTATTCAAGTTAACTTTCTTCGCAAGAGC 2999

QY 1000 aArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLy 1020
|||||
Db 3000 TAGCCTTTGGTGGCGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3059

QY 1020 sLeuValThrAla 1024
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Db 3060 ACTAGTAACCTGCT 3072

RESULT 8
US-10-156-733-14
; Sequence 14, Application US/10156733
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; FILE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477
; CURRENT APPLICATION NUMBER: US/10/156,733
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-733-14

Alignment Scores:
Pred. No.: 0 Length: 3219
Score: 923.00 Matches: 1023
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 90.14% Indels: 2
DB: 41 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-156-733-14 (1-3219)
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
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QY 740 rLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuG1 760
Db 2364 CTGTGATTATCATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGG 2423
QY 760 yAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAl 780
Db 2424 TAACTTGAAGAACCTTACAAGCTCATATGATGATAACATAAAGATGAATGAAGAAGATGC 2483
QY 780 aIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi 800
Db 2484 TATAAACTAGCTGAAGGCTGAAAACCTGAAGAGATGCTGTTTATTTCATTTGACCCA 2543
QY 800 sLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCy 820
Db 2544 CTGTCTGCATGTGAGAGGGAATGGATTACATGATGATCAAGTGTCTGCAAGTGAACCTG 2603
QY 820 sAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLe 840
Db 2604 TGACCTTGAAGAAATTCATATTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2663
QY 840 uAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrIle 860
Db 2664 AGCTCAGAAATCTCAAAATTTGGTCAAACTGAGCAATCTTGATTTATCAGAAAATTAACCT 2723
QY 860 uGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluG1 880
Db 2724 GGAAGAAGATGAATGAAGCTTTCATGAACTGATGCACAGATGAACGCTGCTAGAACA 2783
QY 880 nLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLe 900
Db 2784 GCTACCGCAGCTGATGCTGCGCTGGGCTGTGACGTGCAAGGCGAGCCTGAGCAGCTGTT 2843
QY 900 uLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuTh 920
Db 2844 GAAACATTTGGAGGAGGTCCTCAAACTGCTCAAGCTTGGTTGAAAAACTGGAGACTCAC 2903
QY 920 rAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheG1 940
Db 2904 ACATACAGAGATTAGAAATTTTAGTGATTTTGGAAAGAACCTCTGAAAAACTTCCA 2963
QY 940 nGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVa 960
Db 2964 GCAGTTGATTTGGGGGAAATCGTGTGAGCAGTGTGATGGATGGCTTGCCTTCATGGGTG 3023
QY 960 lPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAs 980
Db 3024 ATTTGGAATCTTAAGCAATTAGTGTTTTGACTTTTAGTAAAGAAATTTCTACCTGA 3083
QY 980 pProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAl 1000
Db 3084 TCCAGCATTAGTCAGAAAACTTAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGC 3143
QY 1000 aArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3144 TAGGCTGTGGTGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3203
QY 1020 sLeuValThrAla 1024
Db 3204 ACTAGTAACCTGCT 3216
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RESULT 9

PCT-US01-07143-23

; Sequence 23, Application PC/TUS0107143

; GENERAL INFORMATION:

; APPLICANT: SMITHKLINE BEECHAM CORPORATION

; APPLICANT: SMITHKLINE BEECHAM p.l.c.

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP50016

; CURRENT APPLICATION NUMBER: PCT/US01/07143

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/187,107

; PRIOR FILING DATE: 2000-03-06

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; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-07143-23
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Alignment Scores:
Pred. No.: 0 Length: 3213
Score: 922.00 Matches: 1022
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 90.04% Indels: 2
Db: 1 Gaps: 0
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US-09-697-089-2 (1-1024) x PCT-US01-07143-23 (1-3213)

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QY 2 AsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLys 21
Db 142 AATTTCAATAAGGACAAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTGCTATATAAG 201
QY 22 GlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIleIle 41
Db 202 CAAATCACAGATGACATATTGTATGGAATGTTCTGAATCGCGAAGAAAGTAACATCAT 261
QY 42 CysCysGluLysValGluLysAspAlaArgGlyIleIleHisMetIleLeuLysLys 61
Db 262 TCGTCGGAGAGGTGGAGCAGGATGCTGCTAGAGGATCAATTCACATGATTTTGAAGAAAG 321
QY 62 GlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeuPhe 81
Db 322 GGTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCTCTATTT 381
QY 82 GlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspLeu 101
Db 382 CAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTG 441
QY 102 AlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGly 121
Db 442 GCTCAGATTAAAGACTTGTACCAATCCCATCTTTCTGAACCTTTTATCCCTGCT 501
QY 122 GluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrpArg 141
Db 502 GAAGATATTGACATTTATTTTAACTTGAAGACACCTTCACAGAACCTCTCCTGTGGAGG 561
QY 142 LysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeu 161
Db 562 AAGGACCAACACCATCAGCGCTGGAGCAGCTGACCCCTGAATGGCTCTCCTGAGGCTCT 621
QY 162 GlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArg 181
Db 622 CAGACCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAGCGCA 681
QY 182 IleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhe 201
Db 682 ATTGCCATGCTCTGGGGCTCCGAAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCCT 741
QY 202 PheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuLeu 221
Db 742 TTCTCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTC 801
QY 222 AspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGln 241
Db 802 GATATACCTGGCAATCAGGAAGCAGACATTCATGGCCATCTGCTGANGCTGGCGAG 861
QY 242 ArgValLeuPheLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGluIle 261
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Db 862 AGGGTCTTTCTCTTCTGATGGCTACAAATGAATTCAGAGCCCAAGCTGCCAGAAATC 921  
 QY 262 GluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 281  
 Db 922 GAAGCCCTGATAAAGAAACACCCGCTTCAGAGCATGGTCATCGTCACCACTACCAC 981  
 QY 282 GluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThr 301  
 Db 982 GAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGTGGGGGATATGACA 1041  
 QY 302 GluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeu 321  
 Db 1042 GAAGACAGCGCCAGGCTCTCATCCGAGAGTGGCTGATCAAGGAGCTTCTGAAGGCTTG 1101  
 QY 322 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheVal 341  
 Db 1102 TTGCTCCAAATTCAGAAATCCAGGTGCTTGGAGAAATCTCATGNAGACCCCTCTCTTGTG 1161  
 QY 342 ValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThr 361  
 Db 1162 GTCATCTGTGTCATTCAGATGGGTGAAAGTGAGTTCACCTCTCACACAAACAAG 1221  
 QY 362 LeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGlyVal 381  
 Db 1222 CTGTTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGGTGTG 1281  
 QY 382 AlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyVal 401  
 Db 1282 GCTGCAAGTGACTTCATTCGAGCCCTGGACCATCTGGAGACCTAGCTCTGGAGGTGTG 1341  
 QY 402 PheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspValLeu 421  
 Db 1342 TTCTCCACAAAGTTTGATTTGCAAGTGCAGGATGCTGCCAGCGTGAATGAGGATGCTCTG 1401  
 QY 422 LeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhe 441  
 Db 1402 CTGACAACTGGGCTCTCTTAATATACAGCTCAAGGTTCAAGGCCAAAGTATAAATTC 1461  
 QY 442 PheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThrSer 461  
 Db 1462 TTTCAAGTCATTCAGAGTACACAGCAGGACGAGACTCAGCAGTTTATTTGAGCTCT 1521  
 QY 462 HisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSer 481  
 Db 1522 CATGAGCCAGAGGTGACCAAGGGAATGTTACTTGCAGAAATGGTTTCCATTTTCG 1581  
 QY 482 AspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAla 501  
 Db 1582 GACATTACATCCACTTATAGACGCTGCTCCGGTACACCTGTGGGTCACTGTGGAAGCC 1641  
 QY 502 ThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeu 521  
 Db 1642 ACCAGGCTGTATGAAGACCTCGCAGCAGTGTATCAACACCGCTGCCCTTCGGACTT 1701  
 QY 522 SerIleAlaLysArgProLeuThrArgGlnGlnLysSerLeuGlnSerValLysAsnThrThr 541  
 Db 1702 TCCATGCCCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCCACT 1761  
 QY 542 GluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHisLeu 561  
 Db 1762 GAGCAAGAAATTTCTGAAGGCATTAACATCAATTCCTTTGTAGAGTGTGCATCCCAATTA 1821  
 QY 562 TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGlnGly 581  
 Db 1822 TATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGNAGCTTTCTTCAAGGT 1881  
 QY 582 LysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrIleuPheAspPheGluHis 601  
 Db 1882 AAAAGCTTATATATCAACTCAGGGAACATCCCGATTACTTATTTGACTTCTTTGAAACAT 1941  
 QY 602 LeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAlaMet 621

Db 1942 TTGCCCAATTTGCAAGTGCCCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATG 2001  
 QY 622 AlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaProGlu 641  
 Db 2002 GCTTCATGGAAAGGCTGCAAGAGACACAGGTGGAATCCACATGAAGAGCCCAAGAA 2061  
 QY 642 ThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThr 661  
 Db 2062 ACCTACATTTCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGACT 2121  
 QY 662 LeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlu 681  
 Db 2122 CTGAGGTCACACTCCGGGATTTAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGG 2180  
 QY 681 YLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAla 701  
 Db 2181 GAAATATTTACGCTCTGCCACAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGC 2240  
 QY 701 aGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAl 721  
 Db 2241 TGGAAAGCCTCAGTTGGTCTCTCAGCACCTGTAAAGACATTTATTTCTCATGGTGGAGC 2300  
 QY 721 aSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLe 741  
 Db 2301 CAGTCCCTCACCATAGAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAACTT 2360  
 QY 741 uSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAs 761  
 Db 2361 GAGTATTTCATGACTACAGAAATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGGTAA 2420  
 QY 761 nLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 781  
 Db 2421 CTTGAAGAACCTTACAAAGCTCATATGGATGAATAACATAAGATGAATGAAGAGATGCTAT 2480  
 QY 781 eLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLe 801  
 Db 2481 AAAACTAGCTGAAGGCTGNAANAACCTGAAGAAGATGTGTTTATTTTCACTTGACCACCT 2540  
 QY 801 uSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAs 821  
 Db 2541 GTCTGACATTTGGAGAGGAATGGATTACATAGTCAAGTCTCTCTCAAGTGAACCCCTGTA 2600  
 QY 821 pLeuGluGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIleLeuAl 841  
 Db 2601 CCTTGAAGAAATTCAAATTAGTCTCTGCTGCTTGTCTGCAAAATGCAGTGAATTCCTAGC 2660  
 QY 841 aGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 861  
 Db 2661 TCAGATCTTCACAAATTTGGTCAAACTGACCATCTTGATTTATCAGAAATTTACCTGGA 2720  
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 Db 2721 AAAAGATGGAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACGTGTAGAACAGCT 2780  
 QY 881 uThrAlaLeuMetLeuProThrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 901  
 Db 2781 CACCGCCTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCGCTGAGCAGCCTGTGTGAA 2840  
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 Db 2841 ACATTTGGAGGAGGTCCCACTCGTCAAGCTTGGGTTGAAAGAACTGGAGACTCACAGA 2900  
 QY 921 pThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlu 941  
 Db 2901 TACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAGAACCCCTGTAAAAAATTTCCAGCA 2960  
 QY 941 nLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrTrpLeuAlaPheMetGlyValPh 961  
 Db 2961 GTTGAATTTGGCGGGAATCGTGTGACAGTGTGATGGCTTGCCTTCATGGGTGATTT 3020  
 QY 961 eGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspPr 981  
 Db 3021 TGAGATCTTAAGCAATTAGTGTGTTTTGACTTTTAGTACTAAAGAAATTTCTACCTGATCC 3080

QY 981 oAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAlaAr 1001  
|||||  
Db 3081 AGCATAGTCAGAAACTAGCCAGTGTATCCAAAGTAATTTCTGCAGAGAGCTAG 3140  
QY 1001 gLeuValGlyTrpGlnPheAspAspLeuSerValIleThrGlyAlaPheLysLe 1021  
|||||  
Db 3141 GCTTGTGGTGGCAATTTGATGATGATCTCAGTGTATTACAGGTGCTTTTAAACT 3200  
QY 1021 uValThrAla 1024  
|||||  
Db 3201 AGTAACTGCT 3210

## RESULT 10

US-10-221-097-23  
; Sequence 23, Application US/10221097  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdock, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Xiang, Zhaoying  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GPS0016  
; CURRENT APPLICATION NUMBER: US/10/221,097  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: PCT/US01/07143  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/187,107  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: 60/236,874  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/188,916  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/237,846  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 3213  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-221-097-23

## Alignment Scores:

Pred. No.:	0	Length:	3213
Score:	922.00	Matches:	1022
Percent Similarity:	99.80%	Conservative:	0
Best Local Similarity:	99.80%	Mismatches:	1
Query Match:	90.04%	Indels:	2
DB:	42	Gaps:	0

US-09-697-089-2 (1-1024) x US-10-221-097-23 (1-3213)

QY 2 AsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLys 21  
|||||  
Db 142 AATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATAAAG 201  
QY 22 GlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIleIle 41  
|||||  
Db 202 CAAATCACAGATGACCTATTGTATGGAAATGTTCTGAATCGCGAAGAAATCAATCATTT 261  
QY 42 CysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLys 61  
|||||  
Db 262 TGCTCGGAGAGGTGGACGAGGATGCTGCTAGAGGATCATTCACATGATGTTTGAAGAAG 321  
QY 62 GlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeuPhe 81  
|||||  
Db 322 GGTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGGAGTGAACATATCCTCTATT 381  
QY 82 GlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspLeu 101  
|||||  
Db 382 CAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTG 441

QY 102 AlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGly 121  
|||||  
Db 442 GCTCAGAGATTTAAAGGACTGTGACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGT 501  
QY 122 GluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrpArg 141  
|||||  
Db 502 GAAGATATTGACATATTATTTTAACTTGAAAAGCACCTTCACAGAACCTGCTCTGTGGAGG 561  
QY 142 LysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuGlnAlaLeu 161  
|||||  
Db 562 AAGGACCAACACCATACCGCGTGGAGCAGCTGACCTGAATGGCTCTCGAGGCTCTT 621  
QY 162 GlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArg 181  
|||||  
Db 622 CAGAGCCCTGTCATCTGAAGGGGNACTGGCAAGGCAAGTCCACTCTGCTGCAGCGCA 681  
QY 182 IleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhe 201  
|||||  
Db 682 ATTGCCATGCTCTGGGGCTCCGAAAGTCAAGGCTCTCACCAGTTCAAAATTCGTCTTC 741  
QY 202 PheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuLeu 221  
|||||  
Db 742 TTCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCCG 801  
QY 222 AspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGln 241  
|||||  
Db 802 GATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGGCAG 861  
QY 242 ArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGluIle 261  
|||||  
Db 862 AGGGTCTCTTTCTTCTGATGGCTACAATGAATCAAGCCCAAGAACTGCCAGAAATC 921  
QY 262 GluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 281  
|||||  
Db 922 GAAGCCCTGATAAAGGAAACCCAGCTTCAAGAACATGGTCATCGTCCACCCTACCAC 981  
QY 282 GluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThr 301  
|||||  
Db 982 GAGTGCTCAGGCACATACGGCAGTTGGTGGCTGACTGCTGAGGTGGGGATATGACA 1041  
QY 302 GluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeu 321  
|||||  
Db 1042 GAAGCAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTCTGAAAGGCTTG 1101  
QY 322 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheVal 341  
|||||  
Db 1102 TTGCTCCAAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGG 1161  
QY 342 ValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrThrThr 361  
|||||  
Db 1162 GTCATCAGTTGTGCAATCCAGATGGTGAAGTGAGTTCCACTCTCACACACAAACAAG 1221  
QY 362 LeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGlyVal 381  
|||||  
Db 1222 CTGTTCCATACCTTCTATGATCTGTGTATACAGAAAAACACACAAACATAAAGGTG 1281  
QY 382 AlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlyVal 401  
|||||  
Db 1282 GCTGCAAGTGACTTCTATTCGGAGCCCTGGACCACTGTGGAGAGCCCTAGCTCTGGAGG 1341  
QY 402 PheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspValLeu 421  
|||||  
Db 1342 TTCTCCCAACAAGTTGATTTCCAGCTGCAGGATGTGTCAGCGCTGAATCAGGATGCTCTG 1401  
QY 422 LeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhe 441  
|||||  
Db 1402 CTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATTC 1461  
QY 442 PheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSer 461  
|||||  
Db 1462 TTTTCAAGATCATTCAGGAGTACAGCAGGACGAAGACTCAGCAGTTTATTGAGCTCT 1521

Qy	462	HisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSer	481
Db	1522	CATGAGCCAGAGAGGTGACCAAGGGGATGGTTACTTTCGACAAAAATGGTTTCATTCG	1581
Qy	482	AspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAla	501
Db	1582	GACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGGAAGCC	1641
Qy	502	ThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGlyLeu	521
Db	1642	ACCAGGGCTGTATGAAAGCACCTCGCAGCAGTGTATCAACACGGCTGCTTCGGACTT	1701
Qy	522	SerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrThr	541
Db	1702	TCCATGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGGTGTGAAAAACACCACT	1761
Qy	542	GluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHisLeu	561
Db	1762	GAGCAGAAAAATCTGAAGGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTA	1821
Qy	562	TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGlnGly	581
Db	1822	TATCAAGAGATACATCCAAATCAGCCCTGACCCCAAGAAATTTGAAGCTTCTCTTCAAGT	1881
Qy	582	LysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGluHis	601
Db	1882	AAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTGACTTCTTTTGAACAT	1941
Qy	602	LeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyValMet	621
Db	1942	TTGCCCAATTTGTCCAAGTCCCTGGACTTCATTAACATGGACTTTTATGGGGAGCTATG	2001
Qy	622	AlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaProGlu	641
Db	2002	GCTTCATGGGAAAAGGCTCGACAGACACAGGTGGAAATCCACATGGGAAGAGCCCGCAAA	2061
Qy	642	ThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThr	661
Db	2062	ACCTACATTTCCAGCAGGCGTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACT	2121
Qy	662	LeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlu	681
Db	2122	CTGGAGGTACACTCCGGGATTTCAGCAAGTTGAATAAGCAAGATATACAG-ATATCTGGG	2180
Qy	681	YLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAl	701
Db	2181	GAANAATATTCAGCTCTGCCACAAGCCTCAGGCTGCANAATAAGAGATGTGCTGGTGTGGC	2240
Qy	701	aglySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAl	721
Db	2241	TGGAAGCCTCAGTTTGGTCCTCAGCACCTGTGAAGAACATTATTCTCTCATGGTGGGAAGC	2300
Qy	721	aSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLe	741
Db	2301	CAGTCCCCCTCACATAGAAGATGAGAGGCATCACATCTGTACAACACTGTAAACACTT	2360
Qy	741	uSerIleHisAspLeuGlnAsnGluArgLeuProGlyGlyLeuThrAspSerLeuGlyAs	761
Db	2361	GAGTATTATGACCTACAGAAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGTAA	2420
Qy	761	nLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle	781
Db	2421	CTTGAAGAACCTTACAAAGCTCATATGGAATAACATAAAGATGAATGAAGAAGATGCTAT	2480
Qy	781	eLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLe	801
Db	2481	AAAACTAGCTGAAGGCTTGAAAAACCTGAAGAAGATGTGTTATTATTTGACCCACTT	2540
Qy	801	uSerAspIleGlyGluClyMetAspTyrIleValLysSerLeuSerGluProCysAs	821
Db	2541	GTCTGACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGA	2600
Qy	821	pLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAl	841

[illegible]

QY	89	LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu	108
DB	736	CTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTG	795
QY	109	TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspLeuAspLeuIlePhe	128
DB	796	TACCAATACCCCATCTTTTCUGAACTTTTATCCCTTGGTGAAGATATTGACATTATTTT	855
QY	129	AsnLeuLysSerThrPheThrGluProValLeuTyrArgLysAspGlnHisHisArg	148
DB	856	AACCTTGAAGAAGCACCTTCACAGAACCTGCTCTGTGGAGGAAGGACCAACACCATCACGC	915
QY	149	ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu	168
DB	916	GTGAGCAGCTGACCTCGAATGGCTTCCTGCAAGGCTCTTCAGAGCCCTGCATCATTTGAA	975
QY	169	GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTyrGlySer	188
DB	976	GGGCAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGAATTGCCATGCTCTGGGGCTCC	1035
QY	189	GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla	208
DB	1036	GGAAAGTGCAGAGGCTGTGACCAAGTTCAAATTCGTCTCTCTCCGTCTCAGCAGGGCC	1095
QY	209	GlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg	228
DB	1096	CAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACCAATCAGG	1155
QY	229	LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp	248
DB	1156	AAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGCAGAGGGTCTCTTTCTCTCTTGAT	1215
QY	249	GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn	268
DB	1216	GGCTACAAATCAAGTTCAGCCAGAACTGCCAGAAATCGAAGCCCTGATTAAGGAAAC	1275
QY	269	HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg	288
DB	1276	CACCGCTTCAAGAACATGTCATGTCACCATCACCTGAGTGGCTGAGGCACATACGG	1335
QY	289	GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu	308
DB	1336	CAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTCTC	1395
QY	309	IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer	328
DB	1396	ATCCGAGAAGTGTGATCAAGGAGCTGCTGAAGGCTGTTGTCTCCAAATTCAGAAATCC	1455
QY	329	ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln	348
DB	1456	AGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTGTGGTCATCATCTGTGCAATCCAG	1515
QY	349	MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp	368
DB	1516	ATGGGTCAAAAGTGAGTTCCACTCTCACACACAAACACGCTGTTCATACCTCTCATGAT	1575
QY	369	LeuLeuIleGlnLysAsnLysHisLysGlyValAlaAlaSerAspPheIleArg	388
DB	1576	CTGTTGTATACAGAAAAACAACAACAATAAAGGTGTGGCTGCAAGTGACTTCATTCGG	1635
QY	389	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe	408
DB	1636	AGCCTGGACCACTGTGAGACCTAGCTCTGGAGGGTGTCTCTCCACAGTTTGATTTC	1695
QY	409	GluLeuGlnAspValSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys	428
DB	1696	GAATGTCAGGATGTGTCACGCTGAATGAGGATGTCCTGCTGCACACTGGGCTCCTCTGT	1755
QY	429	LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu	448
DB	1756	AAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATTCCTTCAAGTCAATCCAGGAG	1815

Qy	449	TyrThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGluProGluValThr	468
Db	1816	TACACACAGAGAGAGACTCAGCAGCTTATTGTCGCTCTCATGAGCCAGAGAGGTGACC	1875
Qy	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
Db	1876	ANGGGGAATGGTTACTTGCAGAAATATGGTTTTCCATTTTGGACATTTACATCCACTATTAGC	1935
Qy	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
Db	1936	AGCGTCGTCGGGTACACCTGTGTGGTCATCTGTGGAAGCCACCAGGGCTGTTATGAAGCAC	1995
Qy	509	LeuAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
Db	1996	CTCGACAGCTGTATCAACACGGCTGCCCTCTCGGAGTTTCCATGCCCAAGAGGCCCTCTC	2055
Qy	529	TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla	548
Db	2056	TGGAGACAGGAACTTTTGCNAAGTGTGAACACACCCTGAGCAGAAATTTCTGNAAGCC	2115
Qy	549	IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
Db	2116	ATAAACATCAATTCCTTGTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAA	2175
Qy	569	SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	588
Db	2176	TCAGCCCTGAGCCAGAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCAACTCA	2235
Qy	589	GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla	608
Db	2236	GGGAACATCCCGCATTTACTTTTGTGACTTCTTTGAACATTTGCCCAATTTGTGCAAGTGCC	2295
Qy	609	LeuAspPheIleLysLeuAspPheTyrGlyIleAlaMetAlaSerTrpGluLysAlaAla	628
Db	2296	CTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTTCATGGGAAAGGCTGCA	2355
Qy	629	GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla	648
Db	2356	GAAGACACAGGTGGAATCCACATGGAAGAGGGCCCGCAAAACCTACATTTCCAGCAGGGCT	2415
Qy	649	ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp	668
Db	2416	GTATCTTTGTCTTCAACTGGAGCAGGAATTCAGAGCTCTCGGAGGTCACTCCGGAT	2475
Qy	669	PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaThr	688
Db	2476	TTTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGAAATAATTTCAGCTCTGCCAC	2534
Qy	688	rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe	708
Db	2535	AAGCCTCAGGCTGCATAAAGAGATGTCTGTGTGGTGTGGAGCCCTCAGTTTGGTCTCT	2594
Qy	708	uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs	728
Db	2595	CAGACCTGTGAAGAATTTATTTCTCTATGTGGAAGCCAGTCCCTCCACCATAGAAGA	2654
Qy	728	pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs	748
Db	2655	TGAGGCGCATCATCATCTGTACAAACCTGAAACCTTGAGTATTCATGACCTACAGAA	2714
Qy	748	nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe	768
Db	2715	TCAAGCGCTCCGGTGGTCTGACTGCACAGCTTGGTAACTTGAAGAACCCTTACAAAGCT	2774
Qy	768	uIleMetAspAsnIleLysMetAsnGluAspAlaIleLysLeuAlaGluGlyLeuLys	788
Db	2775	CATTAATGGATAACATAAAGATGAATCAAGAAAGATGCTATAAAACTAGCTGAAGGCCGTAA	2834
Qy	788	sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMe	808
Db	2835	AAACCTCAAGAAGATGGTTTATTTTCATTTGACCCACTTGTCTGCATTTGAGAGGGAAT	2894
Qy	808	tAspTvrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa	828

|||||  
Db 2895 GGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAGAAATTCATTAAGT 2954  
Qy 828 lsercyscysleuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848  
Db 2955 CTCCTGCCTGTCTGCGAAATGCAAGTCAAAATCCTAGCTCAGAAATCTTCACAAATTTGGT 3014  
Qy 848 llyserleuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868  
Db 3015 CAACTGAGCATCTTGATTTATCAGAAATACCTGGAAAAAGATGGAATGAAGCTCT 3074  
Qy 868 whisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888  
Db 3075 TCATGAACATGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTG 3134  
Qy 888 pclycysaspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGl 908  
Db 3135 GGGCTGTGACGTGCAAGCAGCCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCCA 3194  
Qy 908 nLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAspThrGluIleArgIleLeuGl 928  
Db 3195 ACTCGTCAAGCTTGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTAGG 3254  
Qy 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948  
Db 3255 TGCATTTTTTGGAAAGAACCCCTCTGAAAACTTCAGCAGCTGGAATTTGGCGGGAATCG 3314  
Qy 948 gValSerSerAspGlyTyrLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968  
Db 3315 TGTGAGCAGTATGATGGCTTGGCTTCATGGGTATTTGAGAACTTAAGCAATTTAGT 3374  
Qy 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988  
Db 3375 GTTTTTTGACTTTACTAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 3434  
Qy 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrGlnPheAs 1008  
Db 3435 CCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCTAGGCTTGTGGTGGCAATTTGA 3494  
Qy 1008 pAspAspAspLeuSerValIleThr 1016  
Db 3495 TGATGATGATCTCAGTGTTATTACA 3519

RESULT 12

US-09-841-739-6  
; Sequence 6, Application US/09841739  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841.739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 3612  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-6

Alignment Scores:

Pred. No.: 0 Length: 3612  
Score: 827.00 Matches: 927  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 1  
Query Match: 80.76% Indels: 2  
DB: 32 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-841-739-6 (1-3612)

Qy 89 LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu 108  
Db 736 CTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTG 795  
Qy 109 TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIleIlePhe 128  
Db 796 TACCATAACCCCATCTTTTCTGAACCTTTATCCCTTGTGTGAAGATATTGACATTATTTT 855  
Qy 129 AsnLeuLysSerThrPheThrGluProValLeuTyrArgLysAspGlnHisHisArg 148  
Db 856 AACTTGAAAGACACCTTACAGAACCTGCTGTGTGGAGGAAGGACCAACACCATCACGCG 915  
Qy 149 ValGluGlnLeuThrLeuAsnGlyLeuGlnAlaLeuGlnSerProCysIleIleGlu 168  
Db 916 GTGAGACAGCTGACCTGAATGGCTCTCGAGGCTTTCAGAGCCCTTCATCAATTGAA 975  
Qy 169 GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTyrGlySer 188  
Db 976 GGGGAATCTGCAAGGCAAGTCCACTCTGTGCAAGCAATTGCCATGCTCTGGGGCTCC 1035  
Qy 189 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208  
Db 1036 GGAAGTCAAGGCTCTGACCAAGTTCAATTCGTCTTCTTCCCTCGCTCAGCAGGGCC 1095  
Qy 209 GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg 228  
Db 1096 CAGGTGGACATTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCAG 1155  
Qy 229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248  
Db 1156 AAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGAGAGGGTTCTTTCTCTTGAT 1215  
Qy 249 GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn 268  
Db 1216 GGCTACAAATGAATTCAGCCCAAGCTGCCAGAAATCGAAGCCCTGATAAAGAAAC 1275  
Qy 269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288  
Db 1276 CACCGCTTCAAGAACATGGTCATCGTCACCACTACCACCTGAGTGGCTGAGGCACATACGG 1335  
Qy 289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308  
Db 1336 CAGTTTGGTGCCCTGACTGCTGAGTGGGGATATGACAGAGACAGAGCGCCAGGCTCTC 1395  
Qy 309 lIeArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer 328  
Db 1396 ATCCGAGAAGTGTGATCAAGAGCTTCTGAAGCTTGTGTGCTCCAAATTCAGAAATCC 1455  
Qy 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCysAlaIleGln 348  
Db 1456 AGGTGCTTGAGGAATCTCATGAGACCCCTCTCTTTGTGGTCATCCTGTGCAATCCAG 1515  
Qy 349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368  
Db 1516 ATGGGTGAAAGTGAGTTCCACTCTCACACAAACAGCGTGTTCATACCTCTCATGAT 1575  
Qy 369 LeuLeuIleGlnLysAsnLysHisLysHisGlyValAlaAlaSerAspPheIleArg 388  
Db 1576 CTGTTGATACAGAAAAACAAACAAATAAAGGTGGGTGCAAGTTCATTCATTCGG 1635  
Qy 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408  
Db 1636 AGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCCACAAGTTGATTTC 1695  
Qy 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428  
Db 1696 GAACGTGAGGATGTGTCCAGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCCTCTGT 1755  
Qy 429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448  
Db 1756 AAATATACAGCTCAAGGTTTCAAGCCAAAGTATAAATTTCTTTTCAAGTCAATTCAGGAG 1815

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QY 449 TyrThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr 468
Db 1816 TACACAGCAGGACGAGACTCAGCAGTTTTATTGACGCTCTCATCAGCCAGAGAGGTGACC 1875
QY 469 LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer 488
Db 1876 AAGGGAAATGGTTACTTGCAGAAATGGTTTCCATTTGGACATTACATCCACTTTATAGC 1935
QY 489 SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis 508
Db 1936 ACCCTGCTCCGTCACACCTGTGGTCATCTGTGGAAAGCCACCGAGGCTGTATGAAAGCAC 1995
QY 509 LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu 528
Db 1996 CTCGACGAGCTATATCAACACGGCTGCCTTCTCGGACTTTCCATGCCCAAGAGGCTCTFC 2055
QY 529 TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla 548
Db 2056 TGGAGACAGGAATCTTGCAAAGTGTGAAACACACCCTGAGCAAGAAATTCGAAAGCC 2115
QY 549 IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568
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QY 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer 588
Db 2176 TCAGCCCTGAGCAAGAATTTGAAGCTTCTTTCAAGGTAAAAAGCTTATATATCAACTCA 2235
QY 589 GlyAsnIleProAspTyrLeuPheAspPheGluHisLeuProAsnCysAlaSerAla 608
Db 2236 GGGAAATCCCCGGATTACTTATTTGACTTCTTTGAACATTTTCCCAATTTGTGCAAGTGCC 2295
QY 609 LeuAspPheIleLysLeuAspPheTyrGlyAlaMetAlaSerTrpGluLysAlaAla 628
Db 2296 CTGGACTTCATTAAACTGGACTTTTATGGGGAGAGTATGGCTTCATGGGAAAGGCTGCA 2355
QY 629 GluAspThrGlyGlyIleHisMetGluAlaProGluThrTyrIleProSerArgAla 648
Db 2356 GAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGAGGGCT 2415
QY 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgasp 668
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QY 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaThr 688
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QY 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValle 708
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QY 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728
Db 2595 CAGCACCTGTGAAGACATTTATTTCTCTATGTTGGAAGCCAGTCCCTCCACCATAGAAGA 2654
QY 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGluAs 748
Db 2655 TGAGAGGCACATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACAGAA 2714
QY 748 nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768
Db 2715 TCAAGGGCTGCCGGTGGTCTGACTGACAGCTTGGTAACTTGAAGAACCTTTACAAAGCT 2774
QY 768 rIleMetaspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys 788
Db 2775 CATAATGGATAACATAAGATGAATGAAGAGATGCTATAAACTAGCTGAAGGCTCGAA 2834
QY 788 sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMe 808
Db 2835 AAACCTGAAGAGATGTGTTTATTTTCATTTGACCCACCTGCTGACATTTGGAGAGGAA 2894
QY 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828
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Db 2955 CTCCTGCTGCTTGTCTGCAATATGCAGTGAATAATCTTAGCTCAGATCTTCACAAATTTGGT 3014
QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868
Db 3015 CAACTGAGCATCTTGATTTATCAGAAATTTACCTGGAAAAAGATGGAATGAAGCTCT 3074
QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProThr 888
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QY 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGln 908
Db 3135 GGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCACCA 3194
QY 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGln 928
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QY 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
Db 3255 TGCATTTTTTGGAAAGAACCCCTCTGAAAAAATTTCCAGCAGTTGAATTTGGCGGAAATCG 3314
QY 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
Db 3315 TGTGACAGCTGATGATGGCTTGCCTTTCATGGTGTATTTGAGAAATCTTTAAGCAATTAGT 3374
QY 968 lPhePheAspPheSerThrLysGluPheLeuProaspProAlaLeuValArgLysLeuSe 988
Db 3375 GTTTTTTGACTTTAGTACTAAAGAAATTTCTACTGATCCAGCATTAGTCAGAAAACTTAG 3434
QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGlnAlaArgLeuValGlyTrpGlnPheAs 1008
Db 3435 CCAAGTGTATTCAAGTTAACTTTCTGCAAGAAGCTAGGCTGTTGGTGGCAATTTGA 3494
QY 1008 pAspAspLeuSerValIleThr 1016
Db 3495 TGATGATGATCATCAGTTGTTATTACA 3519
RESULT 13
PCT-US00-29643-4
; Sequence 4, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
PCT-US00-29643-4
Alignment Scores:
Pred. No.: 0 Length: 3615
Score: 827.00 Matches: 927
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 80.76% Indels: 2
DB: 1 Gaps: 0
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us-09-697-089-2 (1-1024) x PCT-US00-29643-4 (1-3615)

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QY 109 TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePhe 128  
DB 796 TACCATACCCCATCTTTTCTGAACTTTATCCCTTGGTGAAGATATTGACATTATTTT 855  
QY 129 AsnLeuLysSerThrPheThrGluProValLeuThrPargLysAspGlnHisHisArg 148  
DB 856 AACTTGAAGACACCTTTCACAGAACCTTGTCTGTGGAGGAGGACCAACACCATCACCGC 915  
QY 149 ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu 168  
DB 916 GTGAGGAGCTGACCCGTGAATGGCTCCTCGAGGCTCTTCAGAGCCCTGCATCATTTGAA 975  
QY 169 GlyGluSerGlyLysGlyLysSerThrLeuGlnArgIleAlaMetLeuTrpGlySer 188  
DB 976 GGGGAATCTGGCAAAGCGCAAGTCCACTCTGCTGCAGCGAATTGCCATGCTCTGGGGCTCC 1035  
QY 189 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208  
DB 1036 GGAAGTGCAGGCTCTGACCAAGTTCAAATTCGTCTTCTCTCCCTCCTCAGCAGGGCC 1095  
QY 209 GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg 228  
DB 1096 CAGGTGGACTTTTGAACCCCTCTGATCAACTCTCGATATACCTGGCAACATCAGG 1155  
QY 229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248  
DB 1156 AAGCAGACATTCATGGCCATGCTCTGAAGCTGGCGCAGAGGGTCTTTTCTTCTTGAT 1215  
QY 249 GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn 268  
DB 1216 GGCTACAAATGAATTCAGAGCCCAAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAAC 1275  
QY 269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288  
DB 1276 CACCGCTTCAGAACATGGTCTATCGTCCACACTACCACTGAGTGCCGAGGCACATACGG 1335  
QY 289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308  
DB 1336 CAGTTTGGTGCCTGCTGCTGAGGTGGGGATATGACAGAGACACGCGCCAGGCTCTC 1395  
QY 309 IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer 328  
DB 1396 ATCCGAGAAGTGTGATCAAGGAGCTTGTGAAGGCTTGTGTCCAAATTCAGAAATCC 1455  
QY 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCysAlaIleGln 348  
DB 1456 AGTGTCTTGAGGAATCTCATGAGACCCCTCTCTTGTGGTCATACCTGTGCAATCCAG 1515  
QY 349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368  
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QY 369 LeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIleArg 388  
DB 1576 CTGTTGATACAGAAAAACAACAACATAAAGGTGTGGCTGCAAGTCACTTCATTTCGG 1635  
QY 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408  
DB 1636 AGCTGACCACCTGTGAGACCTAGCTCTGGAGGGTGTGTCTCCCAAGTTTGATTTTC 1695  
QY 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428  
DB 1696 GAATCGAGATGTGTCACCGTGAATGAGGATGTCTGCTGACAACTGGGCTCTCTGT 1755  
QY 429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448  
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DB 1756 AAATATACAGCTCAAGGTTTCAAGCCAAAGTATAAAATTTCTTTCCAAAGTCATTCCAGGAG 1815  
QY 449 TyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr 468  
DB 1816 TACACAGCAGGAGCAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGAGGAGTGACC 1875  
QY 469 LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer 488  
DB 1876 AAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATTTCGGACATTACATCCACTTATAGC 1935  
QY 489 SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis 508  
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QY 509 LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu 528  
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DB 2056 TGGAGACAGGAATCTTTTGCAAGTGTGAAAAACACCACTGAGCAAGAAATTTCTGAAAGCC 2115  
QY 549 IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568  
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QY 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer 588  
DB 2176 TCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCAACTCA 2235  
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QY 609 LeuAspPheIleLysLeuAspPheTyrGlyAlaAlaMetAlaSerTrpGluLysAlaAla 628  
DB 2296 CTGACTTCAATAAAGTGGACTTTATGGGGAGCTATGCTTTCATGGGAAAAAGGCTGCA 2355  
QY 629 GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla 648  
DB 2356 GAAGACACAGGTGGATCCACATGGAGAGGCCCCAGAAACCTACATTCGCCAGCGGCT 2415  
QY 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp 668  
DB 2416 GTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCAACATCCGGAT 2475  
QY 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh 688  
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QY 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe 708  
DB 2535 AAGCCTCAGCTGCAATAAAGAGATGTGCTGTGGTGGAGCCCTCAGTTTGGTCTCT 2594  
QY 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728  
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QY 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisaspLeuGlnAs 748  
DB 2655 TGAGAGCAGATCAGATCTCTAAACACCTGAAACCTTGAGTATTTCATGACCTACAGAA 2714  
QY 748 nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768  
DB 2715 TCACGCTGCCGGTGGTCTGACTGACGCTTGGGTGAATTTGAAGAACCTTTACAAAGCT 2774  
QY 768 uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys 788  
DB 2775 CATATGGATAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCGCTGAA 2834  
QY 788 sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyLys 808  
DB 2835 AAACCTGAAGAAGATGTGTTTATTTCATTTGACCCACTTGTCTGACATTTGGAGAGGAAT 2894



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QY 808 tAspTvrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828
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QY 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
Db 2955 CTCCTGCTGCTGTCTGCAATGCAGTGAATAATCCTAGCTCAGAAATCTTCACAATTTGGT 3014
QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrIleLeuGluLysAspGlyAsnGluAlaLe 868
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QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProfr 888
Db 3075 TCATGAACGTGACGAGATGACGTGTGAACAGCTCACCAGCTGATGCTGCCCTG 3134
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Db 3135 GGGCTGTGACGTGCAAGGCAGCGCTGAGCAGCGCTGTGAAACATTTGGAGGAGTCCACCA 3194
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Db 3255 TGCATTTTGGAAAGAACCCCTCTGAAAACTTCACAGATTGAATTTGGCGGGAAATCG 3314
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QY 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988
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QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
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PCT-US00-29643-6/c
; Sequence 6, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-6
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Alignment Scores:
Pred. No.: 0 Length: 3615
Score: 827.00 Matches: 927
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 80.76% Indels: 2
Gaps: 1
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US-09-697-089-2 (1-1024) x PCT-US00-29643-6 (1-3615)

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Db 2820 TACCATACCCCATCTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTATTTT 2761
QY 129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisArg 148
Db 2760 AACTTTGAAAGCACCCTTCACAGAACCTGTCTCTGTGGAGAGACCAACACCATCACCG 2701
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Db 2460 AAGCAGACATTCATGCCATGCTGCTGAAGCTGCGCAGAGGGTCTTTTCTCTTCTGAT 2401
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Db 2400 GGCTCAATGAATTCAGCCCCAGAACTGCCAGAAATTCGCAAGCCCTGATAAGGAAAC 2341
QY 269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288
Db 2340 CACCGCTTCAAGAACATGGTCACTGTCACCACTACCACTGAGTGCTGAGGCGACATACGG 2281
QY 289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
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QY 309 IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer 328
Db 2220 ATCCGAGAAGTCTGATCAAGGAGCTTGTGAAGGCTTGTGCTCAAAATTCAGAAATCC 2161
QY 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln 348
Db 2160 AGTGTCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGGTCACTCACTGTGCAATCCAG 2101
QY 349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368
Db 2100 ATGGGTGAAAGTGAGTTCCACTCTCACACACAAACAAACGCTGTTCATACCTTCTATGAT 2041
QY 369 LeuLeuIleGlnLysAsnLysHisLysLysGlyValAlaAlaSerAspPheIleArg 388
Db 2040 CTGTTGATACAGAAAAACAAACACAAATAAAGGTGGCTGCAAGTGACTTTCATTCCG 1981
QY 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408
Db 1980 AGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCACAAAGTTTGTATTC 1921
QY 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428
Db 1920 GAACTGCAGGATGTGTCCACGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCTCTGT 1861
QY 429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448
Db 1860 AAATATACAGCTCAAAAGGTTCAAGCCAAAGTATAAATCTTTTCAAGATCATTTCCAGGAG 1801
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Qy	449	TyThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGluProGluValThr	468
Db	1800	TACACGACGAGCAAGACTCAGCAGTTATTATTCAGCTCTCATGAGCCAGAGAGGTGACC	1741
Qy	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
Db	1740	AAGGGGAATGGTTACTTGTGCAGAAATGGPTTCCATTTCGGACATTACATCCACTATAGC	1681
Qy	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
Db	1580	AGCTGCTCCGGTACACCTGTGGGTATCTGTGAAGCCACCAGGCGTGTTATGAAGCAC	1621
Qy	509	LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
Db	1620	CTCGACGAGTGATCAACACGCGCTCTCTCGGACTTCATCGCCCAAGAGCGCTCTC	1561
Qy	529	TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla	548
Db	1560	TGGAGACAGGAATCTTTGTCAAAAGTGTGAAAAACACCCTGAGCAAGAAATTTCTGAAAGCC	1501
Qy	549	IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
Db	1500	ATAAACATCAATTTCTTTGTAGAGTGTGCATCCCAATTATATCAAGAGAGTACATCCAAA	1441
Qy	569	SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	588
Db	1440	TCAGCCCTGAGCCACGAATTTGAGCTTTCTTTCAAGGTAAAGCTTATATATCACTCA	1381
Qy	589	GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla	608
Db	1380	GGGAACATCCCGATTACTATTTTGACTTCTTTTGAACATTTGCCCAATTTGTGCAAGTGCC	1321
Qy	609	LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaAla	628
Db	1320	CTGGACTTCATTAACTTGACATTTTATGGGGAGACTATGGCTTCATGGGAAAAGGCTGCA	1261
Qy	629	GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla	648
Db	1260	GAAGACACAGTGGAAATCCACATGGNAGAGGCCCCAGAAACCTTACATTTCCACAGAGGCT	1201
Qy	649	ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp	668
Db	1200	GTATCTTTGTTCTTCAACTTGAAGCAGGAATTCAGGACTCGGAGTCCACATCCCGGAT	1141
Qy	669	PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaIle	688
Db	1140	TTCAGCAAGTTGAATTAAGCAAGATATCAG-ATATCTGGGGAAAATATTTCAGCTCTGGCAC	1082
Qy	688	rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe	708
Db	1081	AGCCTCAGGCTGCAATTAAGAGATGTGCTGGTGGCTGGAAGCCTCAGTTTGGTCTCT	1022
Qy	708	uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs	728
Db	1021	CAGCACTGTGAAGAACATTTATTTCTCATGTGTGAAGCCAGTCCCTCCACATAGAAGA	962
Qy	728	pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs	748
Db	961	TGAGAGGCACATCATCTGTAAACAACCTGAAAACCTTGAGTATTATGACCTTACAGAA	902
Qy	748	nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe	768
Db	901	TCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGCT	842
Qy	768	uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys	788
Db	841	CATAATGGATAAACATAAAGATGAATGAAGAGATGCTATAAACTAGCTGAAGCGCTGAA	782
Qy	788	sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMe	808
Db	781	AAACCTTGAAGAGATGTGTTTATTTTCATTTGACCACCTTGCTGCACATTTGAGAGGAAT	722

Qy	808	tAsPtyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa	820
Db	721	GGATTACATAGTCGAAGTCTCTGTCAAGTGAACCTCTGACCTTGAAGAAATTCAAATTAGT	662
Qy	828	lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa	848
Db	661	CTCTCTGCTGTGTCGCAATGCAGTGAATAATTCCTAGCTCAGATCTTCACAAATTTTGGT	602
Qy	848	lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe	868
Db	601	CAAACTGAGCATCTCTGATTTATCAGAAAATTAACCTGGAAAAAGATGGAATGAAGACTCT	542
Qy	868	uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr	888
Db	541	TCATGAACGTGATCAGCAGGATGAAGCTGTGTAGAACAAGCTCACGCGACTGATCTGCCCTG	482
Qy	888	pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProG1	908
Db	481	GGGTGTGACGTGCAAGCGCAGCCTGAGCAGCCCTGTGTGAACAATTTTGGAGGAGTCCCACA	422
Qy	908	nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuG1	928
Db	421	ACTCGTCAAGCTTGGGTGTGAACAACCTGGAGACTCACAGATACAGAGATTTAGAAATTTTAGG	362
Qy	928	yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr	948
Db	361	TGCATTTTTTGGAAAGAACCTCTGAAAAAATTCAGCAGTGTGAATTTGGCGGGAAATCG	302
Qy	948	gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa	968
Db	301	TGTGAGCAGTGATGCATGGCTGCTTCATGGGTGTATTGTAGAATCTTTAAGCAATTAGT	242
Qy	968	lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe	988
Db	241	GTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG	182
Qy	988	rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs	1008
Db	181	CCAAGTGTATCCAAGTTAACCTTTCTGCAAGAGCTAGCTTGTGGTGGCAATTTGA	122
Qy	1008	pAspAspLeuSerValIleThr	1016
Db	121	TGATGATGATCTCAGTGTATTACA	97
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US-09-697-089-4			
; Sequence 4, Application US/09697089			
; GENERAL INFORMATION:			
; APPLICANT: Bertin, John			
; APPLICANT: Robison, Keith E.			
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
; FILE REFERENCE: 07334-136001			
; CURRENT APPLICATION NUMBER: US/09/697,089			
; CURRENT FILING DATE: 2000-10-26			
; PRIOR APPLICATION NUMBER: US 60/161,822			
; PRIOR FILING DATE: 1999-10-27			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 4			
; LENGTH: 3615			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(3612)			
US-09-697-089-4			
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Pred. No.: 0 Length: 3615			
Score: 827.00 Matches: 927			
Percent Similarity: 99.78% Conservative: 0			
Best Local Similarity: 99.78% Mismatches: 1			

Query Match:	80.76%	Indels:	2
DB:	27	Gaps:	0
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QY	89	LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu	108
DB	736	CTTTTTCATCAGACATCAGAAAGCAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTG	795
QY	109	TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleIlePhe	128
DB	796	TACCATACCCCATCTTCTCGAATCTTTATCCCTTGGTGAAGATATTGACATATTATTTT	855
QY	129	AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisAsArg	148
DB	856	AACCTGAAAGACACTTCAGAACCTCTCTGTGGAGGAGACCAACACCATCACCGC	915
QY	149	ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu	168
DB	916	GTGGAGCAGCTGACCTGAATGCCCTCTCTGCAGGCTCTTCAGAGCCCTGCATCATTTGAA	975
QY	169	GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer	188
DB	976	GGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGAATGCCATGCTCTGGGGCTCC	1035
QY	189	GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla	208
DB	1036	GGAAGTGCAAGGCTCTGCACCAAGTTCAATTCGTCTCTCTCCGTCTCAGCAGGGCC	1095
QY	209	GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg	228
DB	1096	CAGGGTGGACATTTTGTAAACCCCTCTGTGATCAACTCTCGTATACCTGCGACAAATCAGG	1155
QY	229	LysGlnThrPheMetAlaMetLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp	248
DB	1156	AACGACACATTCATGGCCATGCTGCTGAAGCTCGCGCAGAGGGTCTTTCTCTCTTGAT	1215
QY	249	GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGluAsn	268
DB	1216	GGCTACAATGAATTCGAAGCCCAAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAAC	1275
QY	269	HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg	288
DB	1276	CACCGCTTCAAGAACATGTGTCATCGTCACCACTTACCACCTGAGTGCCTGAGGCACATACGG	1335
QY	289	GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu	308
DB	1336	CAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAGACAGCCCGCCAGGCTCTC	1395
QY	309	IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer	328
DB	1396	ATCCGAGAAGTGTGATCAAGGAGCTTGTGAAAGGCTTGTGTGCTCCAAATTCAGAAATCC	1455
QY	329	ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln	348
DB	1456	AGTGTCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGTCTATCACTTGTGCAATCCAG	1515
QY	349	MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp	368
DB	1516	ATGGGTGAAGTAGTGTCCACTCTACACAAACCAACCGCTGTTCCTACCTTCTATGAT	1575
QY	369	LeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIleArg	388
DB	1576	CTGTTGATACAGAAAAACAACAACATAAAGGTGTGGCTGCAAGTCACTTCATTCGG	1635
QY	389	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe	408
DB	1636	AGCCTGGACCACTGTGTGAGACCTTAGCTCTGGAGGTGTCTCTCCACAAAGTTTGATTTC	1695
QY	409	GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys	428
DB	1696	GAACTCGAGGATGTGCCAGCGTGAATGAGATGTCTCTGCTGCAACTGGGCTCCTCTGT	1755
QY	429	LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu	448
DB	1756	AAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTCACAAGTCATTCAGGAG	1815
QY	449	TyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr	468
DB	1816	TACACAGCAGGACCAAGACTCAGCAGTTTATTGACGCTCTCATGAGCCAGAGGAGTGACC	1875
QY	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
DB	1876	AAGGGAAATGGTTACTTGCAGAAAATGGTTTCCATTTCCGACATTCATCCACTTATAGC	1935
QY	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
DB	1936	AGCCTCTCCGGTACACCTGTGGTCTCATCTGTGAAAGCCACCAAGGCTGTATTATGAAGCAC	1995
QY	509	LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
DB	1996	CTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGACTTTCATCCGCAAGAGCGCTCTC	2055
QY	529	TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla	548
DB	2056	TGGAGACAGAATCTTTGCAAGGTGTGAAAACACCACTGAGCAGCAAGAAATTCGAAAGCC	2115
QY	549	IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
DB	2116	ATAAACATCAATTCCTTTGTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAA	2175
QY	569	SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	588
DB	2176	TCAGCCCTCAGCCAGAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCAACTCA	2235
QY	589	GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla	608
DB	2236	GGAAACATCCCGCATTTACTATTGTGACTTCTTTTGAACATTTGGCCAAATTTGTGCAAGTGC	2295
QY	609	LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaAla	628
DB	2296	CTGGACTTCATTAACATGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCA	2355
QY	629	GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla	648
DB	2356	GAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAACCTTACATTTCCACAGCGGCT	2415
QY	649	ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp	668
DB	2416	GTATCTTCTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGCTCACCTCCGGAT	2475
QY	669	PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh	688
DB	2476	TTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGGAAAATATTGAGCTCTGCCAC	2534
QY	688	rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValle	708
DB	2535	AAGCCTCAGGCTGCAATAAAGAGATGTGCTGTGTGGTGGAGGCTCAGTTTGTGCTCT	2594
QY	708	uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs	728
DB	2595	CAGCAGCTGTAGAACAATTTATCTCTCATGGTGGAGGAGCCAGTCCCTCCACATAGAGA	2654
QY	728	pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs	748
DB	2655	TGAGGAGCACATCACATCTGTAAACAACTGAAACCTTGGAGTATTTCATGACCTACAGAA	2714
QY	748	nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe	768
DB	2715	TCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAAGCTTACAAAGCT	2774
QY	768	uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys	788
DB	2775	CATAATGGATACATAAAGATGAATGAAGAAGATGCTATAAAACTAGCTGAAGGCTCGAA	2834
QY	788	sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyLeuMe	808

Db 2835 AAACCTGAAGAGAGTGTCTTTATTTCATTGACCACCTGTCTGACATTGGAGAGGAAT 2894  
Qy 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluIleGlnLeuVa 828  
Db 2895 GGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCATTAGT 2954  
Qy 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848  
Db 2955 CTCCTGTGCTGTGTCTGCAATGCAGTGAATACTCTAGCTCAGATCTTCACAATTTGGT 3014  
Qy 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868  
Db 3015 CAAACTGAGCATCTTGATTATCAGAAAATTACCTGGAAGATGCAATGAAGCTCT 3074  
Qy 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888  
Db 3075 TCATGAACGTGTCGACAGGATGAAGCTGTAGAACAGCTACCGCAGCTGCTGCCCTG 3134  
Qy 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluValProGl 908  
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Qy 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928  
Db 3195 ACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAGG 3254  
Qy 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948  
Db 3255 TGCATTTTTTGGAAAGAACCCCTCTGAAAAACTTCAGCAGTTGAATTTGGCGGGAATTCG 3314  
Qy 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968  
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Qy 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988  
Db 3375 GTTTTTTCACCTTAGTACTAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 3434  
Qy 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008  
Db 3435 CCAAGTGTATCCAAGTTAACTTTCTCGAAGAAGCTAGGCTTGTGGGTGGCAATTGA 3494  
Qy 1008 pAspAspLeuSerValIleThr 1016  
Db 3495 TGATGATGATCTCAGTGTATTACA 3519

Search completed: January 31, 2003, 08:40:32  
Job time : 5269 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	923	90.1	3075	1	PCT-US02-21946A-1	Sequence 1, Appli	
2	923	90.1	3219	1	PCT-US02-21946A-14	Sequence 14, Appl	
3	721	70.4	3545	6	US-10-276-781-111	Sequence 111, App	
4	80	7.8	421	6	US-10-203-138A-4307	Sequence 4307, Ap	
5	73	7.1	220	6	US-10-203-138A-9429	Sequence 9429, Ap	
6	9	0.9	1956	5	US-09-620-312D-68	Sequence 68, Appl	
7	9	0.9	2685	5	US-09-134-000C-2326	Sequence 2326, Ap	
8	9	0.9	2685	5	US-09-134-000C-2326	Sequence 2326, Ap	
9	8	0.8	25	7	US-60-427-836-236146	Sequence 236146,	
10	8	0.8	212	5	US-09-531-113-8971	Sequence 8971, Ap	
11	8	0.8	331	6	US-10-240-445-558	Sequence 558, App	



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Qy 760 yAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAl 780
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Qy 780 aileLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi 800
Db 2340 TATAAACTAGCTGAAGCCCTGAAACCTGAAGAAGATGTGTTATTTCATTGACCCA 2399
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Db 2400 CTTGCTGTGACATTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTG 2459
Qy 820 sAspLeuGluGluIleGlnValSerCysLysSerCysLeuSerAlaAsnAlaValLysIleLe 840
Db 2460 TGACCTTGAAGAAATTCAAATAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2519
Qy 840 uAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLe 860
Db 2520 AGCTCAGAACTTCACAAATTTGGTCAAACTGAGCAATCTTGATTTATCAGAAATACCT 2579
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Qy 880 nLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLe 900
Db 2640 GCTACCGGCATGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGCAGCCTGAGCAGCCTGT 2699
Qy 900 uLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuTh 920
Db 2700 GAACATTTGGAGAGGTCCCAACACGTCGCAAGCTTGGGTGGAAACCTGGAGACTCAC 2759
Qy 920 rAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGl 940
Db 2760 AGATACAGAGATTAGAATTTAGTGTGATTTTGGGAAAGAACCTCTCGAAGAACTTCCA 2819
Qy 940 nGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVa 960
Db 2820 GCAGTTGAATTTGGCGGGAATCGTGTGACAGTGTGATGGATGGCTTGCCTTCATGGGTGT 2879
Qy 960 lPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAs 980
Db 2880 ATTTGAGAACTTAAGCAATTAGTGTGTTTGTGACTTTAGTACTTAAGAAATTTCTACCTGA 2939
Qy 980 pProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAl 1000
Db 2940 TCCAGCATTAGTCAGAAACTTAGCCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGC 2999
Qy 1000 aArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLy 1020
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Qy 1020 sLeuValThrAla 1024
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RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
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; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21946A-14

Alignment Scores:
Pred. No.: 0 Length: 3219
Score: 923.00 Matches: 1023
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 90.14% Indels: 2
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-14 (1-3219)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 145 ATGAATTTTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 204
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
Db 205 AAGCAATATCAGATGACCTATTGTTGATGGAATGTTCTGAATCCGGAAGAAGTAACATC 264
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 265 ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAAA 324
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 325 AAGGGTTACAGATCTCTGTAACCTCTTTCTTAAATCCCTTAAGGAGTGGAATATCCTCTA 384
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Db 385 TTTCAGAGACTTGAATGACAAGAGCTTTTTCATCAGACATCAGAAGAGACTTGGAGCAT 444
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
Db 445 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCACTCTTTCTGAAGTCTTATCCCTT 504
Qy 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 505 GGTGAGATATTGACATATTATTTAACTTGAAGAGCACCCTTCACAGAACCTGCTCTGTG 564
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 565 AGAAGGACCACACCATCATCCCGGTGGAGCAGCTGACCTGAATGGCCCTCTGCGAGGCT 624
Qy 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 625 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 684
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 685 CGAATTTGCCATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAATTCGTC 744
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 745 TTCTTCTCCTCTCAGCAGGGCCCGAGGGTGGACTTTTTTGAACCCCTCTGTGATCAACTC 804
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db 805 CTGGATATACCTGGCAATCAGGAAGCAGACATTCATGCCATGCTGCTGAAAGCTCGG 864
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 865 CAGAGGGTCTCTTTTCTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 925 ATCGAAGCCCTGATAAAGGAAACCCCGCTTCAAGAACATGGTCACTGCTCACCCTACC 984
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
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Qy 1020 sLeuValThrAla 1024
Db 3204 ACTAGTAAGTCTGCT 3216
RESULT 3
US-10-276-781-111
; Sequence 111, Application US/10276781
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-781-111

Alignment Scores:
Pred. No.: 0 Length: 3545
Score: 721.00 Matches: 1021
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 3
Query Match: 70.41% Indels: 6
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-276-781-111 (1-3545)
Qy 1 MetAsnPheLeuLysAspAsnSerArgAlaLeuLeuLeuGlnArgMetGlyMetThrValIle 20
Db 232 ATGAATTTTCATAAAGGACATAGCGGAGCCCTTATTCAAAGAAATGGGAATGACTGTTATA 291
Qy 21 LysGlnLeuThrAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
Db 292 AAGCAAAATCACAGATGACTATTGTATGGAATGTTCTGAAATCGCAAGAGAAATAACATC 351
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 352 ATTTGCTCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAA 411
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
Db 412 AAGGTTTCAGAGTCTGTAACTCTTTTAAATCCCTTAAAGGAGTGAACATATCTCTTA 471
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Db 472 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACCAT 531
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
Db 532 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTCAACTTTTATCCCTT 591
Qy 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 592 GGTGAAGATATGACATATTATTTTAACTTGAAGACACTTTCACAGAACCTGTCTGTGG 651
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 652 AGGAAGGCCAACCAATCACCCTGGGAGCAGCTGACCCCTGAATGGCTCTCTGAGGCT 711
Qy 161 LeuGlnSerProCysIleIleGluSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 712 CTTACAGCCCTGCATCATTTAAGGGAATCTGCAAAAGCAAGTCCACCTGCTGTCGAC 771
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 772 CGCATTTGCCATGCTCTGGGGCTCCGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC 831
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Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 832 TTCTTCCCTCCGCTCTCAGCAGGGCCCGAGGTGGACCTTTTGAACCCCTCTGTGATCAACTC 891
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
Db 892 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 951
Qy 241 GlnArgValLeuPheLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 952 CAGAGGGTCTCTTCTTCTTGTATGGCTACATGAATCAAGCCCGCAGAACTGCCAGAA 1011
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 1012 ATCGAAGCCCTGATAAAGAAACCCCGCTTCAAGAACATGGTCTATGCTCACCACCTACC 1071
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 1072 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGTGGGGATATG 1131
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db 1132 ACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGCATCAGGAGCTTGCTGAAGGC 1191
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 1192 TGTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1251
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 1252 GTGGTCACTACTTGTGCAATCCAGATGGTGAAGTGAAGTTCCTCACTCTCACACAAACA 1311
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
Db 1312 ACGCTGTTTCCATACCTTCTATGATCTGTGTATACAGAAACAAACACAAACATAAAGT 1371
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAsp-LeuAlaLeuGluGln 400
Db 1372 GTGGCTGCAAGTGACTTCATTCGGAGCCCTGGACCACTGTGGATA-CCTAGCTCTGGAGG 1430
Qy 400 yValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420
Db 1431 TGTGTTCTCCCAAGTTTGATTTGCACTGCAGGATGTGTCCAGCGTGAATGAGGATGT 1490
Qy 420 IleLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrIle 440
Db 1491 CCTGCTGACAACTGGGCTCCTCTGTAAATATATACGCTCAAAGGTTCAAGCCAAAGTATAA 1550
Qy 440 sPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuTh 460
Db 1551 ATCTTTTCAAGTCAATTCAGGAGTACACAGCAGCAGCAGACCTCAGCAGTTTATTGAC 1610
Qy 460 rSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1611 GTCTCATGAGCAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAAATGGTTTCCAT 1670
Qy 480 eSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGln 500
Db 1671 TTCGACATTAATCACTTATAGCAGCTGCTCGGTTACCTGTGGGTCACTGTGTGGA 1730
Qy 500 uAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGln 520
Db 1731 AGCCACAGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACAGCGCTGCTTCTCGG 1790
Qy 520 yLeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnTh 540
Db 1791 ACTTTCCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACAC 1850
Qy 540 rThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH 560
Db 1851 CACTGAGCAAGAAATTTCTGAAGGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCA 1910
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Qy	560	sLeuTyRGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGluAlaPhePheG1	580
Db	1911	TTTTATATCAAGAGATACATCCAAATTCAGCCCTGAGCCAAGAAATTTGAAGCTTCTTTTCA	1970
Qy	580	nGlyLysSerLeuTyRileAsnSerClyAsnIleProAspTyRLeuPheAspPheG1	600
Db	1971	AGGTAAAGCTTATATATCACTCAGGGAACATCCCCGATACTATTATTGACTTCTTTTGA	2030
Qy	600	uHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuLeuAsp - PheTyRGlyGlyA	620
Db	2031	ACATTGCCCAATYTGCAAGTGCTCTGCAGCTCATTAACACTGGG - CTTTTATGGGGAG	2089
Qy	620	laMeAlaSerTPGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlap	640
Db	2090	CTATGGCTTCATGGAAAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCC	2149
Qy	640	roGluThrTyRileProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheA	660
Db	2150	CAGAAACCTACATCCCGCAGGGCTGTATCTTTGTTCTTCAACTGGGAAGCAGGAATTC	2209
Qy	660	rgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr - Tyr	679
Db	2210	GGACTCTGGAGGTCACACTCCGGGATTCAGCAAGTTGAAATAGCAAGATATCAG - ATAT	2268
Qy	680	LeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGly	699
Db	2269	CTGGGAAAATATTACGCTCTGCCACAAGCCTCAGGCTGCRAAATAAGAGATGTGCTGGT	2328
Qy	700	ValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTySerLeuMetVal	719
Db	2329	GTGGCTGGAAAGCCTCAGTTTGGTCTCAGCAGCCTGTAAGAACATTTATCTCTCATGTG	2388
Qy	720	GluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLys	739
Db	2389	GAAGCCAGTCCCCTCACCATTAGAAAGATGAGAGGCACATCACATCTGTAAACAACTGAAA	2448
Qy	740	ThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeu	759
Db	2449	ACCTTGAGTATTATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTGCACAGCTTG	2508
Qy	760	GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysP	779
Db	2509	GGTAACCTGAAGAACCTTCAAGAGCTCATATATGGATTAACAATAAGATCAATGAAGAAG	2568
Qy	780	AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr	799
Db	2569	GCTATAAACTAGCTGAAGCCTTGAAAAACCTGAGAAGATGTGTTTATTTTCATTTGACC	2628
Qy	800	HisLeuSerAspIleGlyGluGlyMetAspTyRileValLysSerLeuSerSerGluPro	819
Db	2629	CACCTTGCTGACATTCGAGAGGGAATGATACATAGTCAAGTCTCTGCTCAAGTGAACCC	2688
Qy	820	CysAspLeuGluIleGlnLeuValSerCysLysSerAlaAsnAlaValLysIle	839
Db	2689	TGTGACCTTGAAGAAATTCAAATTAGTCTCCTGCTGTTCTGCAAAATGCAGTCAAAATC	2748
Qy	840	LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyR	859
Db	2749	CTAGCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAAAATAC	2808
Qy	860	LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu	879
Db	2809	CTGGAAAAAGATGGAATGAGCTCTTCATGAACATGATCGACAGGATGAAGCTGCTAGAA	2868
Qy	880	GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu	899
Db	2869	CAGCTCACCCGACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCTG	2928
Qy	900	LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu	919
Db	2929	TTGAACATTTTGAGAGAGTCCCAACACTCGTCAAGCTTGGGTTGGTAACACTGGAGACT	2988
Qy	920	ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe	939

Db	2989	ACAGATACAGAGATTAGAAATTTAGTGTGCATTTTGGAAAGAACCCCTCTGAAAACCTTC	3048
Qy	940	GlnGlnLeuAsnLeuAlaGlyAsnArqValSerSerAspGlyTrpLeuAlaPheMetGly	959
Db	3049	CAGCAGTGTGAATTTGGCGGAATCTGTGCACAGTGATGATGCTTGCCTTCATGGT	3108
Qy	960	ValPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuPro	979
Db	3109	GTATTTTCAGAAATCTTAAGCAATTAGTGTTTTTGACTTTAGTACTAAAAGAATTTCTACCT	3168
Qy	980	AspProAlaLeuValLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlu	999
Db	3169	GATCCAGCATAGTACGAAACCTTATGCCAAGTGTTATCCAGTTAACTTTTCTGCAAGAA	3288
Qy	1000	AlaArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPhe	1019
Db	3229	GCTAGGCTTGTGGTGCAATTTGATGATGATCATCTCAGTGTATTACAGGTGCTTTT	3288
Qy	1020	LysLeuValThrAla 1024	
Db	3289	AAACTAGTAAC TGCT 3303	

RESULT 4

US-10-203-138A-4307

; Sequence 4307, Application US/10203138A

; GENERAL INFORMATION:

; APPLICANT: Molecular Dynamics, Inc.

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 47



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RESULT 7
US-09-134-000C-2326
; Sequence 2326, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2326
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2326

Alignment Scores:
Pred. No.: 152 Length: 2685
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.88% Indels: 0
Gaps: 0
DB:

US-09-697-089-2 (1-1024) x US-09-134-000C-2326 (1-2685)
QY 236 LeuLeuLysLeuArgGlnArgValLeu 244
Db 686 TTGTTGAAATTCGACACGCGTCTG 712

RESULT 8
US-09-134-000C-2326
; Sequence 2326, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2326
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2326

Alignment Scores:
Pred. No.: 152 Length: 2685
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.88% Indels: 0
Gaps: 0
DB:

US-09-697-089-2 (1-1024) x US-09-134-000C-2326 (1-2685)
QY 236 LeuLeuLysLeuArgGlnArgValLeu 244
Db 686 TTGTTGAAATTCGACACGCGTCTG 712

RESULT 9
US-60-427-836-236146
; Sequence 236146, Application US/60427836
; GENERAL INFORMATION:
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```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 236146
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-236146

Alignment Scores:
Pred. No.: 17 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
Gaps: 0
DB:

US-09-697-089-2 (1-1024) x US-60-427-836-236146 (1-25)
QY 151 GlnLeuThrLeuAsnGlyLeuLeu 158
Db 1 CAGTTAACACTCAATGGCTTGCTT 24

RESULT 10
US-09-531-113-8971
; Sequence 8971, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531,113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 8971
; LENGTH: 212
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: Jc-gmf102220098f04d1
US-09-531-113-8971

Alignment Scores:
Pred. No.: 139 Length: 212
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
Gaps: 0
DB:

US-09-697-089-2 (1-1024) x US-09-531-113-8971 (1-212)
QY 930 PhePheGlyLysAsnProLeuLys 937
Db 88 TTTTGGAAAAACCCCTTAAA 111

RESULT 11
US-10-240-425-558
; Sequence 558, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
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; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 558  
; LENGTH: 331  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AI309223  
US-10-240-425-558

Alignment Scores:  
Pred. No.: 215 Length: 331  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-240-425-558 (1-331)

Qy 759 SerSerAlaThrLeuLysAsnLeuThr 766  
Db 145 CTGGTAATTTAAATTCCTTACA 168

#### RESULT 12

US-10-152-319A-1150  
; Sequence 1150, Application US/10152319A  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1150  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:

; OTHER INFORMATION: Genbank Accession No. AI179407  
US-10-152-319A-1150  
Alignment Scores:  
Pred. No.: 232 Length: 357  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-152-319A-1150 (1-357)

Qy 685 SerSerAlaThrSerLeuArgLeu 692  
Db 163 TCCAGCGCCACCTCACTGAGACTT 186

#### RESULT 13

US-10-301-856-641  
; Sequence 641, Application US/10301856  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Nephrotoxicology Modeling  
; FILE REFERENCE: 44921-5089-01  
; CURRENT APPLICATION NUMBER: US/10/301,856  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US 10/152,319  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1261  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 641  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:

; OTHER INFORMATION: Genbank Accession No. AI179407

US-10-301-856-641

Alignment Scores:  
Pred. No.: 232 Length: 357  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-301-856-641 (1-357)

Qy 685 SerSerAlaThrSerLeuArgLeu 692

Db 163 TCCAGCGCCACCTCAGAGACTT 186  
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## RESULT 14

US-10-301-856-417/c  
; Sequence 417, Application US/10301856  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgins, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Nephrotoxicology Modeling  
; FILE REFERENCE: 44921-5089-01  
; CURRENT APPLICATION NUMBER: US/10/301,856  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US 10/152,319  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: PatentIn Ver. 2.1  
; NUMBER OF SEQ ID NOS: 1261  
; SEQ ID NO 417  
; LENGTH: 369  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AI029017

US-10-301-856-417

Alignment Scores:  
Pred. No.: 239 Length: 369  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-301-856-417 (1-369)

QY 849 LysLeuSerIleLeuAspLeuSer 856  
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Db 84 AAGCTGAGTACTACTGACTTATCA 61  
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## RESULT 15

US-10-203-138A-3084/c  
; Sequence 3084, Application US/10203138A  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

; FILE REFERENCE: PB 0004 WO 8  
; CURRENT APPLICATION NUMBER: US/10/203,138A  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: CB 24263.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 15438  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 3084  
; LENGTH: 392  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL031864.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 2.6  
US-10-203-138A-3084

Alignment Scores:  
Pred. No.: 254 Length: 392  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 0.78% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-203-138A-3084 (1-392)

QY 316 GluLeuAlaGluGlyLeuLeuLeu 323  
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Db 174 GAACTGCAGAGGTCGTCTCTT 151  
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Search completed: January 31, 2003, 08:44:50  
Job time : 336 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:46:10 : Search time 7683 seconds  
(without alignments)  
11636.577 Million cell updates/sec

Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaatttcataaagacaa.....cttttaactagtaactgct 3072

Scoring table: **OLIGO\_NUC**  
Gapop 60.0, Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

**Word size 6 12**  
Total number of hits satisfying chosen parameters: 824982

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rpod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3072	100.0	3133	9	AY032589	Homo sapi
2	2919	95.0	3219	9	AY035391	Homo sapi
3	2919	95.0	3360	9	BC031555	Homo sapi
4	2868	93.4	3355	9	AK095467	Homo sapi
5	2868	93.4	3396	6	AX318091	Sequence
6	2868	93.4	3396	9	AY027787	Homo sapi
7	2868	93.4	3581	9	AF376061	Homo sapi
8	1946	63.3	160583	2	AC010968	Homo sapi
9	1844	60.0	138909	9	CNS01DS3	Sequence
10	1267	41.2	1355	9	IR2005417	BAC sequ
11	840	27.3	891	6	AX318174	Homo sapi
12	815	26.5	1395	6	AX318093	Sequence
13	815	26.5	1395	9	AY027788	Homo sapi
14	618	20.1	618	6	AX318176	Sequence
15	461	15.0	768	6	AX318097	Sequence
16	461	15.0	768	9	AY027789	Homo sapi
17	292	9.5	162692	9	CNS01DS8	BAC sequ
18	292	9.5	185281	2	AC011232	Homo sapi
19	269	8.8	578	6	AX318095	Sequence
20	269	8.8	578	9	AY027790	Homo sapi
21	261	8.5	261	6	AX318172	Sequence
22	170	5.5	553	11	G55568	SHGC-100923
23	114	3.7	165	6	AX318178	Sequence
24	39	1.3	185469	2	AC101793	Mus muscu
25	29	0.9	29	6	AX318155	Sequence
26	25	0.8	25	6	AX318156	Sequence
27	25	0.8	25	6	AX318157	Sequence
28	25	0.8	25	6	AX318160	Sequence
29	25	0.8	175205	2	AC128434	Rattus no
30	24	0.8	24	6	AX318154	Sequence
31	24	0.8	33	6	AX318152	Sequence
32	23	0.7	23	6	AX318148	Sequence
33	23	0.7	23	6	AX318158	Sequence
34	23	0.7	169406	2	AC090582	Homo sapi
35	23	0.7	175152	2	AC074195	Homo sapi
36	23	0.7	183556	2	AC019059	Homo sapi
37	22	0.7	42513	9	AL592438	Human DNA
38	22	0.7	79431	2	AC098256	Rattus no
39	22	0.7	87834	9	AF002957	Homo sapi
40	22	0.7	137897	9	AL161913	Human DNA
41	22	0.7	151088	9	AC020917	Homo sapi
42	22	0.7	153733	2	AC011980	Homo sapi
43	22	0.7	155531	2	AL592213	Homo sapi
44	22	0.7	157021	2	AC129066	Didelphis
45	22	0.7	159946	2	AC079194	Homo sapi
46	21	0.7	21	6	AX318151	Sequence
47	21	0.7	30	6	AX318153	Sequence
48	21	0.7	7067	6	AX286953	Sequence
49	21	0.7	7595	4	BTCAK35	Bovine gene
50	21	0.7	9257	1	AE010385	Methanopy
51	21	0.7	35357	2	AC131526	Rattus no
52	21	0.7	37906	9	AC005199	Homo sapi
53	21	0.7	45496	2	AC017948	Drosophil
54	21	0.7	76526	2	AC027055	Homo sapi
55	21	0.7	80346	8	ATM4E13	Arabidops
56	21	0.7	84499	8	ATT1235	Arabidops
57	21	0.7	86710	8	ATF23E12	Arabidops
58	21	0.7	91573	10	AL732313	Mouse DNA
59	21	0.7	119141	2	AC096826	Rattus no
60	21	0.7	130117	9	AC004907	Homo sapi
61	21	0.7	157308	2	AC079351	Homo sapi
62	21	0.7	160931	3	AC093498	Drosophil
63	21	0.7	180176	10	AL671190	Mouse DNA
64	21	0.7	181277	2	AC120594	Rattus no
65	21	0.7	181477	9	AC024590	Homo sapi

c 66	21	0.7	184864	9	AC013553	AC013553 Homo sapi	139	20	0.7	163604	4	AC092727	AC092727 Bos tauru
c 67	21	0.7	194874	8	AC080090	AC080090 Homo sapi	c 140	20	0.7	164067	2	AC115162	AC115162 Rattus no
c 68	21	0.7	195165	8	ATCHRIV82	AL161586 Arabidops	c 141	20	0.7	164648	2	AC115014	AC115014 Mus muscu
c 69	21	0.7	197859	8	ATCHRIV83	AL161587 Arabidops	c 142	20	0.7	164688	2	AL732360	AL732360 Mus muscu
c 70	21	0.7	198935	2	AC068573	AC068573 Homo sapi	c 143	20	0.7	165333	9	AC023822	AC023822 Homo sapi
c 71	21	0.7	200398	9	AC025566	AC025566 Homo sapi	c 144	20	0.7	165953	3	AC093104	AC093104 Drosophil
c 72	21	0.7	201415	2	AC107239	AC107239 Mus muscu	c 145	20	0.7	167031	2	AC113882	AC113882 Rattus no
c 73	21	0.7	206452	10	AL593857	AL593857 Mouse DNA	c 146	20	0.7	167469	2	AC113882	AC113882 Rattus no
c 74	21	0.7	211194	10	AL513468	AL513468 Mouse DNA	c 147	20	0.7	168038	2	AC112052	AC112052 Rattus no
c 75	21	0.7	213473	2	AC094371	AC094371 Rattus no	c 148	20	0.7	168231	9	AL589863	AL589863 Human DNA
c 76	21	0.7	214433	2	AL627184	AL627184 Mus muscu	c 149	20	0.7	170279	2	AC027053	AC027053 Homo sapi
c 77	21	0.7	221341	2	AC092992	AC092992 Homo sapi	c 150	20	0.7	171031	2	AC104020	AC104020 Homo sapi
c 78	21	0.7	227194	2	AC020727	AC020727 Homo sapi	c 151	20	0.7	171256	9	AC105193	AC105193 Homo sapi
c 79	21	0.7	242265	2	AC126460	AC126460 Mus muscu	c 152	20	0.7	172526	2	AC107467	AC107467 Rattus no
c 80	21	0.7	256933	10	AC099771	AC099771 Mus Muscu	c 153	20	0.7	174098	9	AC005737	AC005737 Homo sapi
c 81	21	0.7	303367	3	AE003538	AE003538 Drosophil	c 154	20	0.7	174612	9	CNS07EF6	AL512357 Human Chr
c 82	20	0.7	475	6	AX437848	AX437848 Sequence	c 155	20	0.7	175274	9	AP004286	AP004286 Homo sapi
c 83	20	0.7	768	6	AX318097	AX318097 Sequence	c 156	20	0.7	175345	9	AP003065	AP003065 Homo sapi
c 84	20	0.7	768	9	AY027789	AY027789 Homo sapi	c 157	20	0.7	178861	2	AC068231	AC068231 Homo sapi
c 85	20	0.7	1198	14	REOS3NSB	M18390 Reovirus se	c 158	20	0.7	178864	9	AC022535	AC022535 Homo sapi
c 86	20	0.7	1688	8	SCYBR141C	236010 S.cerevisia	c 159	20	0.7	178868	9	AL357752	AL357752 Human DNA
c 87	20	0.7	2833	8	SCYBR142W	236011 S.cerevisia	c 160	20	0.7	180110	2	AC122001	AC122001 Mus muscu
c 88	20	0.7	3709	3	AF116341	AF116341 Drosophil	c 161	20	0.7	180303	9	AL672045	AL672045 Human DNA
c 89	20	0.7	10467	1	AE010860	AE010860 Methanosa	c 162	20	0.7	180836	2	AC025241	AC025241 Homo sapi
c 90	20	0.7	12595	8	SCIRAI	X78937 S.cerevisia	c 163	20	0.7	182870	2	AC016563	AC016563 Homo sapi
c 91	20	0.7	25474	2	AC110773	AC110773 Homo sapi	c 164	20	0.7	184003	2	AC011058	AC011058 Homo sapi
c 92	20	0.7	36631	9	HUMCOL7A1X	L23982 Homo sapien	c 165	20	0.7	185104	2	AC118763	AC118763 Rattus no
c 93	20	0.7	40937	3	CER01E6	758118 Caenorhabdi	c 166	20	0.7	185108	2	AC101860	AC101860 Mus muscu
c 94	20	0.7	45459	2	AC066103	AC066103 Homo sapi	c 167	20	0.7	185405	2	AP001887	AP001887 Homo sapi
c 95	20	0.7	69672	2	AC107863	AC107863 Mus muscu	c 168	20	0.7	185835	2	AC092007	AC092007 Bos tauru
c 96	20	0.7	71463	9	AC080088	AC080088 Homo sapi	c 169	20	0.7	186183	9	AC026827	AC026827 Homo sapi
c 97	20	0.7	81875	2	AC131203	AC131203 Rattus no	c 170	20	0.7	186381	9	AC109708	AC109708 Rattus no
c 98	20	0.7	83969	9	AC005210	AC005210 cithr_179	c 171	20	0.7	186869	2	AC102392	AC102392 Mus muscu
c 99	20	0.7	86155	9	AL159169	AL159169 Human DNA	c 172	20	0.7	187998	2	AC125909	AC125909 Rattus no
c 100	20	0.7	86719	9	AP000885	AP000885 Homo sapi	c 173	20	0.7	189291	2	AC102326	AC102326 Mus muscu
c 101	20	0.7	88326	2	AC005923	AC005923 Homo sapi	c 174	20	0.7	191748	2	AL662902	AL662902 Mus muscu
c 102	20	0.7	88839	3	AC084447	AC084447 Caenorhab	c 175	20	0.7	192029	2	AC123986	AC123986 Mus muscu
c 103	20	0.7	89748	2	AC106195	AC106195 Rattus no	c 176	20	0.7	193999	2	AC113413	AC113413 Homo sapi
c 104	20	0.7	91733	2	AL391278	AL391278 Homo sapi	c 177	20	0.7	194973	9	AP002008	AP002008 Homo sapi
c 105	20	0.7	93409	2	AC073294	AC073294 Mus muscu	c 178	20	0.7	196031	2	AL844564	AL844564 Mus muscu
c 106	20	0.7	99225	2	AC114149	AC114149 Rattus no	c 179	20	0.7	197576	2	AC123476	AC123476 Rattus no
c 107	20	0.7	102165	2	AC083819	AC083819 Mus muscu	c 180	20	0.7	198501	2	AC118410	AC118410 Rattus no
c 108	20	0.7	106601	9	AL357352	AL357352 Human DNA	c 181	20	0.7	199903	2	AC113503	AC113503 Mus muscu
c 109	20	0.7	109810	9	AL139036	AL139036 Human DNA	c 182	20	0.7	204618	10	AF146793	AF146793 Mus muscu
c 110	20	0.7	111777	2	AP004089	AP004089 Oryza sat	c 183	20	0.7	206745	2	AC096481	AC096481 Rattus no
c 111	20	0.7	11851	9	AC090564	AC090564 Homo sapi	c 184	20	0.7	207411	2	AC084746	AC084746 Mus muscu
c 112	20	0.7	114169	9	AC010902	AC010902 Homo sapi	c 185	20	0.7	207541	2	AC121252	AC121252 Homo sapi
c 113	20	0.7	120733	9	AC022124	AC022124 Homo sapi	c 186	20	0.7	207873	2	AL807753	AL807753 Mus muscu
c 114	20	0.7	121931	9	AC008390	AC008390 Homo sapi	c 187	20	0.7	208095	2	AC118606	AC118606 Mus muscu
c 115	20	0.7	121963	2	AC095337	AC095337 Rattus no	c 188	20	0.7	208524	2	AC123260	AC123260 Mus muscu
c 116	20	0.7	124347	9	AC010072	AC010072 Homo sapi	c 189	20	0.7	213889	2	AL807242	AL807242 Mus muscu
c 117	20	0.7	129837	9	AC004829	AC004829 Homo sapi	c 190	20	0.7	216698	2	AC092006	AC092006 Bos tauru
c 118	20	0.7	130221	2	AC125495	AC125495 Oryza sat	c 191	20	0.7	217217	2	AC129085	AC129085 Mus muscu
c 119	20	0.7	130981	2	AC087702	AC087702 Trypanoso	c 192	20	0.7	218074	9	AC023283	AC023283 Homo sapi
c 120	20	0.7	132171	3	AC008370	AC008370 Drosophil	c 193	20	0.7	221689	2	AC097195	AC097195 Rattus no
c 121	20	0.7	132641	2	AC100539	AC100539 Mus muscu	c 194	20	0.7	226060	2	AC079583	AC079583 Mus muscu
c 122	20	0.7	132641	2	AC100539	AC100539 Mus muscu	c 195	20	0.7	226833	3	AE003838	AE003838 Drosophil
c 123	20	0.7	135497	9	AL359752	AL359752 Mus muscu	c 196	20	0.7	228257	2	AC125329	AC125329 Mus muscu
c 124	20	0.7	137955	9	AL359752	AL359752 Human DNA	c 197	20	0.7	275314	2	AC121848	AC121848 Mus muscu
c 125	20	0.7	141079	8	AP002868	AP002868 Oryza sat	c 198	20	0.7	327357	2	AC098504	AC098504 Rattus no
c 126	20	0.7	142203	2	AC079521	AC079521 Mus muscu	c 199	20	0.7	340000	9	AP001707	AP001707 Homo sapi
c 127	20	0.7	145576	8	AP002541	AP002541 Oryza sat	c 200	19	0.6	223	4	AF152590	AF152590 Capreolus
c 128	20	0.7	147474	2	AC117872	AC117872 Rattus no	c 201	19	0.6	275	11	G41356	G41356 21351 Zebra
c 129	20	0.7	147728	9	AC034113	AC034113 Homo sapi	c 202	19	0.6	375	14	AV655518	AV655518 Hepatitis
c 130	20	0.7	149207	9	AC010435	AC010435 Homo sapi	c 203	19	0.6	384	14	AV657142	AV657142 Hepatitis
c 131	20	0.7	150183	2	AC126985	AC126985 Rattus no	c 204	19	0.6	422	11	G21255	G21255 human STS W
c 132	20	0.7	151991	9	AP004289	AP004289 Homo sapi	c 205	19	0.6	558	1	AF437054	AF437054 Unculture
c 133	20	0.7	153031	2	AC105458	AC105458 Felis cat	c 206	19	0.6	581	11	G62797	G62797 SHGC-140335
c 134	20	0.7	155798	2	AC099431	AC099431 Rattus no	c 207	19	0.6	669	11	G58716	G58716 SHGC-105508
c 135	20	0.7	157559	2	AC020344	AC020344 Drosophil	c 208	19	0.6	755	8	STPOACUTR	X55748 S.tuberosum
c 136	20	0.7	158574	2	AC024895	AC024895 Homo sapi	c 209	19	0.6	770	9	HUMLC07	M61840 human lacta
c 137	20	0.7	159158	9	AL359915	AL359915 Human DNA	c 210	19	0.6	888	3	DDU66524	U66524 Dictyostell
c 138	20	0.7	160392	9	AC104236	AC104236 Homo sapi	c 211	19	0.6	1260	1	S38128	S38128 lciA-lactoc



c 212	19	0.6	1494	10	RNU09228	U09228 Rattus norv	c 285	19	0.6	88735	2	AFI65178	AFI65178 Homo sapi
c 213	19	0.6	1578	9	AF236882	AF236882 Homo sapi	c 286	19	0.6	90041	2	AC095553	AC095553 Rattus no
c 214	19	0.6	1843	2	AC014303	AC014303 Drosophil	c 287	19	0.6	90902	8	ATF28420	ATF28420 Arabidops
c 215	19	0.6	2005	10	MUSKTEPII	K02108 Mouse kerat	c 288	19	0.6	91081	2	AC096165	AC096165 Rattus no
c 216	19	0.6	2064	8	AF191494	AF191494 Arabidops	c 289	19	0.6	91955	2	AC106613	AC106613 Rattus no
c 217	19	0.6	2249	10	BC003756	BC003756 Mus muscu	c 290	19	0.6	92138	9	AL590391	AL590391 Human DNA
c 218	19	0.6	2490	8	AF105142	AF105142 Brassica	c 291	19	0.6	93173	2	AC094918	AC094918 Rattus no
c 219	19	0.6	2494	9	HS801051	AL117408 Homo sapi	c 292	19	0.6	94081	9	HSJ820B18	AL109946 Human DNA
c 220	19	0.6	2533	9	HS805082	AL833769 Homo sapi	c 293	19	0.6	94366	2	AC112468	AC112468 Rattus no
c 221	19	0.6	2626	5	AK002145	AB002145 Rana cate	c 294	19	0.6	94453	9	AC019070	AC019070 Homo sapi
c 222	19	0.6	2790	9	AK054790	AK054790 Homo sapi	c 295	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 223	19	0.6	2800	8	STPOAC58	X55749 S. tuberosum	c 296	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 224	19	0.6	2825	9	AK023073	AF203971 Homo sapi	c 297	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 225	19	0.6	3037	3	AF203971	AF203971 Entamoeba	c 298	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 226	19	0.6	3151	8	AF089003	AF089003 Arabidops	c 299	19	0.6	9781	9	AC115082	AC115082 Homo sapi
c 227	19	0.6	3173	8	AF160500	AF160500 Arabidops	c 300	19	0.6	100099	10	AE008684_3	Continuation (4 of
c 228	19	0.6	4048	8	AF277377	AF277377 Arabidops	c 301	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 229	19	0.6	4830	8	SCADR6	XL12493 Yeast ADP6	c 302	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 230	19	0.6	6274	9	HSLPH	X07994 Human mRNA	c 303	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 231	19	0.6	8801	14	AY037273	AY037273 Human imm	c 304	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 232	19	0.6	10029	1	AE006202	AE006202 Pasteurel	c 305	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 233	19	0.6	10379	1	AE007943	AE007943 Agrobacte	c 306	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 234	19	0.6	10581	1	AE008975	AE008975 Agrobacte	c 307	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 235	19	0.6	10917	6	AX384783	AX384783 Methanoba	c 308	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 236	19	0.6	10939	1	AE000813	AE000813 Helicobac	c 309	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 237	19	0.6	12496	1	AE000634	AE000634 Helicobac	c 310	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 238	19	0.6	12526	1	AE001548	AE001548 Helicobac	c 311	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 239	19	0.6	13684	1	AE010466	AE010466 Fusobacte	c 312	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 240	19	0.6	14515	4	CFY15484	Y15484 Canis famli	c 313	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 241	19	0.6	22939	3	CEW04E12	Z82070 Caenorhabdi	c 314	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 242	19	0.6	23087	1	SCD40A	AL161691 Streptomy	c 315	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 243	19	0.6	27413	2	AC127051	AC127051 Rattus no	c 316	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 244	19	0.6	30589	3	CEZK666	Z49132 Caenorhabdi	c 317	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 245	19	0.6	31638	10	AF259073	AF259073 Mus muscu	c 318	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 246	19	0.6	35550	8	U33335	U33335 Saccharomyc	c 319	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 247	19	0.6	36019	9	AC108726	AC108726 Homo sapi	c 320	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 248	19	0.6	36630	9	AC006541	AC006541 Homo sapi	c 321	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 249	19	0.6	40638	10	AC005403	AC005403 Mus muscu	c 322	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 250	19	0.6	42248	2	AC105943	AC105943 Homo sapi	c 323	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 251	19	0.6	43351	9	AC004800	AC004800 Homo sapi	c 324	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 252	19	0.6	44027	3	CBRG41F07	AC084587 Caenorhab	c 325	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 253	19	0.6	44236	3	U80027	U80027 Caenorhabdi	c 326	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 254	19	0.6	47733	3	L14433	L14433 Caenorhabdi	c 327	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 255	19	0.6	49393	2	AC101083	AC101083 Mus muscu	c 328	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 256	19	0.6	52831	2	AC100274	AC100274 Mus muscu	c 329	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 257	19	0.6	54727	9	AL357336	AL357336 Human DNA	c 330	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 258	19	0.6	55801	2	AC131505	AC131505 Lytechinu	c 331	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 259	19	0.6	58330	2	AL353694_3	Continuation (4 of	c 332	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 260	19	0.6	58796	2	AC112983	AC112983 Mus muscu	c 333	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 261	19	0.6	58796	2	AC112983	AC112983 Mus muscu	c 334	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 262	19	0.6	61796	2	AC100321	AC100321 Mus muscu	c 335	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 263	19	0.6	61973	2	AC094631	AC094631 Rattus no	c 336	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 264	19	0.6	63347	2	AC110526	AC110526 Mus muscu	c 337	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 265	19	0.6	63809	2	AC100512	AC100512 Mus muscu	c 338	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 266	19	0.6	66204	2	AC084699	AC084699 Homo sapi	c 339	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 267	19	0.6	6204	2	AC084699	AC084699 Homo sapi	c 340	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 268	19	0.6	69208	2	AC020466	AC020466 Drosophil	c 341	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 269	19	0.6	71225	9	AL358196	AL358196 Human DNA	c 342	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 270	19	0.6	72085	2	AC118655	AC118655 Homo sapi	c 343	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 271	19	0.6	72891	2	AC124128	AC124128 Mus muscu	c 344	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 272	19	0.6	73546	2	AC129938	AC129938 Mus muscu	c 345	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 273	19	0.6	73579	2	AC117704	AC117704 Mus muscu	c 346	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 274	19	0.6	73656	2	AC027536	AC027536 Homo sapi	c 347	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 275	19	0.6	76193	9	AL451081	AL451081 Human DNA	c 348	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 276	19	0.6	77547	2	AC016804	AC016804 Homo sapi	c 349	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 277	19	0.6	77690	8	NC18A7	AL670542 Neurospor	c 350	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 278	19	0.6	78215	2	AC105803	AC105803 Rattus no	c 351	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 279	19	0.6	79376	2	AC105652	AC105652 Rattus no	c 352	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 280	19	0.6	79829	2	AC036211	AC036211 Homo sapi	c 353	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 281	19	0.6	83698	8	AB010072	AB010072 Arabidops	c 354	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 282	19	0.6	83341	2	AC106700	AC106700 Rattus no	c 355	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 283	19	0.6	88098	9	AL451042	AL451042 Human DNA	c 356	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 284	19	0.6	88211	2	AC130247	AC130247 Rattus no	c 357	19	0.6	101846	9	AL450324	AL450324 Human DNA

358	19	0.6 131753	9	AL358790	Human DNA	431	19	0.6 158095	2	AC016224	AC016224 Homo sapi
359	19	0.6 133708	2	AC120074	Rattus no	c 432	19	0.6 158591	9	AC012597	AC012597 Homo sapi
c 360	19	0.6 133708	2	AC092270	Homo sapi	433	19	0.6 158677	2	CNS01DUR	AL133316 Homo sapi
361	19	0.6 134965	9	AL354923	Human DNA	c 434	19	0.6 158817	2	AC127442	AC127442 Rattus no
362	19	0.6 135245	2	AC116286	Rattus no	435	19	0.6 159312	2	AC096878	AC096878 Pan trogl
c 363	19	0.6 135430	9	AC112131	Homo sapi	436	19	0.6 159476	9	AL441963	AL441963 Human DNA
c 364	19	0.6 135598	9	AC099344	Homo sapi	437	19	0.6 159510	9	AC023156	AC023156 Homo sapi
365	19	0.6 137150	2	AC125856	Rattus no	438	19	0.6 159859	2	AC074010	AC074010 Homo sapi
c 366	19	0.6 137539	2	AC130193	Felis cat	c 439	19	0.6 160242	9	AP002778	AP002778 Homo sapi
c 367	19	0.6 138783	9	HS564M11	Human DNA	c 440	19	0.6 160509	2	AC121749	AC121749 Rattus no
c 368	19	0.6 140150	9	AC072057	Homo sapi	441	19	0.6 160736	2	AC027477	AC027477 Homo sapi
369	19	0.6 140756	9	AL139038	Human DNA	442	19	0.6 160804	2	AC011828	AC011828 Homo sapi
370	19	0.6 141212	2	AC113859	Rattus no	c 443	19	0.6 161003	2	AC121888	AC121888 Mus muscu
c 371	19	0.6 142225	9	AC110053	Homo sapi	444	19	0.6 161150	9	AC126240	AC126240 Felis cat
372	19	0.6 142367	2	AC109899	Rattus no	c 445	19	0.6 161648	9	AC108462	AC108462 Homo sapi
373	19	0.6 142776	10	AC006404	Mus muscu	446	19	0.6 161682	2	AC024438	AC024438 Homo sapi
c 374	19	0.6 143124	2	AC129074	Felis cat	447	19	0.6 161757	2	AC044901	AC044901 Homo sapi
c 375	19	0.6 143281	2	AP000614	Homo sapi	448	19	0.6 161879	9	AC017005	AC017005 Homo sapi
376	19	0.6 143677	2	AC102481	Mus muscu	c 449	19	0.6 162208	9	AC073321	AC073321 Homo sapi
c 377	19	0.6 143710	2	AC036109	Homo sapi	450	19	0.6 162322	9	AC093027	AC093027 Homo sapi
378	19	0.6 143723	2	AC012248	Homo sapi	c 451	19	0.6 162599	9	AL360230	AL360230 Human DNA
c 379	19	0.6 143823	9	AC019195	Homo sapi	c 452	19	0.6 163108	2	AC016741	AC016741 Homo sapi
c 380	19	0.6 143842	2	AC096401	Rattus no	c 453	19	0.6 163228	2	AC127812	AC127812 Rattus no
c 381	19	0.6 144480	2	AP004276	Homo sapi	454	19	0.6 163528	2	AC130416	AC130416 Homo sapi
c 382	19	0.6 146327	9	AL162253	Human DNA	455	19	0.6 163632	2	AC069057	AC069057 Homo sapi
383	19	0.6 147061	2	AC119597	Rattus no	456	19	0.6 164223	2	AC109727	AC109727 Rattus no
c 384	19	0.6 147140	9	AC010226	Homo sapi	c 457	19	0.6 164302	9	AC127457	AC127457 Homo sapi
c 385	19	0.6 148137	2	AC025309	Homo sapi	c 463	19	0.6 165191	9	HSDJ140A9	AL109917 Human DNA
c 391	19	0.6 148352	2	AC025309	Homo sapi	c 464	19	0.6 165337	2	AC096212	AC096212 Rattus no
c 392	19	0.6 148459	2	AC128226	Rattus no	c 465	19	0.6 165456	9	AC090733	AC090733 Homo sapi
c 393	19	0.6 148517	2	AC011147	Homo sapi	c 466	19	0.6 165589	9	AL356584	AL356584 Human DNA
394	19	0.6 148557	2	AC116827	Mus muscu	c 467	19	0.6 165743	9	AL691459	AL691459 Homo sapi
395	19	0.6 148703	2	AP004879	Oryza sat	468	19	0.6 165854	2	AC091539	AC091539 Canis fam
396	19	0.6 148930	9	AC073316	Homo sapi	469	19	0.6 165945	2	AC104296	AC104296 Mus muscu
c 397	19	0.6 149061	2	AC118888	Rattus no	470	19	0.6 166022	9	AL354950	AL354950 Human DNA
c 398	19	0.6 149794	2	AC007273	Homo sapi	471	19	0.6 166143	9	AC013447	AC013447 Homo sapi
399	19	0.6 150889	9	AC007881	Homo sapi	472	19	0.6 166305	9	AC012447	AC012447 Homo sapi
c 400	19	0.6 151104	2	AC096123	Rattus no	c 473	19	0.6 166765	9	AC009721	AC009721 Homo sapi
c 401	19	0.6 151117	2	AL357128	Homo sapi	c 474	19	0.6 167269	10	AC083894	AC083894 Mus muscu
c 402	19	0.6 151321	2	AC012276	Homo sapi	475	19	0.6 167446	2	AC122292	AC122292 Mus muscu
c 403	19	0.6 152349	2	AP004790	Oryza sat	c 476	19	0.6 167463	9	AC108489	AC108489 Homo sapi
c 404	19	0.6 152408	2	AP005537	Oryza sat	c 477	19	0.6 167611	9	AL583859	AL583859 Human DNA
c 405	19	0.6 152546	9	AL391221	Human DNA	478	19	0.6 167614	2	AC119641	AC119641 Rattus no
c 406	19	0.6 152787	2	AC026623	Homo sapi	c 479	19	0.6 167616	2	AC106290	AC106290 Rattus no
407	19	0.6 153300	2	AC011933	Homo sapi	480	19	0.6 167783	2	AC094651	AC094651 Rattus no
408	19	0.6 153328	2	AC122111	Rattus no	481	19	0.6 167888	2	AC121651	AC121651 Rattus no
409	19	0.6 153590	9	AP001284	Homo sapi	c 482	19	0.6 167998	9	AL353662	AL353662 Human DNA
410	19	0.6 154001	9	AC083904	Homo sapi	c 483	19	0.6 168239	2	AC021367	AC021367 Homo sapi
c 411	19	0.6 154076	2	AC023273	Homo sapi	c 484	19	0.6 168367	2	AC107830	AC107830 Mus muscu
c 412	19	0.6 154159	2	AC104645	Homo sapi	c 485	19	0.6 168468	9	AC005510	AC005510 Homo sapi
c 413	19	0.6 154289	2	AC027714	Homo sapi	c 486	19	0.6 168668	2	CNS07YQ8	AL713908 Oryza sat
c 414	19	0.6 154371	9	AP003466	Homo sapi	c 487	19	0.6 169106	2	AP005261	AP005261 Oryza sat
c 415	19	0.6 154686	9	AP001595	Homo sapi	c 488	19	0.6 169184	9	AC022398	AC022398 Homo sapi
c 416	19	0.6 155507	2	AL831747	Danio rer	c 489	19	0.6 169204	9	AP001486	AP001486 Homo sapi
417	19	0.6 155619	9	CNS01DFF	Human chr	c 490	19	0.6 169514	2	AC122449	AC122449 Mus muscu
c 418	19	0.6 155705	9	AC093823	Homo sapi	c 491	19	0.6 169833	2	AC107249	AC107249 Rattus no
c 419	19	0.6 155763	2	AC099449	Rattus no	c 492	19	0.6 169880	2	AC107288	AC107288 Rattus no
c 420	19	0.6 155818	9	AC073504	Homo sapi	c 493	19	0.6 170000	2	OSJN00133	AL662943 Oryza sat
c 421	19	0.6 156149	2	AC027556	Homo sapi	c 494	19	0.6 170387	9	AC115225	AC115225 Rattus no
c 422	19	0.6 156238	2	AC104862	Mus muscu	495	19	0.6 170494	2	AP001919	AP001919 Homo sapi
423	19	0.6 156361	2	AC108612	Rattus no	496	19	0.6 170676	9	AC026258	AC026258 Homo sapi
424	19	0.6 156381	2	AC021087	Homo sapi	497	19	0.6 170711	2	AC032020	AC032020 Homo sapi
c 425	19	0.6 156452	2	AC096043	Rattus no	c 498	19	0.6 170829	2	AP001316	AP001316 Homo sapi
426	19	0.6 156856	2	AC097235	Rattus no	c 499	19	0.6 170906	2	AC084314	AC084314 Mus muscu
c 427	19	0.6 156891	2	AC108550	Rattus no	c 500	19	0.6 171349	2	AC020735	AC020735 Homo sapi
428	19	0.6 156992	2	AC093581	Homo sapi	c 501	19	0.6 171369	2	AC113690	AC113690 Rattus no
429	19	0.6 157511	2	AC021383	Homo sapi	c 502	19	0.6 171486	2	AC120330	AC120330 Rattus no
c 430	19	0.6 157562	2	AC011574	Homo sapi	503	19	0.6 171676	9	AC107904	AC107904 Homo sapi

c 504	19	0.6 171826	2	AC119810	Mus muscu	577	19	0.6 182166	2	AC098066	Rattus no
c 505	19	0.6 172210	9	AC098656	Homo sapi	578	19	0.6 182166	2	AC126658	Rattus no
c 506	19	0.6 172341	2	AC095490	Homo sapi	579	19	0.6 182170	2	AC120775	Rattus no
c 507	19	0.6 172573	9	AC007276	Homo sapi	c 580	19	0.6 182205	2	AC104478	Sus scrof
c 508	19	0.6 172692	2	AP001013	Homo sapi	c 581	19	0.6 182401	2	AC112034	Rattus no
c 509	19	0.6 172936	2	AC027154	Mus muscu	c 582	19	0.6 182500	2	AC026988	Homo sapi
c 510	19	0.6 173037	2	AC124155	Danio rer	c 583	19	0.6 182779	2	AC113783	Rattus no
c 511	19	0.6 173251	2	AC114469	Rattus no	c 584	19	0.6 183023	2	AC095955	Rattus no
c 512	19	0.6 173260	9	CNS07ECU	Human chr	c 585	19	0.6 183251	9	AP002848	Homo sapi
c 513	19	0.6 173709	9	AP001010	Homo sapi	c 586	19	0.6 183251	9	AC013555	Homo sapi
c 514	19	0.6 173758	9	AC009144	Homo sapi	c 587	19	0.6 183287	2	AC122493	Mus muscu
c 515	19	0.6 173769	10	AL669819	Mouse DNA	c 588	19	0.6 183499	2	AL607153	Homo sapi
c 516	19	0.6 173844	2	AC040904	Homo sapi	c 589	19	0.6 184081	2	AC103625	Mus muscu
c 517	19	0.6 174031	4	AC091507	Sus scrof	c 590	19	0.6 184114	2	AC121882	Mus muscu
c 518	19	0.6 174149	9	AC009227	Homo sapi	c 591	19	0.6 184184	2	AC120545	Mus muscu
c 519	19	0.6 174494	30	AC068744	Homo sapi	c 592	19	0.6 184868	2	AC102310	Mus muscu
c 520	19	0.6 174539	2	AP000875	Homo sapi	c 593	19	0.6 185242	2	AC112103	Rattus no
c 521	19	0.6 174647	2	AC009452	Homo sapi	c 594	19	0.6 185259	9	AC063953	Homo sapi
c 522	19	0.6 175037	2	AC118879	Rattus no	c 595	19	0.6 185399	9	AC098133	Rattus no
c 523	19	0.6 175118	3	AC010842	Drosophill	c 596	19	0.6 185596	9	AC021553	Homo sapi
c 524	19	0.6 175306	9	AC079948	Homo sapi	c 597	19	0.6 185789	2	AC127224	Mus muscu
c 525	19	0.6 175345	2	AC022301	Mus muscu	c 598	19	0.6 186052	9	AC104187	Homo sapi
c 526	19	0.6 175403	9	AC093268	Homo sapi	c 599	19	0.6 186394	2	AC012551	Homo sapi
c 527	19	0.6 175432	2	AC114711	Rattus no	c 600	19	0.6 186690	2	AC023553	Homo sapi
c 528	19	0.6 175448	2	AC009662	Homo sapi	c 601	19	0.6 187083	2	AC117050	Rattus no
c 529	19	0.6 175781	3	AC008091	Drosophill	c 602	19	0.6 187332	2	AC110401	Rattus no
c 530	19	0.6 176065	2	AC024046	Homo sapi	c 603	19	0.6 187449	9	AC016450	Homo sapi
c 531	19	0.6 176097	2	AC112282	Rattus no	c 604	19	0.6 187645	2	AC102191	Mus muscu
c 532	19	0.6 176221	2	AC011111	Homo sapi	c 605	19	0.6 187816	10	AL606919	Mouse DNA
c 533	19	0.6 176295	2	AC026176	Homo sapi	c 606	19	0.6 187965	2	AC110729	Mus muscu
c 534	19	0.6 176498	9	AC003035	Homo sapi	c 607	19	0.6 188197	2	AL845361	Mus muscu
c 535	19	0.6 176524	9	AC0010726	Homo sapi	c 608	19	0.6 188272	3	AC005639	Drosophill
c 536	19	0.6 176604	2	AC120569	Rattus no	c 609	19	0.6 189086	2	AC009921	Homo sapi
c 537	19	0.6 176613	2	AC102554	Mus muscu	c 610	19	0.6 189191	2	AC104682	Sus scrof
c 538	19	0.6 177027	9	AC097514	Homo sapi	c 611	19	0.6 189729	2	AC073930	Homo sapi
c 539	19	0.6 177080	9	AC027288	Homo sapi	c 612	19	0.6 189894	2	AC115722	Mus muscu
c 540	19	0.6 177402	9	AC007406	Homo sapi	c 613	19	0.6 189978	2	AC097532	Homo sapi
c 541	19	0.6 177795	9	AC067743	Homo sapi	c 614	19	0.6 190304	2	AC114439	Rattus no
c 542	19	0.6 177901	9	AC011893	Homo sapi	c 615	19	0.6 190369	10	AL590429	Mouse DNA
c 543	19	0.6 177969	9	AC068107	Homo sapi	c 616	19	0.6 190803	2	AC111090	Mus muscu
c 544	19	0.6 178080	2	AC026319	Homo sapi	c 617	19	0.6 190925	2	AL606665	Homo sapi
c 545	19	0.6 178113	10	AC121917	Mus muscu	c 618	19	0.6 191134	2	AC122376	Mus muscu
c 546	19	0.6 178144	2	AC073929	Homo sapi	c 619	19	0.6 191286	9	AC012050	Homo sapi
c 547	19	0.6 178182	2	AC114980	Homo sapi	c 620	19	0.6 191891	2	AC010443	Homo sapi
c 548	19	0.6 178184	10	AL683866	Mouse DNA	c 621	19	0.6 192296	9	AC009654	Homo sapi
c 549	19	0.6 178192	2	AC099045	Homo sapi	c 622	19	0.6 192388	2	AC118926	Mus muscu
c 550	19	0.6 178314	9	CNS01RHH	Homo sapi	c 623	19	0.6 192388	2	AC118926	Mus muscu
c 551	19	0.6 178433	9	AC006427	Human chr	c 624	19	0.6 192960	2	AC098808	Paplo cyn
c 552	19	0.6 178524	9	AC008427	Homo sapi	c 625	19	0.6 193135	2	AC122466	Mus muscu
c 553	19	0.6 178716	2	AC099216	Rattus no	c 626	19	0.6 193916	2	AC123184	Rattus no
c 554	19	0.6 178733	9	AC026003	Homo sapi	c 627	19	0.6 194106	2	AL606756	Mus muscu
c 555	19	0.6 178779	2	AC117442	Homo sapi	c 628	19	0.6 194453	2	AC010862	Homo sapi
c 556	19	0.6 178892	2	AC130794	Felis cat	c 629	19	0.6 194809	4	AC091506	Sus scrof
c 557	19	0.6 178997	2	AC126611	Mus muscu	c 630	19	0.6 194809	4	AC091506	Sus scrof
c 558	19	0.6 179242	2	AC099470	Rattus no	c 631	19	0.6 195137	2	AL845507	Danio rer
c 559	19	0.6 179641	2	AC073694	Mus muscu	c 632	19	0.6 195159	2	AC102500	Mus muscu
c 560	19	0.6 179783	2	AC094349	Rattus no	c 633	19	0.6 195191	9	AC024339	Homo sapi
c 561	19	0.6 179868	9	AC106746	Homo sapi	c 634	19	0.6 195319	2	AC119470	Rattus no
c 562	19	0.6 180137	2	AC023081	Homo sapi	c 635	19	0.6 195348	2	AC127081	Rattus no
c 563	19	0.6 180189	9	AL365510	Human DNA	c 636	19	0.6 195964	2	AC114410	Mus muscu
c 564	19	0.6 180216	2	AC015756	Homo sapi	c 637	19	0.6 196067	2	AC068560	Mus muscu
c 565	19	0.6 180487	2	AC113228	Bos tauru	c 638	19	0.6 196242	8	ATCHRIV75	Arabidops
c 566	19	0.6 180689	2	AC124913	Sus scrof	c 639	19	0.6 196267	2	AC116145	Mus muscu
c 567	19	0.6 180897	9	AC106782	Homo sapi	c 640	19	0.6 196493	2	AL831764	Mus muscu
c 568	19	0.6 180900	2	AC018975	Homo sapi	c 641	19	0.6 197054	2	AC094179	Rattus no
c 569	19	0.6 180948	2	AC098800	Homo sapi	c 642	19	0.6 197351	2	AC127204	Rattus no
c 570	19	0.6 181041	2	AC108666	Rattus no	c 643	19	0.6 197452	2	AL355513	Homo sapi
c 571	19	0.6 181043	2	AC011833	Homo sapi	c 644	19	0.6 197622	2	AC115300	Mus muscu
c 572	19	0.6 181083	2	AP001268	Homo sapi	c 645	19	0.6 198064	2	AC121611	Mus muscu
c 573	19	0.6 181145	10	AP0079819	Mus muscu	c 646	19	0.6 198334	9	AF411849S1	Homo sapi
c 574	19	0.6 181202	2	AC108432	Mus muscu	c 647	19	0.6 198602	10	AL450395	Mouse DNA
c 575	19	0.6 181293	2	AC112548	Rattus no	c 648	19	0.6 199071	10	AL669938	Mouse DNA
c 576	19	0.6 181700	2	AC128595	Rattus no	c 649	19	0.6 199102	2	AC079315	Homo sapi



796	18	0.6	960	6	AX122205	AX122205 Sequence	c 869	18	0.6	2689	1	BSU19898	UI9898 Bacillus sp
c 797	18	0.6	962	4	SHPPLAC	M31660 Ovine place	c 870	18	0.6	2740	1	P30TRA	M62986 Plasmid p30
798	18	0.6	1023	8	AF155762	AF155762 Pismum sat	c 871	18	0.6	2841	10	RATTCBC3	M63795 Rat T-cell
799	18	0.6	1047	5	AF317271	AF317271 Pelvicach	c 872	18	0.6	2854	8	SCYDL180W	Z74228 S. cerevisia
800	18	0.6	1083	6	AX064929	AX064929 Sequence	c 873	18	0.6	2904	9	AK096138	AK096138 Homo sapi
801	18	0.6	1094	9	HSU3	X14945 Human gene	c 874	18	0.6	2987	10	MMIDDGENE	X95480 M. musculus
c 802	18	0.6	1205	6	AX013773	AX013773 Sequence	c 875	18	0.6	3000	6	ARI72809	ARI72809 Sequence
c 803	18	0.6	1216	4	OAPLE2	AF079546 Ovis arie	c 876	18	0.6	3157	3	AY058362	AY058362 Drosophill
c 804	18	0.6	1254	1	ECPSU028	AF369028 Streptoco	c 877	18	0.6	3165	3	DMP13K59F	X99912 D.melanogas
c 805	18	0.6	1264	1	ECPSU233	X55896 E.coli plas	c 878	18	0.6	3275	6	AX078760	AX078760 Sequence
c 806	18	0.6	1323	9	AB014486	AB014486 Homo sapi	c 879	18	0.6	3566	8	ENU86619	U86619 Emericella
c 807	18	0.6	1339	3	AY058340	AY058340 Drosophill	c 880	18	0.6	3614	8	RCCHS2	DI0160 Rhizopus oi
c 808	18	0.6	1348	3	AF252639	AF252639 Drosophill	c 881	18	0.6	3671	14	AF291703	AF291703 Andes vir
c 809	18	0.6	1348	3	AF252641	AF252641 Drosophill	c 882	18	0.6	3881	8	SCU07228	U72228 Saccharomyc
c 810	18	0.6	1348	3	AF252641	AF252641 Drosophill	c 883	18	0.6	3968	1	MYCMBPRP	L11447 Mycoplasma
c 811	18	0.6	1353	9	HS3A326249	AJ326249 Homo sapi	c 884	18	0.6	3969	6	AR203450	AR203450 Sequence
c 812	18	0.6	1389	9	AF154847	AF154847 Homo sapi	c 885	18	0.6	3969	6	AX034666	AX034666 Sequence
c 813	18	0.6	1390	9	AF044670	AF044670 Homo sapi	c 886	18	0.6	3999	6	AX305640	AX305640 Sequence
c 814	18	0.6	1420	5	AF358668	AF358668 Oncorhync	c 887	18	0.6	4116	8	AB055105	D78641 Mouse mRNA
c 815	18	0.6	1433	3	AFSECAATP	AF358668 Oncorhync	c 888	18	0.6	4116	8	AB055105	AB055105 Oryza sat
c 816	18	0.6	1473	8	AF084564	X79331 A.francisca	c 889	18	0.6	4197	3	AF163835	AF163835 Dictyoste
c 817	18	0.6	1506	8	AY052232	AY084564 Arabidops	c 890	18	0.6	4220	8	ENU86620	U86620 Emericella
c 818	18	0.6	1515	6	AR170122	AY052232 Arabidops	c 891	18	0.6	4255	9	AK024455	AK024455 Homo sapi
c 819	18	0.6	1561	9	HUMNELI	ARI70122 Sequence	c 892	18	0.6	4451	1	WSAJ3049	AJ003049 Wolinella
c 820	18	0.6	1579	9	AK000918	ARI70123 Sequence	c 893	18	0.6	4796	5	XLXOLL	Y09661 X.laevis mR
c 821	18	0.6	1600	10	AF157497	M20199 Human neutr	c 894	18	0.6	4982	6	AR107128	AR107128 Sequence
c 822	18	0.6	1609	9	BC002992	AF157497 Mus muscu	c 895	18	0.6	4982	6	AR181017	AR181017 Sequence
c 823	18	0.6	1634	10	MMU09930	BC002992 Homo sapi	c 896	18	0.6	5028	8	SCU49845	U49845 Saccharomyc
c 824	18	0.6	1645	9	BC034772	U09930 Mus musculu	c 897	18	0.6	5072	1	LLNISG	AJ000993 Lactococc
c 825	18	0.6	1650	6	AR170152	BC034772 Homo sapi	c 898	18	0.6	5131	10	MMU83913	U83913 Mus musculu
c 826	18	0.6	1650	6	AR170153	ARI70152 Sequence	c 899	18	0.6	5173	6	AR204612	AR204612 Sequence
c 827	18	0.6	1664	3	DMRPS3	ARI70153 Sequence	c 900	18	0.6	5191	10	MMU28789	U28789 Mus musculu
c 828	18	0.6	1668	10	BC003866	X72921 D.melanogas	c 901	18	0.6	5292	9	HSMED	Y00477 Human bone
c 829	18	0.6	1700	3	AF273766	BC003866 Mus muscu	c 902	18	0.6	5376	9	AF352051	AF352051 Homo sapi
c 830	18	0.6	1789	9	BC011702	AF273766 Perna can	c 903	18	0.6	5430	3	PFU27339	PFU27339 Plasmodium
c 831	18	0.6	1792	9	BC007391	BC011702 Homo sapi	c 904	18	0.6	5867	9	HSL241B9A	Z69362 Human DNA s
c 832	18	0.6	1800	6	AK048215	BC007391 Homo sapi	c 905	18	0.6	6040	9	AC108054	AC108054 Homo sapi
c 833	18	0.6	1839	5	DRU17600	AR048215 Sequence	c 906	18	0.6	6471	9	HSSTTV	X96783 H.sapiens S
c 834	18	0.6	1878	6	AX078761	U17600 Danio rerio	c 907	18	0.6	6562	5	AF197944	AF197944 Xenopus l
c 835	18	0.6	1905	10	MUSVCRB2X	AX078761 Sequence	c 908	18	0.6	7383	2	AC014643	AC014643 Drosophill
c 836	18	0.6	1909	9	AB063086	M28601 Mouse T cel	c 909	18	0.6	7894	8	AF004964	AF004964 Lotus jap
c 837	18	0.6	1909	10	AF134805	AB063086 Macaca fa	c 910	18	0.6	8329	4	AB013085	AB013085 Potorous
c 838	18	0.6	1923	1	AF323029	AF134805 Mus muscu	c 911	18	0.6	8615	5	GGU28143	U28143 Gallus gall
c 839	18	0.6	1930	9	AK057359	AF323029 Sphingomo	c 912	18	0.6	8810	9	AY040206	AY040206 Homo sapi
c 840	18	0.6	1935	9	D83730	AK057359 Homo sapi	c 913	18	0.6	8868	6	AX399206	AX399206 Sequence
c 841	18	0.6	1943	5	GM6PR46K	D83730 Homo sapien	c 914	18	0.6	8868	9	HSU16720	U16720 Human inter
c 842	18	0.6	1962	6	AR170120	X95501 G.gallus mR	c 915	18	0.6	8873	6	AX251820	AX251820 Sequence
c 843	18	0.6	1982	6	AR170120	AX014865 Sequence	c 916	18	0.6	8873	6	AX344206	AX344206 Sequence
c 844	18	0.6	1982	6	AR170121	ARI70120 Sequence	c 917	18	0.6	8873	6	AX348605	AX348605 Sequence
c 845	18	0.6	1982	8	SCYDL179W	ARI70121 Sequence	c 918	18	0.6	8958	1	LLU17233	LLU17233 Lactococcus
c 846	18	0.6	1996	9	AF217993	Z74227 S.cerevisia	c 919	18	0.6	9084	6	AX346506	AX346506 Sequence
c 847	18	0.6	2003	9	HSM804811	AF217993 Homo sapi	c 920	18	0.6	9865	2	AC013172	AC013172 Drosophill
c 848	18	0.6	2024	9	BC014156	AL833498 Homo sapi	c 921	18	0.6	9953	3	PCU43145	U67553 Mechanococc
c 849	18	0.6	2064	10	BC021411	BC014156 Homo sapi	c 922	18	0.6	10029	1	AE013639	AE013639 Yersinia
c 850	18	0.6	2144	6	AR170150	BC021411 Mus muscu	c 923	18	0.6	10503	1	AE000819	AE000819 Methanoba
c 851	18	0.6	2144	6	AR170151	ARI70150 Sequence	c 924	18	0.6	10503	1	AE000819	AE000819 Yersinia
c 852	18	0.6	2160	5	AF184244	AF184244 Danio rer	c 925	18	0.6	10607	1	AE009555	AE009555 Brucella
c 853	18	0.6	2180	9	BC033165	BC033165 Homo sapi	c 926	18	0.6	11094	1	AE005854	AE005854 Caulobact
c 854	18	0.6	2204	8	TAIB38	X56782 T.aestivum	c 927	18	0.6	11499	1	AE009957	AE009957 Streptoco
c 855	18	0.6	2248	9	AF051323	BC051323 Homo sapi	c 928	18	0.6	11683	1	AE013669	AE013669 Yersinia
c 856	18	0.6	2251	9	BC002893	BC002893 Homo sapi	c 929	18	0.6	12311	8	AF004559	AF004559 Venturia
c 857	18	0.6	2254	8	AF239719	AF239719 Arabidops	c 930	18	0.6	13187	1	AE005701	AE005701 Caulobact
c 858	18	0.6	2276	5	OWTKS	X92522 Oncorhynch	c 931	18	0.6	13732	6	AX346722	AX346722 Sequence
c 859	18	0.6	2285	3	AY070955	AY070955 Drosophill	c 932	18	0.6	14544	9	AF386492	AF386492 Homo sapi
c 860	18	0.6	2285	3	AX113518	AY113518 Drosophill	c 933	18	0.6	15854	9	AF148319	AF148319 Homo sapi
c 861	18	0.6	2285	5	AF077830	AF077830 Gallus ga	c 934	18	0.6	17114	9	AC112704	AC112704 Homo sapi
c 862	18	0.6	2300	10	AF134804	AF134804 Mus muscu	c 935	18	0.6	17509	6	AX409450	AX409450 Sequence
c 863	18	0.6	2309	9	BC009469	BC009469 Homo sapi	c 936	18	0.6	17509	6	HUMPAFA	J03764 Human, plas
c 864	18	0.6	2320	5	AK026954	AK026954 Homo sapi	c 937	18	0.6	17963	1	AE007009	AE007009 Mycobacte
c 865	18	0.6	2336	5	AF022946	AF022946 Gallus ga	c 938	18	0.6	18124	3	CEU26736	U26736 Caenorhabdi
c 866	18	0.6	2520	8	AF395906	AF395906 Saccharom	c 939	18	0.6	18540	2	AC014834	AC014834 Drosophill
c 867	18	0.6	2648	3	DMCALB32A	X68566 D.melanogas	c 940	18	0.6	21261	3	AE002935	AE002935 Drosophill
c 868	18	0.6	2667	8	AF443590	AF443590 Morinda c	c 941	18	0.6	21688	9	AC117413	AC117413 Homo sapi











Db 625 CTTAGAGCCCTGTCATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 684  
QY 541 CGCATGGCCATGCTCTGGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAAATTCGTC 600  
Db 685 CGAAATGGCCATGCTCTGGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAAATTCGTC 744  
QY 601 TTCCTTCCCTCGCTCTCAGCAGGGCCAGGGTGACATTTTGAACCCCTCTGTCATCAACTC 660  
Db 745 TTCCTTCCCTCGCTCTCAGCAGGGCCAGGGTGACATTTTGAACCCCTCTGTCATCAACTC 804  
QY 661 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGCGCATGCTGTCGAAGCTGCGG 720  
Db 805 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGCGCATGCTGTCGAAGCTGCGG 864  
QY 721 CAGAGGGTTCTTTTCTCTCTGATGGCTACATGAATTCAGGCCCCAGAACTGCCCAGAA 780  
Db 865 CAGAGGGTTCTTTTCTCTCTGATGGCTACATGAATTCAGGCCCCAGAACTGCCCAGAA 924  
QY 781 ATCGAAGCCCTGATAAAGGAAACACCCGCTTCAAGAACATGGTCATCGTCACCACTACC 840  
Db 925 ATCGAAGCCCTGATAAAGGAAACACCCGCTTCAAGAACATGGTCATCGTCACCACTACC 984  
QY 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGGATATG 900  
Db 985 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGGATATG 1044  
QY 901 ACAGAAGACAGCGCCAGGCTCTATCCGAGAAGTCTGATCAAGGAGCTTCTGTAAGGC 960  
Db 1045 ACAGAAGACAGCGCCAGGCTCTATCCGAGAAGTCTGATCAAGGAGCTTCTGTAAGGC 1104  
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Db 1105 TTGTTGCTCCAAATTCAGAAATCCAGGTCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1164  
QY 1021 GTGGTCATCAGTTGTGCAATCCAGATGGGTGAAAGTGAGTTCACCTCTCACACACAAACA 1080  
Db 1165 GTGGTCATCAGTTGTGCAATCCAGATGGGTGAAAGTGAGTTCACCTCTCACACACAAACA 1224  
QY 1081 ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACACACAAACATAAAGT 1140  
Db 1225 ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACACACAAACATAAAGT 1284  
QY 1141 GTGGCTGCAAGTGACTTCAATCCGAGCCCTGGACCCTGTGGAGACCTAGCTCTGGAGGGT 1200  
Db 1285 GTGGCTGCAAGTGACTTCAATCCGAGCCCTGGACCCTGTGGAGACCTAGCTCTGGAGGGT 1344  
QY 1201 GTGTTCTCCCAAGTTGATTTCCAGTGCAGAGTGTGCCAGGTGAATGAGGATGTC 1260  
Db 1345 GTGTTCTCCCAAGTTGATTTCCAGTGCAGAGTGTGCCAGGTGAATGAGGATGTC 1404  
QY 1261 CTGCTGACAACTGGGCTCCTCTGTAATATACAGCTCAAAGTTTCAAGCCAAAGTATAAA 1320  
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Qy	2761	GATACAGAGATTAGAATTTAGTGCATTTTTTGGAAAGAACCCCTCGAAAACTTCCAG	2820	BASE COUNT	986 a	after 9-days ODF induction.-primary culture, CD34+ Cells"
Db	2992	GATACAGAGATTAGAATTTAGTGCATTTTTTGGAAAGAACCCCTCGAAAACTTCCAG	3051	ORIGIN	726 c	774 g 869 t
Qy	2821	CAGTTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGGCTTGCTTCATGGGTGA	2880	Query Match	93.4%	Score 2868; DB 9; Length 3355;
Db	3052	CAGTTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGGCTTGCTTCATGGGTGA	3111	Best Local Similarity	99.9%	Pred. No. 0;
Qy	2881	TTTGAGAACTTAGCAATAGTGTGTTTGGACCTTAGTACTAAGAAATTTCTACCTGAT	2940	Matches 3069; Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
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RESULT 4						
AK095467		3355 bp mRNA linear	PRI 15-JUL-2002			
LOCUS						
DEFINITION		Homo sapiens cDNA FLJ38148 fis, clone D90ST2003791, highly similar to Homo sapiens ICB-protease activating factor mRNA.				
ACCESSION		AK095467				
VERSION		AK095467.1	GI:21754727			
KEYWORDS		oligo capping; fis (full insert sequence).				
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ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS		1. Nimomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, K., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.				
		NEDO human cDNA sequencing project				
		Unpublished				
TITLE		2 (bases 1 to 3355)				
JOURNAL		Isogai, T. and Yamamoto, J.				
REFERENCE		Direct Submission				
AUTHORS		Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7				
TITLE		kazusa-kametar, Kisarazu, Chiba 292-0812, Japan				
JOURNAL		(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)				
		NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.				
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LOCUS AX318091 3396 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 96 from Patent WO0190156.  
ACCESSION AX318091  
VERSION AX318091.1 GI:17900820  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Reed J.C., Pio F.F., Godzik A., Stehlik C., Damiano J.S., Lee S.H.,  
Oliveira V.A., Hayashi H. and Pawlowski K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 96 29-NOV-2001;  
The Burnham Institute (US)  
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ORIGIN  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Gingras, M.-C., Qiu, J. and Margolin, J.F.  
Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation  
Unpublished  
-2 (bases 1 to 3581)  
Gingras, M.-C., Qiu, J. and Margolin, J.F.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,  
Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX  
77030, USA  
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QY 383 TTAACCTTGAAGAGCACCCTTCACAGAACCTGTCCTGTGGAGGAAGACCAACACCATCAC 442

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of library C17B_978_SKB from chromosome 2 of Homo sapiens (Human).
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VERSION AL121653.2 GI:7159616
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SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 138909)
AUTHORS Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brothier,P., Cattolico,L., Barbe,V., Burgunder,J.M.,
Prud'Homme,J.F., Brice,A., Fontaine,B., Heilig,R. and
Weissenbach,J.
TITLE Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
JOURNAL Nat. Genet. (1999) In press
REFERENCE 2 (bases 1 to 138909)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1355)  
Auffray,C., Ansoenge,W., Ballabio,A., Estivill,X., Gibson,K.,  
Lehrach,H., Poustka,A. and Lundberg,J.  
The European IMAGE consortium for Integrated Molecular analysis of  
human gene transcripts  
Unpublished  
2 (bases 1 to 1355)  
Pluvinet,R., Estivill,X., Escarceller,M. and Sumoy,L.  
Direct Submission  
Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de  
Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via  
s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,  
SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:  
http://www.iro.es e-mail enquiries: lsumoy@iro.es  
EURO-IMAGE Consortium Contact: Auffray C  
CNRS UPR 420 - Genetique Moleculaire et Biologie du Developement  
IFR 1221 - Rue Guy Moquet 19, Batiment G - Bp 8  
94801 Villejuif Cedex, FRANCE  
Tel: ++33-1-49 58 34 98  
Fax: ++33-1-49 58 35 09  
e-mail: auffray@infobiogen.fr  
This clone is available royalty-free through IMAGE Consortium  
Distributors.  
IMPORTANT: This sequence represents the full insert of this IMAGE  
cDNA clone. No attempt has been made to verify whether this  
corresponds to the full-length of the original mRNA from which it  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 179 29-NOV-2001;  
The Burnham Institute (US)  
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BASE COUNT 237 a 228 c 217 g 209 t  
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 481 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 540  
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QY 721 CAGAGGTTCTTTTCTCTTGTGATGCTACAATGAATTCAGCCCCCAGAACTCCCGCAGAA 780  
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Qy	1081	ACGCTGTTCCATACCTCTTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT	1140
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Db	661	GTGGTTCGAAGTGACTTCATTTCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGT	720
Qy	1201	GTGTTCTCCCAAGTTTGTATTTCCGAAGTGCAGGATGTGTCCAGCGTGAATGAGGATGTC	1260
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Qy	1261	CTGCTGACAACTGGGCTCCTCTGTAAATATATACAGCTCAAGGTTCAAGCCAAAGTATAAA	1320
Db	781	CTGCTGACAACTGGGCTCCTCTGTAAATATATACAGCTCAAGGTTCAAGCCAAAGTATAAA	840
Qy	1321	TTCTTTTCAAGAGTCAATCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGT	1371
Db	841	TTCTTTTCAAGAGTCAATCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGT	891
RESULT 12			
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DEFINITION	Sequence 98 from Patent WO0190156.		
ACCESSION	AX318093		
VERSION	AX318093.1	GI:17900822	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Read, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H., Oliveira, V.A., Hayashi, H. and Pawlowski, K.		
JOURNAL	Card domain containing polypeptides, encoding nucleic acids, and methods of use		
FEATURES	Patent: WO 0190156-A 98 29-NOV-2001; The Burnham Institute (US)		
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Qy	2378	TGTGTTATTTTCATTTGACCCACCTTGTCTGACATTTGGAGAGGGAATGGATTACATAGTCA	2437
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Qy	2438	AGTCTCTGTCGAAGTGAACCCCTGTGACCTTGAAGAAATTCATTTAGTCTCTGCTCTGCT	2497
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Qy	2498	CTGCANATGCAGTGAANAATCTAGCTCAGAAATCTTCACAATTTGGTCAAACTGACATTC	2557
Db	779	CTGCANATGCAGTGAANAATCTAGCTCAGAAATCTTCACAATTTGGTCAAACTGACATTC	838
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Db	839	TTGATTTATCAGAAAATTTACCTGGAAAAAGATGGAATGAAGCTCTTCATGAACGTGATCG	898
Qy	2618	ACAGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGC	2677
Db	899	ACAGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGC	958
Qy	2678	AAGCAGCGCTGAGCAGCGCTGTTGAACATTTGGAGGAGTCCCACAACCTCGTCAAGCTTG	2737
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Qy	2738	GTTTGAANAACCTGGAGACTCACAGATACAGATTTAGTAATTTTAGTGCATTTTGGAA	2797
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Db	1259	AGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATTTTGATGATGATGATCTCA	1318
Qy	3038	GTGTTATTACAGGTGCTTTTAACTAGTAACTGCT	3072
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DEFINITION	Homo sapiens CLANB (CLAN1) mRNA, complete cds.		
ACCESSION	AY027788		
VERSION	AY027788.1	GI:14324114	
KEYWORDS	Homo sapiens.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1395)		
TITLE	Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C.		
JOURNAL	Clan, a novel human ced-4-like gene		
MEDLINE	Genomics 75 (1-3), 77-83 (2001)		
PUBMED	21365712		
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REFERENCE 2 (bases 1 to 1395)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA
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QY 3038 GTGTTATTACAGGTGCTTTTAAACTAGTAAGTCTGT 3072
DB 1319 GTGTTATTACAGGTGCTTTTAAACTAGTAAGTCTGT 1353
RESULT 14
AX318176 618 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 181 from Patent WO0190156.
DEFINITION AX318176
ACCESSION AX318176
VERSION AX318176.1 GI:17900867
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 181 29-NOV-2001;
The Burnham Institute (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2818 CAGCAGTTGAATTCGCGGGAATCGTGTGACAGCTGATGATGCTTGCCTTCATGGGT 2877
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RESULT 15
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LOCUS AX318097 768 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 102 from Patent W00190156.
ACCESSION AX318097
VERSION AX318097.1 GI:17900826
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
TITLE Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,
Oliveira, V.A., Hayashi, H. and Pawlowski, K.
METHODS Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 102 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source
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ACCESSION AY027789
VERSION AY027789.1 GI:14324116
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 768)
Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C.
JOURNAL Clan, a novel human ced-4-like gene
MEDLINE Genomics 75 (1-3), 77-83 (2001)
21365712
PUBMED 11472070
REFERENCE
2 (bases 1 to 768)
Stehlik, C., Damiano, J.S., Pio, F., Godzik, A. and Reed, J.C.
AUTHORS Direct Submission
TITLE Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
JOURNAL Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
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BASE COUNT 218 a 157 c 180 g 213 t
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Db 637 GTGAGATATTCACATATTTTACCTTGAAGACACCTTCACAGAACTGCTGTGG 696
QY 421 AGGAGGACCAACACCATCACCGCTGGAGCAGTGACCT 461
Db 697 AGGAGGACCAACACCATCACCGCTGGAGCAGTGACCT 737

RESULT 17
CNS01DS8/c
LOCUS
DEFINITION
BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 563N04
of library RPCI-11 from chromosome 2 of Homo sapiens (Human).
ACCESSION
AL121658
VERSION
AL121658.4 GI:20218783
KEYWORDS
SPG4 genomic DNA interval.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brottier,P., Catolico,L., Barbe,V., Burgunder,J.M.,
Pru'd'Homme,J.F., Brice,A., Fontaine,B., Hellig,R. and
Weissenbach,J.
Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
Nat. Genet. (1999) In press
2 (bases 1 to 162692)
Direct Submission
Genoscope.
Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : ww.genoscope.cns.fr)
On Apr 19, 2002 this sequence version replaced gi:20160242.
FEATURES
Location/Qualifiers
1..162692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="563N04"
BASE COUNT
44981 a 32017 c 32887 g 52792 t 15 others
ORIGIN

Query Match 9.5%; Score 292; DB 9; Length 162692;
Best Local Similarity 100.0%; Pred. No. 6e-146;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTTTGGAAAGAACCCCTCTGAAAACTTTCCAGCAGTTGAAATTTGGCGGAAA 2840
Db 152218 AGGTGCATTTTTTGGAAAGAACCCCTCTGAAAACTTTCCAGCAGTTGAAATTTGGCGGAAA 152159
QY 2841 TCGTGTGACAGTGGATGGCTTGCCTTCATGGGTGTATTGAGAACTTTAAGCAAT 2900
Db 152158 TCGTGTGACAGTGGATGGCTTGCCTTCATGGGTGTATTGAGAACTTTAAGCAAT 152099
QY 2901 AGTGTTTTTTGTACTTTAGTACTAAAGAAATTTCTACCTGTATCCAGCAATTAGTCAGAAAACT 2960
Db 152098 AGTGTTTTTTGTACTTTAGTACTAAAGAAATTTCTACCTGTATCCAGCAATTAGTCAGAAAACT 152039
QY 2961 TAGCCAAGTGTATCCAACTTAACCTTTCTGCAAGAAGTAGCTTTGTTGGGTGGCAAT 3020
Db 152038 TAGCCAAGTGTATCCAACTTAACCTTTCTGCAAGAAGTAGCTTTGTTGGGTGGCAAT 151979
QY 3021 TGATGATGATGATCTCAGTGTATTATACAGTGTCTTTAACTAGTAACTGCT 3072
Db 151978 TGATGATGATGATCTCAGTGTATTATACAGTGTCTTTAACTAGTAACTGCT 151927

RESULT 18
AC011232/c
LOCUS
DEFINITION
Homo sapiens chromosome 2 clone RP11-78E13, WORKING DRAFT SEQUENCE,
7 unordered pieces.
ACCESSION
AC011232
VERSION
AC011232.7 GI:13270720
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTROP.
SOURCE
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 185281)
Waterston,R.H.
Direct Submission
Submitted (04-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 10, 2001 this sequence version replaced gi:9799811.
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0078E13
----- Summary Statistics -----
Sequencing vector: M13; 57%
Sequencing vector: plasmid; 40%
Chemistry: Dye-primer ET; 48% of reads
Chemistry: Dye-terminator Big Dye; 50% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182798 bases at least Q40
Consensus quality: 183538 bases at least Q30
Consensus quality: 184045 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 184681; sum-of-contigs
Quality coverage: 7.07 in Q20 bases; agarose-fp
Quality coverage: 7.33 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
```

\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1985: contig of 1985 bp in length  
\* 1986 2085: gap of unknown length  
\* 2086 8183: contig of 6098 bp in length  
\* 8184 8283: gap of unknown length  
\* 8284 22741: contig of 14458 bp in length  
\* 22742 22841: gap of unknown length  
\* 22842 41446: contig of 18605 bp in length  
\* 41447 41547: gap of unknown length  
\* 41548 69183: contig of 27636 bp in length  
\* 69184 69283: gap of unknown length  
\* 69284 112131: contig of 42849 bp in length  
\* 112132 112232: gap of unknown length  
\* 112233 185281: contig of 73050 bp in length.

## FEATURES

source  
1. 185281  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/clone="RP11-78E13"  
1. 1985  
/note="assembly\_name:Contig11"  
2086. 8183  
/note="assembly\_name:Contig12"  
8284. 22741  
/note="assembly\_name:Contig13"  
22842. 41446  
/note="assembly\_name:Contig14"  
41547. 69182  
/note="assembly\_name:Contig15"  
69283. 112131  
/note="assembly\_name:Contig16"  
112232. 185281  
/note="assembly\_name:Contig17"  
BASE COUNT 52719 a 36957 c 37187 g 57816 t 602 others  
ORIGIN

misc\_feature  
1. 1985  
/note="assembly\_name:Contig11"  
misc\_feature  
2086. 8183  
/note="assembly\_name:Contig12"  
misc\_feature  
8284. 22741  
/note="assembly\_name:Contig13"  
misc\_feature  
22842. 41446  
/note="assembly\_name:Contig14"  
misc\_feature  
41547. 69182  
/note="assembly\_name:Contig15"  
misc\_feature  
69283. 112131  
/note="assembly\_name:Contig16"  
misc\_feature  
112232. 185281  
/note="assembly\_name:Contig17"

BASE COUNT 52719 a 36957 c 37187 g 57816 t 602 others  
ORIGIN

Query Match 9.58; Score 292; DB 2; Length 185281;  
Best Local Similarity 100.0%; Pred. No. 5.9e-146;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2781 AGGTGCATTTTTTGGAAAGAACCTCTGAAAACTTCAGCAGTTGAATTTGGCGGAAA 2840  
|||||  
Db 160183 AGGTGCATTTTTTGGAAAGAACCTCTGAAAACTTCAGCAGTTGAATTTGGCGGAAA 160124  
|||||

Qy 2841 TCGTGTGAGCAGTGATGGCTTGCCCTTCATGGGTATTTGAGAACTTTAAGCAATT 2900  
|||||  
Db 160123 TCGTGTGAGCAGTGATGGCTTGCCCTTCATGGGTATTTGAGAACTTTAAGCAATT 160064  
|||||

Qy 2901 AGTGTGTTTGCATTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 2960  
|||||  
Db 160063 AGTGTGTTTGCATTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 160004  
|||||

Qy 2961 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAACTAGGCTTGTGGGTGGCAATT 3020  
|||||  
Db 160003 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAACTAGGCTTGTGGGTGGCAATT 159944  
|||||

Qy 3021 TGATGATGATGATCTCAGTGTATTACAGGTCGTTTTAACTAGTAACTGCT 3072  
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Db 159943 TGATGATGATGATCTCAGTGTATTACAGGTCGTTTTAACTAGTAACTGCT 159892  
|||||

## RESULT 19

AX318095  
LOCUS AX318095 578 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 100 from Patent WO0190156.  
ACCESSION AX318095  
VERSION AX318095.1 GI:17900824  
KEYWORDS

SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1

REFERENCE  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use

JOURNAL Patent: WO 0190156-A 100 29-NOV-2001;  
The Burnham Institute (US)

FEATURES  
source  
1. 578  
Location/Qualifiers

CDS  
277..555  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD19342.1"  
/db\_xref="GI:17900825"  
/translation="MNFKDSRLIORMGMTVIKQITDLDLFVNNVLRREVNICCE  
KVEQDAARGIIHMLKKGSESLFLKSLKWNYPFLQDLNGQSLLTA"

BASE COUNT 172 a 106 c 143 g 157 t  
ORIGIN

Query Match 8.88; Score 269; DB 6; Length 578;  
Best Local Similarity 100.0%; Pred. No. 2.3e-133;  
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTTTCATAAAGGACAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTTATA 60  
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Db 277 ATGAATTTTCATAAAGGACAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTTATA 336  
|||||

Qy 61 AAGCAATACAGATGACCTATTGTATGGAATGCTCTGAATCGCGAAGAGTAACATC 120  
|||||

Db 337 AAGCAATACAGATGACCTATTGTATGGAATGCTCTGAATCGCGAAGAGTAACATC 396  
|||||

Qy 121 ATTTGCTGCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 180  
|||||

Db 397 ATTTGCTGCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 456  
|||||

Qy 181 AAGGTTTCAGAGTCTCTGAACCTCTTCTTAAATCCCTTAAGGAGTGAACATCTCTCTA 240  
|||||

Db 457 AAGGTTTCAGAGTCTCTGAACCTCTTCTTAAATCCCTTAAGGAGTGAACATCTCTCTA 516  
|||||

Qy 241 TTTTCAGGACTTGAATGGACAAGTCTTTT 269  
|||||

Db 517 TTTTCAGGACTTGAATGGACAAGTCTTTT 545  
|||||

## RESULT 20

AY027790  
LOCUS AY027790 578 bp mRNA linear PRI 20-JUL-2001  
DEFINITION Homo sapiens CLAND (CLAN1) mRNA, complete cds.  
ACCESSION AY027790  
VERSION AY027790.1 GI:14324118  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens.  
Eukaryota;  
Mammalia;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 578)

Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.

Clan, a novel human ced-4-like gene

JOURNAL Genomics 75 (1-3), 77-83 (2001)

MEDLINE 21365712

PUBMED 11472070

REFERENCE  
2 (bases 1 to 578)

Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.

Direct Submission

Submitted (21-FEB-2001) Program on Apoptosis and Cell Death

Research, The Burnham Institute, 10901 North Torrey Pines Road, La

Jolla, CA 92037, USA

FEATURES

source  
Location/Qualifiers  
1..578  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="2p22-p21"  
/tissue\_type="lung"  
1..578  
/gene="CLAN1"  
277..555  
/gene="CLAN1"  
/note="CARD protein; alternatively spliced"  
/codon\_start=1  
/product="CLAND"  
/protein\_id="AAK14779.1"  
/db\_xref="GI:14324119"  
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KVEDAARGIIHMLKKGSECNFLKSLKWNYPFLQDLNGQSLTTA"  
BASE COUNT 172 a 106 c 143 g 157 t  
ORIGIN

Query Match 8.8%; Score 269; DB 9; Length 578;  
Best Local Similarity 100.0%; Pred. No. 2.3e-133;  
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTGTATA 60  
Db 277 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTGTATA 336  
QY 61 AAGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 120  
Db 337 AAGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 396  
QY 121 ATTGCTCGGAGAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180  
Db 397 ATTGCTCGGAGAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 456  
QY 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240  
Db 457 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 516  
QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTT 269  
Db 517 TTTCAGGACTTGAATGGACAAAGTCTTTT 545

RESULT 21  
AX318172  
LOCUS AX318172 261 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 177 from Patent WO0190156.  
ACCESSION AX318172  
VERSION AX318172.1 GI:17900863  
KEYWORDS human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 177 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source  
Location/Qualifiers  
1..261  
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/db\_xref="taxon:9606"  
1..>261  
/note="unnamed protein product"  
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/protein\_id="CAD19349.1"  
/db\_xref="GI:17900864"

/translation="MNFIKDNRSRALIQRMGTVIKQITDDLFVWNLNREEVNIICCE  
KVEDAARGIIHMLKKGSECNFLKSLKWNYPFLQDLNGQ"  
BASE COUNT 86 a 44 c 59 g 72 t  
ORIGIN  
Query Match 8.5%; Score 261; DB 6; Length 261;  
Best Local Similarity 100.0%; Pred. No. 5.1e-129;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTGTATA 60  
Db 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTGTATA 60  
QY 61 AAGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 120  
Db 61 AAGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 120  
QY 121 ATTGCTCGGAGAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180  
Db 121 ATTGCTCGGAGAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180  
QY 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240  
Db 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240  
QY 241 TTTCAGGACTTGAATGGACAA 261  
Db 241 TTTCAGGACTTGAATGGACAA 261  
RESULT 22  
G55568/c  
LOCUS G55568 553 bp DNA linear STS 30-MAR-2000  
DEFINITION SHGC-100923 Human Homo sapiens STS genomic, sequence tagged site.  
ACCESSION G55568  
VERSION G55568.1 GI:6120887  
KEYWORDS STS.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 553)  
AUTHORS Olivier,M. and Cox,D.R.  
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)  
JOURNAL Unpublished (2000)  
COMMENT  
Contact: Michael Olivier, David R. Cox  
Stanford Human Genome Center  
Stanford University School of Medicine  
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA  
Tel: (650) 320-5800  
Fax: (650) 320-5801  
Email: olivier@shgc.stanford.edu  
Primer A: AATTAAGGGGGCAAAATAAGCAAA  
Primer B: TAACACCCCTTTGTTCTTCTCTCA  
STS size: 322  
PCR Profile:  
Initial incubation: 95 degrees C for 10 minutes  
Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 30 seconds  
Polymerization: 72 degrees C for 23 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9700  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
AmpliTaq Gold Polymerase: 0.07 units/uL  
Total Vol: 5 uL  
Buffer: MgCl2: 2.5 mM  
KCl: 50 mM

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Tris-HCl: 10 mM
pH: 8.3

BAC ends sequenced at TIGR from the RPC111 BAC library. Designed
and developed at the Stanford Human Genome Center.

FEATURES             source
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            1..553
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                primer_bind
            complement(304..326)
BASE COUNT  170 a 107 c 114 g 162 t
ORIGIN
    Query Match      5.5%; Score 170; DB 11; Length 553;
    Best Local Similarity 100.0%; Pred. No. 9.4e-80;
    Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2615 TCGACAGATGAAGCTGTAGACAGCTCACCAGCTGATGCTGCCCTGGGGCTGTGACG 2674
Db 258 TCGACAGATGAAGCTGTAGACAGCTCACCAGCTGATGCTGCCCTGGGGCTGTGACG 199
Qy 2675 TCGAAGGCGAGCTGAGCAGCTGTGTAACATTTGGAGGAGTCCACAACTCGTCAAGC 2734
Db 198 TCGAAGGCGAGCTGAGCAGCTGTGTAACATTTGGAGGAGTCCACAACTCGTCAAGC 139
Qy 2735 TTGGTTTCAAAACTGGAGACTCACAGTACAGATAGATTTTAGGT 2784
Db 138 TTGGTTTCAAAACTGGAGACTCACAGTACAGATAGATTTTAGGT 89

RESULT 23
AX318178
LOCUS       AX318178             165 bp    DNA    linear    PAT 14-DEC-2001
DEFINITION   Sequence 183 from Patent WO0190156.
ACCESSION   AX318178
VERSION     AX318178.1  GI:17900869
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
            Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE       Card domain containing polypeptides, encoding nucleic acids, and
            methods of use
JOURNAL     Patent: WO 0190156-A 183 29-NOV-2001;
            The Burnham Institute (US)
FEATURES             source
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        Location/Qualifiers
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                SATSLRLQIKR"
BASE COUNT  51 a 37 c 38 g 39 t
ORIGIN
    Query Match      3.7%; Score 114; DB 6; Length 165;
    Best Local Similarity 99.4%; Pred. No. 2.1e-49;
    Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1924 ACCTACATCCACAGCGCTGTATCTTGTCTTCACTGGAAGCAGGAATTCAGGACT 1983
Db 1 ACCTACATCCACAGCGCTGTATCTTGTCTTCACTGGAAGCAGGAATTCAGGACT 60
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Qy 1984 CTGGAGGTCACACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGGG 2043
Db 61 CTGGAGGTCACACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGGG 120
Qy 2044 AAAATATTACGCTCTGCCACAGCCTCAGGCTGCAAAATAAAGAGA 2088
Db 121 AAAATATTACGCTCTGCCACAGCCTCAGGCTGCAAAATAAAGAGA 165

RESULT 24
AC101793/c
LOCUS       AC101793             185469 bp    DNA    linear    HTG 21-AUG-2002
DEFINITION   Mus musculus clone RP24-178L2, WORKING DRAFT SEQUENCE, 43 unordered
            pieces.
ACCESSION   AC101793
VERSION     AC101793.2  GI:22381529
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 185469)
            Birren,B., Nusbaum,C. and Lander,E.
            Mus musculus, clone RP24-178L2
            Unpublished
            2 (bases 1 to 185469)
            Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chararo,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., Lacombe,K.,
            Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
            MacLean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollata,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viell,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
            Direct Submission
            Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            3 (bases 1 to 185469)
            Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
            Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., MacDonald,P., Major,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viell,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
            Direct Submission
            Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
```

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Aug 21, 2002 this sequence version replaced gi:17060568.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L17408  
Center clone name: 178\_L\_2  
----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Pirap; version 0.960731  
Consensus quality: 173992 bases at least Q40  
Consensus quality: 177954 bases at least Q30  
Consensus quality: 180012 bases at least Q20  
Insert size: 168000; agarose-fp  
Insert size: 181269; sum-of-contigs  
Quality coverage: 7.1 in Q20 bases; agarose-fp  
Quality coverage: 6.6 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 43 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 60: contig of 60 bp in length  
\* 61 160: gap of 100 bp  
\* 161 824: contig of 664 bp in length  
\* 825 924: gap of 100 bp  
\* 925 1843: contig of 919 bp in length  
\* 1844 1943: gap of 100 bp  
\* 1944 2615: contig of 672 bp in length  
\* 2616 2715: gap of 100 bp  
\* 2716 3318: contig of 603 bp in length  
\* 3319 3418: gap of 100 bp  
\* 3419 4524: contig of 1106 bp in length  
\* 4525 4624: gap of 100 bp  
\* 4625 5485: contig of 861 bp in length  
\* 5486 5585: gap of 100 bp  
\* 5586 6384: contig of 799 bp in length  
\* 6385 6484: gap of 100 bp  
\* 6485 7162: contig of 678 bp in length  
\* 7163 7262: gap of 100 bp  
\* 7263 7456: contig of 194 bp in length  
\* 7457 7556: gap of 100 bp  
\* 7557 8160: contig of 604 bp in length  
\* 8161 8260: gap of 100 bp  
\* 8261 8941: contig of 681 bp in length  
\* 8942 9041: gap of 100 bp  
\* 9042 9922: contig of 881 bp in length  
\* 9923 10022: gap of 100 bp  
\* 10023 11459: contig of 1437 bp in length  
\* 11460 11559: gap of 100 bp  
\* 11560 12040: contig of 481 bp in length  
\* 12041 12140: gap of 100 bp  
\* 12141 13305: contig of 1165 bp in length  
\* 13306 13405: gap of 100 bp  
\* 13406 14296: contig of 891 bp in length  
\* 14297 14396: gap of 100 bp  
\* 14397 15353: contig of 957 bp in length  
\* 15354 15453: gap of 100 bp  
\* 15454 16520: contig of 1067 bp in length  
\* 16521 16620: gap of 100 bp  
\* 16621 18291: contig of 1671 bp in length  
\* 18292 18391: gap of 100 bp

\* 18392 19794: contig of 1403 bp in length  
\* 19795 19894: gap of 100 bp  
\* 19895 21659: contig of 1765 bp in length  
\* 21660 21759: gap of 100 bp  
\* 21760 23729: contig of 1970 bp in length  
\* 23730 23829: gap of 100 bp  
\* 23830 25103: contig of 1274 bp in length  
\* 25104 25203: gap of 100 bp  
\* 25204 27230: contig of 2027 bp in length  
\* 27231 27330: gap of 100 bp  
\* 27331 29923: contig of 2593 bp in length  
\* 29924 30023: gap of 100 bp  
\* 30024 32248: contig of 2225 bp in length  
\* 32249 32348: gap of 100 bp  
\* 32349 35145: contig of 2797 bp in length  
\* 35146 35245: gap of 100 bp  
\* 35246 38595: contig of 3350 bp in length  
\* 38596 38695: gap of 100 bp  
\* 38696 41857: contig of 3162 bp in length  
\* 41858 41957: gap of 100 bp  
\* 41958 45734: contig of 3777 bp in length  
\* 45735 45834: gap of 100 bp  
\* 45835 50585: contig of 4751 bp in length  
\* 50586 50685: gap of 100 bp  
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\* 58533 58632: gap of 100 bp  
\* 58633 64513: contig of 5881 bp in length  
\* 64514 64613: gap of 100 bp  
\* 64614 72116: contig of 7503 bp in length  
\* 72117 72216: gap of 100 bp  
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\* 79498 79597: gap of 100 bp  
\* 79598 89239: contig of 9642 bp in length  
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\* 100841 112859: contig of 12019 bp in length  
\* 112860 112959: gap of 100 bp  
\* 112960 125403: contig of 12444 bp in length  
\* 125404 125503: gap of 100 bp  
\* 125504 140153: contig of 14650 bp in length  
\* 140154 140253: gap of 100 bp  
\* 140254 160616: contig of 20363 bp in length  
\* 160617 160716: gap of 100 bp  
\* 160717 185469: contig of 24753 bp in length.  
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Best Local Similarity 100.0%; Pred. No. 5.9e-09;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1710 CCTGAGCCCAAGATTTGAAGCTTCTTTCAAGGTAAAG 1748  
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Db 151494 CCTGAGCCAGAAATTGAGCTTCTTTCAGGTAAG 151456

RESULT 25  
AX318155/c  
LOCUS AX318155 29 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 160 from Patent WO0190156.  
ACCESSION AX318155  
VERSION AX318155.1 GI:17900846  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequences.

REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 160 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 TGACTTCATTCGGAGCCTGGACCACCTGTG 1180  
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RESULT 26  
AX318156  
LOCUS AX318156 25 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 161 from Patent WO0190156.  
ACCESSION AX318156  
VERSION AX318156.1 GI:17900847  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequences.

REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 161 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source Location/Qualifiers  
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RESULT 27  
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LOCUS AX318157 25 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 162 from Patent WO0190156.  
ACCESSION AX318157  
VERSION AX318157.1 GI:17900848  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequences.

REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 162 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
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/note="primer"

BASE COUNT 8 a 4 c 5 g 8 t  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 28  
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LOCUS AX318160 25 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 165 from Patent WO0190156.  
ACCESSION AX318160  
VERSION AX318160.1 GI:17900851  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequences.

REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 165 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"

BASE COUNT 11 a 4 c 5 g 5 t  
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Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AATTTCATAAGGACAATAGCCGAG 28  
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Db 1 AATTTCATAAGGACAATAGCCGAG 25

RESULT 29  
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LOCUS AC128434 175205 bp DNA linear HTG 19-JUL-2002  
DEFINITION Rattus norvegicus clone CH230-104C1, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 60 unordered pieces.  
ACCESSION AC128434  
VERSION AC128434.1 GI:21909117



KEYWORDS  
SOURCE  
ORGANISM

HTG: HTGS\_PHASE1.  
Rattus norvegicus.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
AUTHORS

1 (bases 1 to 175205)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,  
Barbieri,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,  
Bouck,J., Bowie,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P.,  
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
Delnathaye,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,  
Douthett,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,  
Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J.,  
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,  
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
Jarlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Ljoulseged,H.,  
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,  
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,  
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,  
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwunolu,G.,  
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,  
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,  
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,  
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,  
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,  
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
Tansey,J., Taylor,C., Taylor,T., Teifrod,B., Thomas,N., Thomas,S.,  
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,D., Watson,S.,  
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 175205)  
Worley,K.C.  
Direct Submission  
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
----- Genome Center  
Center: Baylor College of Medicine  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GYXN  
Center clone name: CH230-104C1  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 117421 bases at least Q40  
Consensus quality: 124465 bases at least Q30  
Consensus quality: 129193 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 60 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1561: contig of 1561 bp in length  
\* 1562: gap of unknown length  
\* 1562 2884: contig of 1223 bp in length  
\* 1562 2884: gap of unknown length  
\* 2885 4160: contig of 1176 bp in length  
\* 2885 4160: gap of unknown length  
\* 4161 5643: contig of 1383 bp in length  
\* 5643: gap of unknown length  
\* 5644 7371: contig of 1628 bp in length  
\* 7371: gap of unknown length  
\* 7372 9191: contig of 1720 bp in length  
\* 9191: gap of unknown length  
\* 9192 10351: contig of 1060 bp in length  
\* 10351: gap of unknown length  
\* 10352 12006: contig of 1555 bp in length  
\* 10352 12006: gap of unknown length  
\* 12007 13864: contig of 1758 bp in length  
\* 12007 13864: gap of unknown length  
\* 13865 15179: contig of 1215 bp in length  
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\* 15180 16514: contig of 1235 bp in length  
\* 16514: gap of unknown length  
\* 16515 17837: contig of 1223 bp in length  
\* 16515 17837: gap of unknown length  
\* 17838 19892: contig of 1955 bp in length  
\* 17838 19892: gap of unknown length  
\* 19893 21501: contig of 1509 bp in length  
\* 19893 21501: gap of unknown length  
\* 21502 23094: contig of 1493 bp in length  
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\* 23095 23194: contig of 1974 bp in length  
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\* 23195 25268: gap of unknown length  
\* 25169 27182: contig of 1914 bp in length  
\* 25169 27182: gap of unknown length  
\* 27183 28532: contig of 1250 bp in length  
\* 27183 28532: gap of unknown length  
\* 28533 30371: contig of 1739 bp in length  
\* 28533 30371: gap of unknown length  
\* 30372 31973: contig of 1502 bp in length  
\* 30372 31973: gap of unknown length  
\* 31974 32073: gap of unknown length  
\* 31974 32073: gap of unknown length  
\* 32074 33635: contig of 2777 bp in length  
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\* 33636 36512: contig of 1221 bp in length  
\* 33636 36512: gap of unknown length  
\* 36512 37832: contig of 1221 bp in length  
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\* 37833 40506: contig of 2574 bp in length  
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\* 43273 45399: contig of 2027 bp in length  
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\* 56135 58230: gap of unknown length  
\* 58231 61935: contig of 3605 bp in length  
\* 58231 61935: gap of unknown length

\* 61936 62035: gap of unknown length  
\* 62036 63849: contig of 1814 bp in length  
\* 63850 63949: gap of unknown length  
\* 63950 66368: contig of 2419 bp in length  
\* 66369 66468: gap of unknown length  
\* 66469 70087: contig of 3619 bp in length  
\* 70088 70187: gap of unknown length  
\* 70188 73499: contig of 3312 bp in length  
\* 73500 73599: gap of unknown length  
\* 73600 73979: contig of 2380 bp in length  
\* 73980 76079: gap of unknown length  
\* 76080 79674: contig of 3595 bp in length  
\* 79675 79774: gap of unknown length  
\* 79775 82514: contig of 2740 bp in length  
\* 82515 82615: gap of unknown length  
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\* 85239 85338: gap of unknown length  
\* 85339 87656: contig of 2318 bp in length  
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\* 87757 89651: contig of 1895 bp in length  
\* 89652 89751: gap of unknown length  
\* 89752 93019: contig of 3268 bp in length  
\* 93020 93119: gap of unknown length  
\* 93120 97532: contig of 4413 bp in length  
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\* 97633 100905: contig of 3273 bp in length  
\* 100906 101005: gap of unknown length  
\* 101006 102927: contig of 1922 bp in length  
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\* 106702 110014: contig of 3313 bp in length  
\* 110015 110114: gap of unknown length  
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\* 119986 120085: gap of unknown length  
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\* 129029 129128: gap of unknown length  
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\* 152959 153058: gap of unknown length

Query Match 0.8%; Score 25; DB 2; Length 175205;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1109 TGATACAGAAACAAACACACAAACA 1133  
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Db 134182 TGATACAGAAACAAACACACAAACA 134206

RESULT 30  
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LOCUS AX318154 24 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 159 from Patent WO0190156.  
ACCESSION AX318154  
VERSION AX318154.1 GI:17900845  
KEYWORDS .  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and

methods of use  
JOURNAL Patent: WO 0190156-A 159 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source Location/Qualifiers  
1. .24  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"  
BASE COUNT 5 a 3 c 12 g 4 t  
ORIGIN  
Query Match 0.8%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 135 GGTGGAGCAGGATGCTGTAGAGG 158  
|||||  
Db 1 GGTGGAGCAGGATGCTGTAGAGG 24  
RESULT 31  
AX318152  
LOCUS AX318152 33 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 157 from Patent WO0190156.  
ACCESSION AX318152  
VERSION AX318152.1 GI:17900843  
KEYWORDS .  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 157 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source Location/Qualifiers  
1.33  
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/db\_xref="taxon:32630"  
/note="primer"  
BASE COUNT 12 a 8 c 6 g 7 t  
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Query Match 0.8%; Score 24; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATTTTCATAAAGGACAATAGC 24  
|||||  
Db 10 ATGAATTTTCATAAAGGACAATAGC 33  
RESULT 32  
AX318148/c  
LOCUS AX318148 23 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 153 from Patent WO0190156.  
ACCESSION AX318148  
VERSION AX318148.1 GI:17900839  
KEYWORDS .  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 153 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source Location/Qualifiers  
1. .23

/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"

BASE COUNT 6 a 6 c 5 g 6 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.4;  
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QY 149 CTGCTAGAGGATCATTCACATG 171  
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Db 23 CTGCTAGAGGATCATTCACATG 1

RESULT 33  
AX318158  
LOCUS AX318158 23 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 163 from Patent WO0190156.  
ACCESSION AX318158  
VERSION AX318158.1 GI:17900849  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1  
Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,  
Oliveira, V.A., Hayashi, H. and Pawlowski, K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 163 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
Location/Qualifiers  
1..23  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 8 a 4 c 5 g 6 t  
ORIGIN

Query Match 0.7%; Score 23; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GTAACATCATTTGTCGCGAGAA 134  
|||||  
Db 1 GTAACATCATTTGTCGCGAGAA 23

RESULT 34  
AC090582/c  
LOCUS AC090582 169406 bp DNA linear HTG 24-AUG-2002  
DEFINITION Homo sapiens chromosome 11 clone RP11-125F14 map 11, \*\*\* SEQUENCING  
IN PROGRESS \*\*\*, 6 unordered pieces.  
ACCESSION AC090582  
VERSION AC090582.6 GI:22474963  
KEYWORDS HTG: HTGS\_PHASE1; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Plrimates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 169406)  
Birken, B., Nusbaum, C. and Lander, E.  
AUTHORS  
TITLE Homo sapiens chromosome 11, clone RP11-125F14  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 169406)  
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,  
Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,  
Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,  
Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,  
Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-pierre, N.,  
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T.,  
Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,  
Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,  
McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
Sounez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 169406)

# REFERENCE AUTHORS

Birken, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,  
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,  
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,  
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,  
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Aug 24, 2002 this sequence version replaced gi:20334596.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

# COMMENT

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L11783  
Center clone name: 125\_F14  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 5671: contig of 5671 bp in length  
\* 5672 5771: gap of 100 bp  
\* 5772 43769: contig of 37998 bp in length  
\* 43770 43869: gap of 100 bp  
\* 43870 51226: contig of 7357 bp in length  
\* 51227 51326: gap of 100 bp  
\* 51327 90886: contig of 39560 bp in length  
\* 90887 90986: gap of 100 bp  
\* 90987 111813: contig of 20827 bp in length  
\* 111814 111913: gap of 100 bp  
\* 111914 169406: contig of 57493 bp in length.  
Location/Qualifiers  
1..169406

# FEATURES source

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/chromosome="11"
/map="11"
/clone="RP11-125F14"
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BASE COUNT 40775 a 44420 c 43265 g 40363 t 583 others
ORIGIN

Query Match 0.78; Score 23; DB:2; Length 169406;
Best Local Similarity 100.0%; Pred. NO. 2.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1887 AGACACAGGTGGATCCACATGG 1909
|||||
Db 96369 AGACACAGGTGGATCCACATGG 96347

RESULT 35
AC074195/c
LOCUS AC074195 175152 bp DNA linear HTG 20-AUG-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-750A9, WORKING DRAFT
AC074195
VERSION AC074195.3 GI:9799883
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 175152)
Waterston,R.H.
Direct Submission
Submitted (16-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 13, 2000 this sequence version replaced gi:9743495.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0750A09
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155181 bases at least Q40
Consensus quality: 161068 bases at least Q30
Consensus quality: 163835 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 172752; sum-of-contigs
Quality coverage: 4.16 in Q20 bases; agarose-fp
Quality coverage: 4.34 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1335: contig of 1335 bp in length
* 1336 1436: gap of unknown length
* 1436 3074: contig of 1639 bp in length

3075 3174: gap of unknown length
3175 5334: contig of 2360 bp in length
5335 5634: gap of unknown length
5635 8287: contig of 2653 bp in length
8288 8388: gap of unknown length
8389 10416: contig of 2028 bp in length
10417 10515: gap of unknown length
10516 12875: contig of 2360 bp in length
12876 12976: gap of unknown length
12977 16283: contig of 3308 bp in length
16284 16384: gap of unknown length
16385 19546: contig of 3163 bp in length
19547 19646: gap of unknown length
19647 24020: contig of 4374 bp in length
24021 24121: gap of unknown length
24122 28747: contig of 4626 bp in length
28748 33535: contig of 4689 bp in length
33536 33636: gap of unknown length
33637 38255: contig of 4620 bp in length
38256 38356: gap of unknown length
38357 43277: contig of 4922 bp in length
43278 43378: gap of unknown length
43379 47903: contig of 4526 bp in length
47904 48003: gap of unknown length
48004 52385: contig of 4381 bp in length
52386 52484: gap of unknown length
52485 58975: contig of 6491 bp in length
58976 59075: gap of unknown length
59076 67304: contig of 8228 bp in length
67305 67404: contig of 7446 bp in length
67405 74850: gap of unknown length
74851 83616: contig of 8666 bp in length
83617 94881: contig of 11166 bp in length
94882 94981: gap of unknown length
94982 104767: contig of 9785 bp in length
104768 104866: gap of unknown length
104867 118097: contig of 13231 bp in length
118098 118197: gap of unknown length
118198 132815: contig of 14618 bp in length
132816 132915: gap of unknown length
132916 148952: contig of 16037 bp in length
148953 149052: gap of unknown length
149053 175152: contig of 26100 bp in length.

FEATURES
Location/Qualifiers
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/clone="RP11-750A9"
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5635..8287
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16384..19546
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/note="assembly_name:Contig24"
28847..33535
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\* 128333 128432: gap of unknown length  
 \* 128433 139368: contig of 10936 bp in length  
 \* 139369 139468: gap of unknown length  
 \* 139469 154140: contig of 14672 bp in length  
 \* 154141 154240: gap of unknown length  
 \* 154241 167223: contig of 13483 bp in length  
 \* 167224 167823: gap of unknown length  
 \* 167824 183556: contig of 15733 bp in length.

## FEATURES

Location/Qualifiers  
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1. 183556  
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 20637. 25264  
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 73942. 79919  
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 128433. 139368  
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vector\_side:right"  
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 154241. 167723  
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 167824. 183556  
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Query Match 0.7%; Score 23; DB 2; Length 183556;  
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 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1887 AGACACAGGTGGTAATCCACATGG 1909  
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 Db 103946 AGACACAGGTGGTAATCCACATGG 103924

## RESULT 37

AL592438/c

LOCUS AL592438 42513 bp DNA linear PRI 21-OCT-2001  
 DEFINITION Human DNA sequence from clone RP11-187G6 on chromosome 9, complete sequence.

ACCESSION AL592438

VERSION AL592438.7 GI:16412381

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 42513)

AUTHORS Wall, M.

TITLE Direct Submission

JOURNAL

Submitted (20-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 Requests: clonerequest@sanger.ac.uk

## COMMENT

On Oct 24, 2001 this sequence version replaced gi:15021052.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em:, EMBL; SW:,  
 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; information on the WORMPEP  
 database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr9  
 RP11-187G6 is from the library RPCI-11.1 constructed by the group  
 of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pBACe3.6  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP11-187G6 it may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true right end of clone RP11-187G6 is at 42513 in this  
 sequence. The true left end of clone RP11-99J1 is at 3799 in this  
 sequence. The true right end of clone RP11-161E22 is at 2000 in  
 this sequence.

## FEATURES

Location/Qualifiers  
 source  
 1. 42513

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/clone="RP11-187G6"
/clone_lib="RP11-11.1"
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1060 TTCACACTCTCACACAAACAA 1081
|||||
Db 42350 TTCACACTCTCACACAAACAA 42329

RESULT 38
AC098256
LOCUS
DEFINITION Rattus norvegicus clone CH230-1G22, *** SEQUENCING IN PROGRESS ***,
48 unordered pieces.
AC098256
VERSION AC098256.3 GI:21953970
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 79431)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbary,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouch,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burrell,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyie,M.D., Dathorne,S.R., David,R.,
Devilay,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseghe,H.,
Lozahar,M., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Monabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,

```

Weinstock,G. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 79431)  
Worley,K.C.  
Direct Submission  
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 79431)  
Worley,K.C.  
Direct Submission  
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 24, 2002 this sequence version replaced gi:20976511.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: TUDU  
Center clone name: CH230-1G22  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 33875 bases at least Q40  
Consensus quality: 35563 bases at least Q30  
Consensus quality: 36799 bases at least Q20  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 48 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1072: contig of 1072 bp in length  
\* 1073 1172: gap of unknown length  
\* 1173 2181: contig of 1009 bp in length  
\* 2182 2281: gap of unknown length  
\* 2282 3489: contig of 1208 bp in length  
\* 3490 3589: gap of unknown length  
\* 3590 4669: contig of 1080 bp in length  
\* 4670 4769: gap of unknown length  
\* 4770 5841: contig of 1072 bp in length  
\* 5842 7188: contig of 1247 bp in length  
\* 7189 7288: gap of unknown length  
\* 7289 8373: contig of 1085 bp in length  
\* 8374 8474: gap of unknown length  
\* 8475 9595: contig of 1122 bp in length  
\* 9596 10856: contig of 1161 bp in length  
\* 10857 10956: gap of unknown length  
\* 10957 12528: contig of 1572 bp in length  
\* 12529 12628: gap of unknown length  
\* 12629 14017: contig of 1389 bp in length  
\* 14018 14117: gap of unknown length  
\* 14118 15306: contig of 1189 bp in length  
\* 15307 15406: gap of unknown length  
\* 15407 16997: contig of 1591 bp in length  
\* 16998 17097: gap of unknown length  
\* 17098 18675: contig of 1578 bp in length  
\* 18676 18775: gap of unknown length  
\* 18776 20264: contig of 1489 bp in length  
\* 20265 20365: gap of unknown length  
\* 20366 21735: contig of 1371 bp in length

```
* 21736 21835: gap of unknown length
* 21836 23176: contig of 1341 bp in length
* 23177 23276: gap of unknown length
* 23277 24327: contig of 1051 bp in length
* 24328 24427: gap of unknown length
* 24428 25499: contig of 1072 bp in length
* 25500 26599: gap of unknown length
* 26600 26756: contig of 1157 bp in length
* 26757 26856: gap of unknown length
* 26857 28201: contig of 1345 bp in length
* 28202 28301: gap of unknown length
* 28302 30133: contig of 1832 bp in length
* 30134 30233: gap of unknown length
* 30234 31984: contig of 1751 bp in length
* 31985 32084: gap of unknown length
* 32085 33479: contig of 1395 bp in length
* 33480 33579: gap of unknown length
* 33580 34838: contig of 1259 bp in length
* 34839 34938: gap of unknown length
* 34939 36511: contig of 1573 bp in length
* 36512 36611: gap of unknown length
* 36612 38672: contig of 2061 bp in length
* 38673 38772: gap of unknown length
* 38773 40686: contig of 1914 bp in length
* 40687 40786: gap of unknown length
* 40787 41840: contig of 1054 bp in length
* 41841 41940: gap of unknown length
* 41941 42364: contig of 1024 bp in length
* 42365 43064: gap of unknown length
* 43065 44307: contig of 1243 bp in length
* 44308 44407: gap of unknown length
* 44409 45721: contig of 1314 bp in length
* 45722 45821: gap of unknown length
* 45822 47317: contig of 1496 bp in length
* 47318 47418: gap of unknown length
* 47419 48844: contig of 1427 bp in length
* 48845 48944: gap of unknown length
* 48945 50750: contig of 1806 bp in length
* 50751 50850: gap of unknown length
* 50851 52232: contig of 1382 bp in length
* 52233 52332: gap of unknown length
* 52333 53122: contig of 1480 bp in length
* 53123 53912: gap of unknown length
* 53913 56448: contig of 2536 bp in length
* 56449 56548: gap of unknown length
* 56549 57716: contig of 1168 bp in length
* 57717 57817: gap of unknown length
* 57818 59387: contig of 1571 bp in length
* 59388 59487: gap of unknown length
* 59489 61488: contig of 2001 bp in length
* 61489 61588: gap of unknown length
* 61589 64695: contig of 3107 bp in length
* 64696 64795: gap of unknown length
* 64796 66580: contig of 1785 bp in length
* 66581 66680: gap of unknown length
* 66681 68096: contig of 1416 bp in length
* 68097 68196: gap of unknown length
* 68197 70443: contig of 2247 bp in length
* 70444 70543: gap of unknown length
* 70544 73543: contig of 3000 bp in length
* 73544 73643: gap of unknown length
* 73644 75974: contig of 2231 bp in length
* 75975 75974: gap of unknown length
* 75975 79431: contig of 3457 bp in length.
      Location/Qualifiers
        1..79431
          /organism="Rattus norvegicus"
          /db_xref="taxon:10116"
          /clone="CH230-1G22"
BASE COUNT 21375 a 15325 c 15238 g 22670 t 4823 others
ORIGIN
Query Match 0.7%; Score 22; DB 2; Length 79431;
Best Local Similarity 100.0%; Pred. No. 9.9; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1117 AAAAAACAAACACATAAAG 1138
Db 18515 AAAAAACAAACACATAAAG 18536
|||||
RESULT 40
AL161913/c
LOCUS
DEFINITION Human DNA sequence from clone Rp11-64P11 on chromosome 9, complete
sequence.
ACCESSION AL161913
VERSION AL161913.11 GI:16972809
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Mashreghi-Mohammadi,M.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:14329900.
COMMENT
```



During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr9>

RP11-64P11 is from the library RPCI-11.1 constructed by the group

of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone

RP11-64P11. It may be shorter because we sequenced overlapping

sections only once, except for a short overlap.

The true left end of clone RP11-36615 is at 135898 in this

sequence. The true right end of clone RP11-18766 is at 2000 in this

sequence.

```

FEATURES
    source
        1..137897
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="9"
            /clone="RP11-64P11"
            /clone_lib="RPCI-11.1"
BASE COUNT    44788 a 26058 c 25186 g 41865 t
ORIGIN

```

```

Query Match      0.7%; Score 22; DB 9; Length 137897;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1060 TTCCACTCTCACACAAACAA 1081
      |||||||
Db 1837 TTCCACTCTCACACAAACAA 1816

```

```

RESULT 41
AC020917
LOCUS      Homo sapiens chromosome 19 clone CTD-2013N17, complete sequence.
DEFINITION
ACCESSION  AC020917
VERSION     AC020917.4 GI:11120760
KEYWORDS   HTG
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE   1 (bases 1 to 151088)
AUTHORS    DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE       Direct Submission
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 151088)
AUTHORS    DOE Joint Genome Institute.
TITLE       Direct Submission
JOURNAL     Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3 (bases 1 to 151088)
AUTHORS    DOE Joint Genome Institute and Stanford Human Genome Center.

```

```

TITLE       Direct Submission
JOURNAL     Submitted (08-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Nov 8, 2000 this sequence version replaced gi:7704958.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu

```

```

Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
STS Content:
SHGC-57513 G37313.

```

```

FEATURES
    source
        1..151088
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="19"
            /clone="CTD-2013N17"
BASE COUNT    40571 a 38233 c 38536 g 33748 t
ORIGIN

```

```

Query Match      0.7%; Score 22; DB 9; Length 151088;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1778 ATTACTTATTGACTTCTTGA 1799
      |||||||
Db 117449 ATTACTTATTGACTTCTTGA 117470

```

```

RESULT 42
AC011980/c
LOCUS      Homo sapiens clone RP11-16H7, WORKING DRAFT SEQUENCE, 11 unordered
            pieces.
DEFINITION  AC011980
ACCESSION  AC011980.3 GI:7230122
VERSION     HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS   Homo sapiens
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE   1 (bases 1 to 153733)
AUTHORS    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE       Homo sapiens, clone RP11-16H7
JOURNAL     Unpublished
AUTHORS

```

```

REFERENCE   2 (bases 1 to 153733)
AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J.,
            Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McSwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Wyman,D., Ye.W.J., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Zimmer,A. and Zody,M.

```

```

TITLE       Direct Submission
JOURNAL     Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 12, 2000 this sequence version replaced gi:6453966.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

```

----- Project Information  
Center project name: L3543  
Center clone name: 16\_H.7  
----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 117952 bases at least Q40  
Consensus quality: 136478 bases at least Q30  
Consensus quality: 146705 bases at least Q20  
Insert size: 157000; agarose-fp  
Insert size: 152733; sum-of-contigs  
Quality coverage: 4.1 in Q20 bases; agarose-fp  
Quality coverage: 4.2 in Q20 bases; sum-of-contigs  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 11 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
\* 3262: contig of 3262 bp in length  
\* 3263 3362: gap of 100 bp  
\* 3363 9412: contig of 6050 bp in length  
\* 9413 9512: gap of 100 bp  
\* 9513 14144: contig of 4632 bp in length  
\* 14145 14244: gap of 100 bp  
\* 14245 24193: contig of 9949 bp in length  
\* 24194 24293: gap of 100 bp  
\* 24294 37092: contig of 12799 bp in length  
\* 37093 37192: gap of 100 bp  
\* 37193 49508: contig of 12316 bp in length  
\* 49509 49608: gap of 100 bp  
\* 49609 60861: contig of 11253 bp in length  
\* 60862 60961: gap of 100 bp  
\* 60962 76206: contig of 15245 bp in length  
\* 76207 76306: gap of 100 bp  
\* 76307 89151: contig of 12845 bp in length  
\* 89152 89251: gap of 100 bp  
\* 89252 107693: contig of 18442 bp in length  
\* 107694 107793: gap of 100 bp  
\* 107794 153733: contig of 45940 bp in length.

FEATURES  
source  
1. .153733  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="RP11-16H7"  
/clone\_lib="RPCI-11 Human Male BAC"  
1. .3262  
/note="assembly\_fragment"  
3363. .9412  
/note="assembly\_fragment"  
9513. .14144  
/note="assembly\_fragment"  
14245. .24193  
/note="assembly\_fragment"  
24294. .37092  
/note="assembly\_fragment"  
37193. .49508  
/note="assembly\_fragment"  
49609. .60861  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right"  
60962. .76206  
/note="assembly\_fragment"  
76307. .89151  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:right"  
89252. .107693

misc\_feature /note="assembly\_fragment"  
107794. .153733  
/note="assembly\_fragment"  
BASE COUNT 42218 a 34152 c 33610 g 42710 t 1043 others  
ORIGIN  
Query Match 0.7%; Score 22; DB 2; Length 153733;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1117 AAAACAACACACACATATAAG 1138  
|||||  
Db 120518 AAAACAACACACACATATAAG 120497  
|||||  
RESULT 43  
AL592213 155531 bp DNA linear HTG 04-AUG-2001  
LOCUS Homo sapiens chromosome 9 clone RP11-99J1, \*\*\* SEQUENCING IN  
DEFINITION PROGRESS \*\*\*, in ordered pieces.  
ACCESSION AL592213 AC007951  
VERSION AL592213.6 GI:15131900  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_CANCELLED.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 155531)  
Hammond.S.  
Direct Submission  
Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Aug 9, 2001 this sequence version replaced gi:15029558.  
Draft Sequence Produced by Whitehead Institute/MIT Center for  
Genome Research, 320 Charles Street,  
Cambridge, MA 02141, USA  
http://www-seq.wi.mit.edu  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: BA99J1  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: M13; M77815; 30% of reads  
Chemistry: Dye-terminator Big Dye; 68% of reads  
Dye-terminator Big Dye; 68% of reads  
Chemistry: Dye-terminator Big Dye; 68% of reads  
Consensus quality: 155436 bases at least Q40  
Consensus quality: 155453 bases at least Q30  
Consensus quality: 155482 bases at least Q20  
Insert size: 155531; sum-of-contigs  
Insert size: 144681; 16.2% error; agarose-fp  
Quality coverage: 15.49x in Q20 bases; sum-of-contigs Quality  
coverage: 16.65x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
FEATURES  
source  
1. .155531  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="9"  
/clone="RP11-99J1"  
/clone\_lib="RPCI-11.1"  
1. .155531  
/note="assembly\_fragment:03518"

clone\_end:SP6  
vector\_side:right"  
BASE COUNT 50143 a 29768 c 28721 g 46899 t  
ORIGIN

Query Match 0.7%; Score 22; DB 2; Length 15531;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1060 TTCCACTCTCACACAAACAA 1081  
|||||  
Db 38569 TTCCACTCTCACACAAACAA 38548

RESULT 44  
AC129066/c 157021 bp DNA linear HTG 16-AUG-2002  
LOCUS Didelphis virginiana clone LB3-8N21, WORKING DRAFT SEQUENCE, 3  
DEFINITION ordered pieces.

ACCESSION AC129066  
VERSION AC129066.2 GI:22267576  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
SOURCE North American opossum.  
ORGANISM Didelphis virginiana

REFERENCE 1 (bases 1 to 157021)  
AUTHORS Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Madero, Q.L., Madero, V.B., Marquies, E.H., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paquirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantropop, S., Thomas, J.W., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 157021)  
Green, E.D.

TITLE Direct Submission  
JOURNAL Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717  
REFERENCE 1 (bases 1 to 157021)  
AUTHORS Government Circle, Gaithersburg, MD 20877, USA  
JOURNAL Green, E.D.  
REFERENCE 3 (bases 1 to 157021)  
AUTHORS Direct Submission  
JOURNAL Submitted (16-AUG-2002) NIH Intramural Sequencing Center, 8717  
TITLE Government Circle, Gaithersburg, MD 20877, USA  
COMMENT On Aug 16, 2002 this sequence version replaced gi:21955001.

----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_zoehghri.nih.gov](mailto:nisc_zoehghri.nih.gov)  
----- Project Information  
Center Project name: dvd  
Center Clone name: 008N21

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 155497 bases at least Q40  
Consensus quality: 156249 bases at least Q30  
Consensus quality: 156658 bases at least Q20  
Insert size: 138000; agarose-fp  
Quality coverage: 7.19x in Q20 bases; agarose-fp  
Quality coverage: 6.33x in Q20 bases; sum-of-contigs  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 31400: contig of 31400 bp in length  
\* 31401 31500: gap of unknown length  
\* 31501 40794: contig of 9294 bp in length  
\* 40795 40894: gap of unknown length  
\* 40895 157021: contig of 116127 bp in length.

FEATURES  
Location/Qualifiers  
1..157021

source  
/organism="Didelphis virginiana"  
/db\_xref="taxon:9267"  
/clone="LB3-8N21"  
/clone\_lib="LB3"

misc\_feature  
1..31400  
/note="assembly\_fragment  
clone\_end:T7  
vector\_side:left"

misc\_feature  
31501..40794  
/note="assembly\_fragment"

misc\_feature  
40895..157021  
/note="assembly\_fragment  
clone\_end:SP6  
vector\_side:right"

BASE COUNT 49123 a 27264 c 26805 g 53629 t 200 others  
ORIGIN

Query Match 0.7%; Score 22; DB 2; Length 157021;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2587 GATGGAATGAAGCTCTTCATG 2608  
|||||  
Db 113039 GATGGAATGAAGCTCTTCATG 113018

RESULT 45  
AC079194/c 159946 bp DNA linear HTG 22-NOV-2000  
LOCUS Homo sapiens chromosome 11 clone RP11-475C4 map 11, WORKING DRAFT  
DEFINITION SEQUENCE, 37 unordered pieces.

ACCESSION AC079194  
VERSION AC079194.2 GI:11276162  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 159946)  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE Homo sapiens chromosome 11, clone RP11-475C4  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 159946)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Bida, F., Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,



misc\_feature 9659. .11181  
/note="assembly\_fragment"  
misc\_feature 11282. .12622  
/note="assembly\_fragment"  
misc\_feature 12723. .14374  
/note="assembly\_fragment"  
misc\_feature 14475. .37771  
/note="assembly\_fragment"  
misc\_feature 37872. .39354  
/note="assembly\_fragment"  
misc\_feature 39455. .40854  
/note="assembly\_fragment"  
misc\_feature 40955. .42709  
/note="assembly\_fragment"  
misc\_feature 42810. .44167  
/note="assembly\_fragment"  
misc\_feature 44268. .46404  
/note="assembly\_fragment"  
misc\_feature 46505. .48310  
/note="assembly\_fragment"  
misc\_feature 48411. .51136  
/note="assembly\_fragment"  
misc\_feature 51237. .53831  
/note="assembly\_fragment"  
misc\_feature 53932. .56439  
/note="assembly\_fragment"  
misc\_feature 56540. .58998  
/note="assembly\_fragment"  
misc\_feature 59099. .63491  
/note="assembly\_fragment"  
misc\_feature 63592. .66743  
/note="assembly\_fragment"  
misc\_feature 66844. .69817  
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misc\_feature 69918. .73103

Query Match 0.7%; Score 22; DB 2; Length 159946;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 AAAACAACACAAACATAAAG 1138  
|||||  
Db 150590 AAAACAACACAAACATAAAG 150569

RESULT 46  
AX318151  
LOCUS AX318151 21 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 156 from Patent WO0190156.  
ACCESSION AX318151  
VERSION AX318151.1 GI:17900842  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 156 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"  
BASE COUNT 5 a 3 c 6 g 7 t  
ORIGIN

Query Match 0.7%; Score 21; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GTATGGAATGTTCTGAATCGC 105  
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Db 1 GTATGGAATGTTCTGAATCGC 21

RESULT 47  
AX318153/c  
LOCUS AX318153 30 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 158 from Patent WO0190156.  
ACCESSION AX318153  
VERSION AX318153.1 GI:17900844  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 158 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source  
1..30  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"  
BASE COUNT 11 a 7 c 6 g 6 t  
ORIGIN

Query Match 0.7%; Score 21; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 TATCCTCTATTTCAGGACTTG 252  
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Db 30 TATCCTCTATTTCAGGACTTG 10

RESULT 48  
AX286953  
LOCUS AX286953 7067 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 21 from Patent WO0181598.  
ACCESSION AX286953  
VERSION AX286953.1 GI:17048966  
KEYWORDS  
SOURCE Candida albicans.  
ORGANISM Candida albicans  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; mitosporic Saccharomycetales; Candida.  
REFERENCE  
1  
AUTHORS Nellissen,B.J., de Backer,M.D. and Luyten,W.H.  
TITLE Multiple retrotransposon families in Candida albicans  
JOURNAL Patent: WO 0181598-A 21 01-NOV-2001;  
JANSSEN PHARMACEUTICA N.V. (BE)  
FEATURES  
source  
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/organism="Candida albicans"  
/db\_xref="taxon:5476"  
BASE COUNT 2539 a 1198 c 1057 g 2273 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2002 GATTCAGCAAGTTGAATAAG 2022  
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Db 4763 GATTCAGCAAGTTGAATAAG 4783

RESULT 49

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BTCSK35          7595 bp      DNA      linear      MAM 24-JUN-2000
LOCUS            Bovine gene for kappa-casein exons 3-5.
DEFINITION      BTFCSK35
ACCESSION      X14908
VERSION      X14908.1 GI:180
KEYWORDS      casein; kappa-casein; repetitive sequence; Alu-like repetitive
              sequence; restriction fragment linked polymorphism.
SOURCE          cow.
ORGANISM        Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE      1 (bases 1 to 7595)
AUTHORS      Valman,D., Mercier,D., Moazami-Goudarzi,K., Eggen,A.,
              Ciampolini,R., Lepingale,A., Velmala,R., Kaukinen,J., Varvio,S.I.,
              Tkach,T.M. and Gordanetsky,S.I.
              Alexander,L.J., Stewart,A.F., Mackinlay,A.G., Kapelinskaya,T.V.,
              Isolation and characterization of the bovine kappa-casein gene
              Eur. J. Biochem. 178 (2), 395-401 (1988)
TITLE          Isolation and characterization of the bovine kappa-casein gene
JOURNAL        Eur. J. Biochem. 178 (2), 395-401 (1988)
MEDLINE        89091174
PUBMED         3208764
REFERENCE      2 (bases 1 to 7595)
AUTHORS      Valman,D., Mercier,D., Moazami-Goudarzi,K., Eggen,A.,
              Ciampolini,R., Lepingale,A., Velmala,R., Kaukinen,J., Varvio,S.I.,
              Martin,P. et al.
              A set of 99 cattle microsatellites: characterization, synteny
              mapping, and polymorphism
              Mamm. Genome 5 (5), 288-297 (1994)
TITLE          A set of 99 cattle microsatellites: characterization, synteny
JOURNAL        Mamm. Genome 5 (5), 288-297 (1994)
MEDLINE        94355772
PUBMED         7545949
REFERENCE      3 (bases 1 to 7595)
AUTHORS      Mackinlay,A.G.
              Direct Submission
              Submitted (16-MAR-1989) A.G. Mackinlay, The University of New South
              Wales, P.O. Box 1 Kensington New South Wales Australia
              Location/Qualifiers
FEATURES         source
                 1..7595
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                 /usedin=X14906:kc_mrna
                 /label=ex3
misc_feature     2886..2891
                 /usedin=X14907:kc_sig
                 /label=sigstop
mat_peptide     join(2892..2918,4930..5412)
                 /product="kappa-casein"
exon             4930..5446
                 /label=kc_mat
                 /usedin=X14906:kc_mrna
                 /label=ex4
misc_feature     4930..5412
                 /usedin=X14907:kc_cds
                 /label=stop
variation        5309
                 /note="c is t in kappa-casein B variant; changes acc (Thr)
                 to atc (Ile)"
variation        5345
                 /note="a is c in kappa-casein B variant; changes gat (Asp)
                 to gct (Ala)"
variation        5406
                 /note="a is g in kappa-casein B variant; loss of PstI
                 site"
variation        5413
                 /note="a is t in kappa-casein B variant"
exon             7296..7416
                 /usedin=X14906:kc_mrna
                 /label=ex5
variation        7382
                 /note="t is c in kappa-casein B variant; loss of BglII
                 site, creates MspI site"
polyA_site      7416
variation        7484

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/Note="t is c in variant clone"
7486
/Note="t is c in variant clone"
7504
/Note="t is c in variant clone"
7534
/Note="g is a in variant clone"
7570..7571
/Note="c is inserted in variant clone"
2646 a 1292 c 1182 g 2475 t
BASE COUNT
ORIGIN
Query Match      0.7%; Score 21; DB 4; Length 7595;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 380 TTTTAACTTGAAGACACCT 400
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Db 6007 TTTTAACTTGAAGACACCT 6027
      |||||
RESULT 50
AE010385/c
LOCUS            Methanopyrus kandleri AV19 section 84 of 157 of the complete
DEFINITION      genome.
ACCESSION      AE010385 AE009439
VERSION      AE010385.1 GI:19887459
KEYWORDS
SOURCE          Methanopyrus kandleri AV19.
ORGANISM        Methanopyrus kandleri AV19
Archaea; Euryarchaeota; Methanopyri; Methanopyrales;
Methanopyraceae; Methanopyrus.
REFERENCE      1 (bases 1 to 9257)
AUTHORS      Slesarev,A.I., Mezhevaya,K.V., Makarova,K.S., Polushin,N.N.,
              Shcherbinina,O.V., Shakhova,V.V., Belova,G.I., Aravind,L.,
              Natile,D.A., Rogozin,I.B., Tatusov,R.L., Wolf,Y.I., Stetter,K.O.,
              Malykh,A.G., Koonin,E.V. and Kozzyavkin,S.A.
              The Complete Genome of the Hyperthermophile Methanopyrus kandleri
              AV19 and Monophyly of Archaeal Methanogens
              Unpublished
              2 (bases 1 to 9257)
              Slesarev,A.I., Mezhevaya,K.V., Makarova,K.S., Polushin,N.N.,
              Shcherbinina,O.V., Shakhova,V.V., Belova,G.I., Aravind,L.,
              Natile,D.A., Rogozin,I.B., Tatusov,R.L., Wolf,Y.I., Stetter,K.O.,
              Malykh,A.G., Koonin,E.V. and Kozzyavkin,S.A.
              Direct Submission
              Submitted (04-FEB-2002) Fidelity Systems, Inc., Gaithersburg, MD
              20879
              Location/Qualifiers
FEATURES         1..9257
                 /organism="Methanopyrus kandleri AV19"
                 /strain="AV19"
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                 complement(371..919)
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                 /transl_table=11
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                 /db_xref="GI:19887460"
                 /translation="MELEVAEFELEDIKVVVLRGDITELNADAVNPANSRGVWGCG
                 VAAAIKAKGGEIEREMERAKALIPVGEAVETTAGDLDLDAEYVIHAPTMERPAQRIGVEN
                 VREATEAALRKABELGVESVAFPGMGTVGVGVPYEDAAETMVEVIERLAPLESVRV
                 YLVGYEELAEAFRRALERRVG"
                 1318..2307
                 /gene="ecm27_2"
                 /note="MK0951"
                 1318..2307
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/transl_table=11
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/protein_id="AA02164.1"
/db_xref="GI:19887461"
/translation="MNGLKPCSVRALPVRGSDRVPWSALAYMMGCFVGFHFLSELLV
DATVGLARKYGLSEVAGATLAAGTSAPEFGSSLSLLEHPNVGVGTILGSAYNVN
TVIPGLAALAGGLTERAVYRRDVLFLVLLVLLVSLMDRVLRVLEALAWLYGL
VLLMRRDESTIGAGDGTGEASLRSVAVVVGTAALSDLAMVATVDFCEGGL
SSRSVSLLLNAGTSVDPDTLASVHAARGFGSLAVSNVAGSNTFFLLVCLGLVPLSLVS
RTPVHGELGALVALGCVLLYLVTVDGKLRNVEALALLGAYAFVACLLVL"
2448..3488
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CDS
2448..3488
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/product="Pyruvate-formate lyase-activating enzyme"
/protein_id="AA02165.1"
/db_xref="GI:19887462"
/translation="MGSRTMSDGLREWEGRTWEEVDGKVRCLVCPKCVIPEGSEGF
CVRNRRGELVLLHGKVSIVAPDPIEKPLPHYKPGDVFSLGTVGCNFRCHCQN
WQISAGPEEVPLEEMPPERIVGAARKTGCSVAFTYNEPIIGLEYTLTFEACREEG
LGVVYTFNGFATRTAKILGEVDAAVNDLKAFTEDFYRDVAKWLPVLTCKTWKD
MGVHVLTTLVTPGYNDSSEEARIRWIRKELGPDTPHWSRFPDPVRLMDVPDTPV
ETIEKFEIGYPEGLYVYVAGNVPGHKYENTYCPCKEPPVVVRRGFSIVKMHVTDDEH
CFHKDAELHFVT"
3682..4497
/gene="ubia"
CDS
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/product="4-hydroxybenzoate polyprenyltransferase"
/protein_id="AA02166.1"
/db_xref="GI:19887463"
/translation="MRAYLELRPINCAMALGVVVVGELIAGARLDVGAVLAPVVAAV
VCAGNAINDYDAVDVAVNRDPRIPSGRVPSRSMFALGCFAGVGMAIVNRMC
LAIALNSVLLYLYSRUKGTPLIGNVMVSYLVGSCFLFEGAAGVGPAPVWFLFLAF
LANLVREILKDELDVEGDAALGKLTPIAYGEGVALRVATVFAIALAVLTPLPYLDGV
VQWPLYLALPAAVLIALLASVLAVAGSWDAGAKQVRVYKVMGLLGLLAFIASLL"
complement(4486..5613)
/gene="MK0954"
CDS
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/codon_start=1
/transl_table=11
/product="Uncharacterized conserved protein"
/protein_id="AA02167.1"
/db_xref="GI:19887464"
/translation="MVSVAEEKVTYVIKADVGGFGPGHSEVHPDLLEACEGVLEDAVD
EVIDIYVTRGDDIDLIMTHTRGEDDEKVELAWNNAQEAATKVAEDLKLKYGADOLL
SDAFSGNVRGVPGAAMELVERPSEPIIVFCCKDTPSAFNLPLRFPADPNNTAGL
VLDPMSHGFEFEVHDVIDOKRVILKCPPEMYDGLLALIGQTORAIKRVYKKGDDGEA
ERIAATVTERLNLAGEYVQKDDPVAVIRQSGFPGVAVGEVLEPFTFPHLVAGWRGS
HNGPLVSEEAHPTRFDGPPRIIALGFOLRNGELVGPQDLFADPAFDRAREIANEV
ADYIRRHGPFOPHLLSEEEVLTLPDLVILKLEDFEEDLEE"
complement(5660..6010)
/gene="egd2"
CDS
complement(5660..6010)
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/product="transcription factor homologous to
NACalpha-BTF3"
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/db_xref="GI:19887465"
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EKQPVIRKIMNQEFYQVAGKAKREKPEEPTDEDVLLVAEQAGVSEEAARKALEET
GGDLAEAIMRLQGE"
complement(6059..6511)
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/transl_table=11
/product="Prefoldin, molecular chaperone implicated in de
novo protein folding, alpha subunit"
/protein_id="AA02169.1"
/db_xref="GI:19887466"
/translation="MSRYVEIVRGITLAIQFGREAADMLDGEVKVYRVRRGRPREVPVD
GKRLLCTVRASDGLVSLAPEGARLHAATEPPEHRVVCADENWEAVRGRDLFCETALR
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6527..7864
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CDS
6527..7864
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/db_xref="GI:19887467"
/translation="MDPDVLLRHAEIISDACVVYALEGELVEIEASNGELRKADSDRV
RTYAVRVLKEGWSVAGSDPPDRDLVERALRTGEGSAIEPEEVPAAEGSYRWEGKLS
PLDSLEAAELAVELSRVSYDCEITYSAGSVRYTITITWSECEVRLDCVNFVGVKVS
GKGTAGREYTERDGANCAGLEFLERAEVRDEAVRRLLEDLEAEPPGERAESVITD
PELLGVIVHEAFGHAVEGLDVARGESVLQDWYGERVASEIIVTVDQTPERGAFSYPPF
DDEGEPRTVLEEGVLRGYLTDLTSAEALOLEVTGNRGLSEIGDHVQVRMSYVIVE
PGDASREELFEAGDGVAYLLGSGQDTDTATGNFQFSAKLYGVVEEGPSPRPVRDVG
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7864..9093
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CDS
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protease of TldD family (PmbA subfamily protein)"
/protein_id="AA02171.1"
/db_xref="GI:19887468"
/translation="MALDDPLSQFEPGPRAVLLEVERVEVTHDTGDRGRVSADRT
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AVDEDELMDLLEAVNEVSDDVTITSVTVGVRRRVIFRTPSDQAEEREESVTVSLDV
IGFESGFAMDVTAVGPRDIDPELLAREASEMASEAPKERVSGGELAVAFHPRAFSELLT
VYLIPALSCLEVLKGTGDFDGRDGRKVCPSLRVYVNDPTLDRRPGSYAFDDDEGSTPK
RWELISDGLRSFYTDLYSSRRLGMESTSGLGIRRPESPANVIVQGDASSEEVELEE
ADLIIVRTLGAHTASKVSGRFSVTALWAETVEGRAVPVSVRGNLYSSLKDALISEETE
RTGVVEPPYALLRCRVG"
BASE COUNT 1481 a 3019 c 3036 g 1721 t
ORIGIN
Query Match 0.7%; Score 21; DB 1; Length 9257;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2710 GAGGAGGTCCCAACTCGTC 2730
|||||
DB 8202 GAGGAGGTCCCAACTCGTC 8182
Search completed: January 31, 2003, 03:11:19
Job time : 10921 secs
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GenCore version 5.1.3  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 21:51:25 : Search time 598 Seconds  
(without alignments)  
11568.794 Million cell updates/sec

Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaatttcataaagacaaa.....cttttaaacactgact 3072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 12

Total number of hits satisfying chosen parameters: 375039

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2	2919	95.0	3545	22	AAH98254	2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*	489	11
3	2918	95.0	3213	22	AAH78219	3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*	461	12
4	2868	93.4	3396	24	ABK22731	4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*	420	13
5	2634	85.7	3615	22	AA503946	5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*	304	14
6	2082	67.1	2215	22	AAH78218	6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*	269	15
7	1781	58.0	2950	22	AAH99581	7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*	261	16
8	840	27.3	891	24	ABK22766	8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*	242	17
9	815	26.5	1395	24	ABK22732	9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*	242	18
SUMMARIES									
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
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1	3072	100.0	3133	22	AA503945				
2	2919	95.0	3545	22	AAH98254				
3	2918	95.0	3213	22	AAH78219				
4	2868	93.4	3396	24	ABK22731				
5	2634	85.7	3615	22	AA503946				
6	2082	67.1	2215	22	AAH78218				
7	1781	58.0	2950	22	AAH99581				
8	840	27.3	891	24	ABK22766				
9	815	26.5	1395	24	ABK22732				

Human cdna encodin	24	ABK22767	618	20.1	24	ABK22767	Human cdna encodin
Human colon cancer	22	AAH34171	2735	15.9	22	AAH34171	Human colon cancer
Human cdna encodin	24	ABK22734	768	15.0	24	ABK22734	Human cdna encodin
Human cdna encodin	22	AA526160	608	13.7	22	AA526160	Human cdna encodin
Human cdna encodin	22	AA526575	522	9.9	22	AA526575	Human cdna encodin
Human cdna encodin	24	ABK22733	578	8.8	24	ABK22733	Human cdna encodin
Human cdna encodin	24	ABK22765	261	8.5	24	ABK22765	Human cdna encodin
Human breast cell	21	ABA45612	421	7.9	21	ABA45612	Human breast cell
Human foetal liver	22	ABA56119	421	7.9	22	ABA56119	Human foetal liver
Probe #4236 for ge	22	ABA25770	421	7.9	22	ABA25770	Probe #4236 for ge
Human brain expres	22	AAK04305	421	7.9	22	AAK04305	Human brain expres
Human bone marrow	22	AAK29801	421	7.9	22	AAK29801	Human bone marrow
Probe #4322 for ge	22	AAI14389	421	7.9	22	AAI14389	Probe #4322 for ge
Probe #4450 used t	22	AAI35764	421	7.9	22	AAI35764	Probe #4450 used t
Probe #4204 used t	22	AAI04213	421	7.9	22	AAI04213	Probe #4204 used t
Human genome-deriv	24	ABS04362	421	7.9	24	ABS04362	Human genome-deriv
Human breast cell	22	ABA50734	220	7.2	22	ABA50734	Human breast cell
Human foetal liver	22	ABA68704	220	7.2	22	ABA68704	Human foetal liver
Probe #14134 for g	22	ABA35668	220	7.2	22	ABA35668	Probe #14134 for g
Human brain expres	22	AAK17044	220	7.2	22	AAK17044	Human brain expres
Human bone marrow	22	AAK42828	220	7.2	22	AAK42828	Human bone marrow
Probe #13523 for g	22	AAI23590	220	7.2	22	AAI23590	Probe #13523 for g
Probe #17590 used	22	AAI48904	220	7.2	22	AAI48904	Probe #17590 used
Probe #9197 used t	22	AAI09206	220	7.2	22	AAI09206	Probe #9197 used t
Human genome-deriv	24	ABS16884	220	7.2	24	ABS16884	Human genome-deriv
Human cdna encodin	24	ABK22768	165	3.7	24	ABK22768	Human cdna encodin
Human spliced tran	24	ABNA0447	60	2.0	24	ABNA0447	Human spliced tran
Human CLAN A PCR p	29	ABK22753	29	0.9	29	ABK22753	Human CLAN A PCR p
Human CLAN B PCR p	25	ABK22754	25	0.8	25	ABK22754	Human CLAN B PCR p
Human CLAN D PCR p	25	ABK22755	25	0.8	25	ABK22755	Human CLAN D PCR p
Human CLAN A PCR p	24	ABK22752	25	0.8	24	ABK22752	Human CLAN A PCR p
Human CLAN CARD do	24	ABK22750	24	0.8	24	ABK22750	Human CLAN CARD do
Human CLAN CDNA PC	23	ABK22746	23	0.7	23	ABK22746	Human CLAN CDNA PC
Human CLAN C PCR p	24	ABK22756	23	0.7	24	ABK22756	Human CLAN C PCR p
Human CLAN CARD do	21	ABK22749	21	0.7	21	ABK22749	Human CLAN CARD do
Long terminal repe	30	ABK22751	30	0.7	30	ABK22751	Long terminal repe
Human prostate exp	23	AAV95269	7067	0.7	23	AAV95269	Human prostate exp
Bacillus clausii g	431	ABV46663	431	0.7	431	ABV46663	Bacillus clausii g
Human cdna encodin	24	ABK78972	475	0.7	24	ABK78972	Human cdna encodin
Drosophila melanog	23	ABL25908	3811	0.7	23	ABL25908	Drosophila melanog
Drosophila melanog	23	ABL04194	4737	0.7	23	ABL04194	Drosophila melanog
Human nervous syst	22	ABAI12901	431	0.6	22	ABAI12901	Human nervous syst
DNA encoding nove	23	AA574824	451	0.6	23	AA574824	DNA encoding nove
Human cdna clone (	22	ABH11452	549	0.6	22	ABH11452	Human cdna clone (
H. pylori cell env	19	AAK30628	579	0.6	19	AAK30628	H. pylori cell env
H. pylori GHPO 875	19	AAK14445	649	0.6	19	AAK14445	H. pylori GHPO 875
DNA encoding nove	23	AA570584	1034	0.6	23	AA570584	DNA encoding nove
CDNA encoding nove	21	AAF13098	1780	0.6	21	AAF13098	CDNA encoding nove
Aspergillus oryzae	24	ABL56644	2379	0.6	24	ABL56644	Aspergillus oryzae
Nucleotide sequenc	22	ABL16202	2825	0.6	22	ABL16202	Nucleotide sequenc
Human cdna sequenc	23	ABL09400	3217	0.6	23	ABL09400	Human cdna sequenc
Drosophila melanog	23	AA59627	8632	0.6	23	AA59627	Drosophila melanog
Propionibacterium	24	ABA97708	10917	0.6	24	ABA97708	Propionibacterium
Wild-type mouse Wo	22	AA532551	14346	0.6	22	AA532551	Wild-type mouse Wo
Human genomic DNA	22	AAK38253	30310	0.6	22	AAK38253	Human genomic DNA
Genomic DNA from t	24	ABL22748	21	0.6	24	ABL22748	Genomic DNA from t
Human CLAN CDNA PC	24	AAK32551	116	0.6	24	AAK32551	Human CLAN CDNA PC
Human secreted pro	22	AAK68570	116	0.6	22	AAK68570	Human secreted pro
Human immune/haema	22	AAK68571	147	0.6	22	AAK68571	Human immune/haema
Human ovarian cano	22	ABL86464	147	0.6	22	ABL86464	Human ovarian cano
Plant microsatelli	24	AAK31261	216	0.6	24	AAK31261	Plant microsatelli
Human gene signatu	16	AAAT24250	274	0.6	16	AAAT24250	Human gene signatu
Plant microsatelli	322	AAK31416	322	0.6	322	AAK31416	Plant microsatelli
Plant microsatelli	355	AAK31325	355	0.6	355	AAK31325	Plant microsatelli
Human polynucleoti	377	AAK88708	377	0.6	377	AAK88708	Human polynucleoti
Human prostate exp	399	ABV00662	399	0.6	399	ABV00662	Human prostate exp
Plant microsatelli	434	AAK31366	434	0.6	434	AAK31366	Plant microsatelli
Human secreted pro	435	AAK09333	435	0.6	435	AAK09333	Human secreted pro
Human breast cell	446	ABA6095	446	0.6	446	ABA6095	Human breast cell
Human foetal liver	454	ABA56643	454	0.6	454	ABA56643	Human foetal liver

c 83	18	0.6	454	22	ABA26250	Probe #4716 for ge	c 156	18	0.6	2824	23	ABL14984	Drosophila melanog
c 84	18	0.6	454	22	AAK30303	Human bone marrow	c 157	18	0.6	2832	23	ABL29982	Drosophila melanog
c 85	18	0.6	454	22	AAI14905	Probe #4838 for ge	c 158	18	0.6	2861	22	AAK79745	Human immune/haema
c 86	18	0.6	454	22	AAI36257	Probe #4943 used t	c 159	18	0.6	2869	23	ABL7056	Drosophila melanog
c 87	18	0.6	454	22	AAI04685	Probe #4676 used t	c 160	18	0.6	3000	20	AAK84399	S. capsulata IF012
c 88	18	0.6	454	24	ABS04888	Human genome-deriv	c 161	18	0.6	3001	21	AAH51776	Chromosome 13q31-q
c 89	18	0.6	466	21	AAC01809	Human secreted pro	c 162	18	0.6	3001	21	AAH51787	Chromosome 13q31-q
c 90	18	0.6	468	21	AAA31287	Plant microsatelli	c 163	18	0.6	3041	23	ABL06950	Drosophila melanog
c 91	18	0.6	472	22	ABA43065	Human breast cell	c 164	18	0.6	3126	23	ABL11736	Drosophila melanog
c 92	18	0.6	472	22	ABA53479	Human foetal liver	c 165	18	0.6	3228	23	AAH81183	DNA encoding novel
c 93	18	0.6	472	22	ABA23248	Probe #1714 for ge	c 166	18	0.6	3275	22	AAF25373	Genomic sequence o
c 94	18	0.6	472	22	AAK01751	Human brain expres	c 167	18	0.6	3368	23	ABL29984	Drosophila melanog
c 95	18	0.6	472	22	AAK27206	Human bone marrow	c 168	18	0.6	3460	22	AAH26682	Human genomic DNA
c 96	18	0.6	472	22	AAI1187	Probe #1720 for ge	c 169	18	0.6	3527	23	ABL09309	Drosophila melanog
c 97	18	0.6	472	22	AAI33101	Probe #1787 used t	c 170	18	0.6	3529	21	AAH31144	Human colon cancer
c 98	18	0.6	472	22	AAI01718	Probe #1709 used t	c 171	18	0.6	3608	24	AAH33243	Human secreted pro
c 99	18	0.6	472	24	ABS01749	Human genome-deriv	c 172	18	0.6	3931	23	ABL29382	Drosophila melanog
c 100	18	0.6	503	23	ABV31005	Human prostate exp	c 173	18	0.6	3942	20	AAV80604	Kidney injury asso
c 101	18	0.6	503	23	ABV39973	Human prostate exp	c 174	18	0.6	3958	23	ABL11720	Drosophila melanog
c 102	18	0.6	529	23	AAH52224	DNA encoding novel	c 175	18	0.6	3969	21	AAH64473	DNA encoding an as
c 103	18	0.6	594	11	AAQ05868	Sequence encoding	c 176	18	0.6	3999	24	AB199451	Mouse ischaemic co
c 104	18	0.6	652	21	AAQ07589	Fusarium venenatum	c 177	18	0.6	4168	23	ABL30172	Drosophila melanog
c 105	18	0.6	682	21	AAC44321	Arabidopsis thalia	c 178	18	0.6	4199	23	ABL30188	Drosophila melanog
c 106	18	0.6	763	23	ABL29983	Drosophila melanog	c 179	18	0.6	4215	22	AAI58415	Human polynucleoti
c 107	18	0.6	814	22	AAH05406	Human cDNA clone (	c 180	18	0.6	4871	22	AAI60201	Human polynucleoti
c 108	18	0.6	824	23	ABL14985	Drosophila melanog	c 181	18	0.6	4911	23	ABL13032	Drosophila melanog
c 109	18	0.6	863	23	ABL11737	Drosophila melanog	c 182	18	0.6	4951	20	AAH13198	Enterococcus faeca
c 110	18	0.6	864	23	ABV09831	Human prostate exp	c 183	18	0.6	4982	18	AAH85267	HMG-CoA reductase
c 111	18	0.6	873	23	ABV11991	Human prostate exp	c 184	18	0.6	4986	23	AAH88902	DNA encoding novel
c 112	18	0.6	888	20	AAH20212	Enterococcus faeca	c 185	18	0.6	5031	23	ABL11822	Drosophila melanog
c 113	18	0.6	888	24	ABN98197	E faecalis EF110 g	c 186	18	0.6	5120	23	AAH84984	DNA encoding novel
c 114	18	0.6	960	22	AAH67086	C glutamicum codin	c 187	18	0.6	5121	22	AAH86008	Human immune/haema
c 115	18	0.6	992	11	AAQ05870	Sequence encoding	c 188	18	0.6	5173	24	AAH33333	Proliferation pote
c 116	18	0.6	1034	22	AAQ52527	Human secreted pro	c 189	18	0.6	5212	9	AAH80317	Transcription cont
c 117	18	0.6	1083	22	AAH71387	Corynebacterium gi	c 190	18	0.6	5292	21	AAH21374	Human low adenosin
c 118	18	0.6	1092	23	AAH82524	DNA encoding novel	c 191	18	0.6	5292	21	AAH35252	Human adenosine re
c 119	18	0.6	1105	23	ABV25236	Human prostate exp	c 192	18	0.6	5511	17	AAH41853	cDNA encoding plas
c 120	18	0.6	1163	22	AAH37592	Human musculoskele	c 193	18	0.6	5890	22	AAH05680	Human reproductive
c 121	18	0.6	1205	20	AAZ42236	Human normal bladd	c 194	18	0.6	6108	22	AAH39728	Genomic sequence #
c 122	18	0.6	1243	24	ABL89619	Human polynucleoti	c 195	18	0.6	6108	22	AAH65557	Human immune/haema
c 123	18	0.6	1250	9	AAH80316	Transcription cont	c 196	18	0.6	6108	22	AAH90069	Human digestive sy
c 124	18	0.6	1343	22	AAH86733	Human polynucleoti	c 197	18	0.6	6111	22	AAH39727	Genomic sequence #
c 125	18	0.6	1473	21	AAH40012	Arabidopsis thalia	c 198	18	0.6	6111	22	AAH90068	Human digestive sy
c 126	18	0.6	1491	21	AAH47150	DNA encoding a ser	c 199	18	0.6	6212	21	AAH21375	Human low adenosin
c 127	18	0.6	1515	19	AAV40737	C. felis esterase,	c 200	18	0.6	6212	21	AAH35253	Human adenosine re
c 128	18	0.6	1515	19	AAV40738	C. felis esterase,	c 201	18	0.6	6231	23	ABL09308	Drosophila melanog
c 129	18	0.6	1561	21	AAH21032	Human low adenosin	c 202	18	0.6	6276	23	ABL26815	Drosophila melanog
c 130	18	0.6	1561	21	AAH34910	Human adenosine re	c 203	18	0.6	6689	23	ABL11814	Drosophila melanog
c 131	18	0.6	1579	22	AAH13702	Human cDNA sequenc	c 204	18	0.6	7380	20	AAH84028	MMP9 promoter beta
c 132	18	0.6	1595	24	ABQ91965	Human NF-kB activa	c 205	18	0.6	7383	22	AAH00153	Matrix metalloprot
c 133	18	0.6	1611	12	AAQ12528	Thymidylate phosph	c 206	18	0.6	7386	22	AAH90294	Human digestive sy
c 134	18	0.6	1611	21	AAH47151	DNA encoding a ser	c 207	18	0.6	7386	22	AAH57671	Human colorectal c
c 135	18	0.6	1618	23	ABL11537	Drosophila melanog	c 208	18	0.6	7897	23	ABL05564	Drosophila melanog
c 136	18	0.6	1619	21	AAH15908	Human protein clon	c 209	18	0.6	8873	24	ABL70173	Chemically treated
c 137	18	0.6	1650	19	AAV40760	C. felis esterase,	c 210	18	0.6	8873	24	AAH61124	Human gene regulat
c 138	18	0.6	1650	19	AAV40761	C. felis esterase,	c 211	18	0.6	8873	24	AAH31210	Signal transductio
c 139	18	0.6	1723	20	AAV71287	Human vesicular bi	c 212	18	0.6	9084	24	ABL33604	Human immune syste
c 140	18	0.6	1761	24	AAH33265	Human secreted pro	c 213	18	0.6	9805	22	AAH34718	Human DNA for a no
c 141	18	0.6	1800	15	AAQ67601	Retinoblastoma pro	c 214	18	0.6	9805	22	AAH05681	Human reproductive
c 142	18	0.6	1878	22	AAH25374	Nucleotide sequenc	c 215	18	0.6	11968	23	ABL26814	Drosophila melanog
c 143	18	0.6	1926	20	AAH25522	Sphingomonas capsu	c 216	18	0.6	13732	24	ABL33820	Human immune syste
c 144	18	0.6	1962	20	AAH27750	Human ovarian tumo	c 217	18	0.6	15915	23	ABL04550	Drosophila melanog
c 145	18	0.6	1982	19	AAV40735	C. felis esterase,	c 218	18	0.6	17252	22	AAH28668	Genomic sequence #
c 146	18	0.6	1982	19	AAV40736	C. felis esterase,	c 219	18	0.6	17509	24	ABH95599	Gene #2097 used to
c 147	18	0.6	1982	22	AAH21167	Ctenocephalides fe	c 220	18	0.6	19040	22	ABA16589	Human nervous syst
c 148	18	0.6	1986	23	ABL30173	Drosophila melanog	c 221	18	0.6	23044	23	ABL11536	Drosophila melanog
c 149	18	0.6	1996	24	ABA04431	Human PPI744 prote	c 222	18	0.6	32205	22	AAH08217	Human ovarian and
c 150	18	0.6	2144	19	AAV40758	C. felis esterase,	c 223	18	0.6	32205	22	AAH07525	Human reproductive
c 151	18	0.6	2144	19	AAV40759	C. felis esterase,	c 224	18	0.6	32986	22	AAH69758	Human immune/haema
c 152	18	0.6	2144	22	AAH21182	Ctenocephalides fe	c 225	18	0.6	32986	22	AAH84629	Human immune/haema
c 153	18	0.6	2299	19	AAH26326	S. pneumoniae deri	c 226	18	0.6	39746	23	ABL113398	Drosophila melanog
c 154	18	0.6	2299	19	AAH42995	Streptococcus pneu	c 227	18	0.6	45186	22	AAH60478	Wild-type human CT
c 155	18	0.6	2619	22	AAH26680	Human genomic DNA	c 228	18	0.6	236303	22	AAH11614	Human genomic DNA

229	18	0.6	325791	22	AAS43104	Human Oestrogen re	302	17	0.6	541	24	ABS17367	Human genome-deriv
230	18	0.6	349980	22	AAH68530	C glutamicum codin	303	17	0.6	542	22	AAD14988	Human NOV9 DNA. H
231	18	0.6	1503900	22	AAK95240	Human neuregulin-1	c 304	17	0.6	551	24	ABK62815	Rat sequence diffe
232	18	0.6	1503900	22	AAK96733	Human neuregulin-1	c 305	17	0.6	575	22	ABA63892	Human foetal liver
233	18	0.6	1664976	19	AAV21209	Methanococcus jann	c 306	17	0.6	575	22	ABA31072	Probe #9538 for ge
234	17	0.6	21	20	AAZ18259	P450 enzyme gene s	c 307	17	0.6	575	22	AAI18893	Probe #8826 for ge
235	17	0.6	32	24	ABK53200	Lipase (tliA) 5' p	c 308	17	0.6	576	20	AAZ29765	Human SOCS16 cDNA.
236	17	0.6	47	21	AAZ67938	Human map-related	c 309	17	0.6	583	22	AAI99056	Human excretory re
237	17	0.6	51	21	AAZ99916	Sequence of the st	c 310	17	0.6	583	22	AAI63406	Human kidney relat
238	17	0.6	60	24	AAZ39012	Human spliced tran	c 311	17	0.6	587	22	AAK63165	Human immune/haema
239	17	0.6	121	21	AAI10211	Human secreted pro	c 312	17	0.6	588	22	AAZ27307	cDNA encoding nove
240	17	0.6	167	23	ABL57927	Human VGS1 exon 8.	c 313	17	0.6	588	23	AAK54335	cDNA encoding nove
241	17	0.6	212	21	AAI13747	Human secreted pro	c 314	17	0.6	590	24	ABK63068	Rat sequence diffe
242	17	0.6	243	22	AAI01773	Human reproductive	c 315	17	0.6	591	20	AAK64907	Human G protein-co
243	17	0.6	243	23	ABL97066	Human testicular a	c 316	17	0.6	591	23	ABV35313	Human prostate exp
244	17	0.6	276	20	AAV88937	EST clone HW846..	c 317	17	0.6	591	23	ABV44145	Human prostate exp
245	17	0.6	290	20	AAZ22458	Internal Transcrib	c 318	17	0.6	591	24	ABK81685	cDNA encoding nove
246	17	0.6	296	22	AAK53772	Murine transport a	c 319	17	0.6	604	23	ABV22637	Human prostate exp
247	17	0.6	308	23	ABV07396	Human prostate exp	c 320	17	0.6	604	23	ABV28460	Human prostate exp
248	17	0.6	312	22	AAH66827	C glutamicum codin	c 321	17	0.6	609	22	AAK89375	Human digestive sy
249	17	0.6	324	22	AAI188588	Human polynucleoti	c 322	17	0.6	619	21	AAO16111	Human colon cancer
250	17	0.6	333	21	AAI22687	Human secreted pro	c 323	17	0.6	621	24	ABQ225194	Oligonucleotide fo
251	17	0.6	354	24	ABN68875	Streptococcus poly	c 324	17	0.6	621	24	ABQ225195	Oligonucleotide fo
252	17	0.6	355	24	ABL85192	Human ovarian canc	c 325	17	0.6	636	21	AAA30448	Human brain cDNA c
253	17	0.6	359	21	AAA44118	Human secreted exp	c 326	17	0.6	644	23	ABV14219	Human prostate exp
254	17	0.6	375	22	AAK59068	Human cancer relat	c 327	17	0.6	644	23	ABV14219	Human prostate exp
255	17	0.6	383	18	AAK83360	Breast cancer tumo	c 328	17	0.6	653	21	AAF08204	Fusarium venenatum
256	17	0.6	383	19	AAV68900	DNA molecule encod	c 329	17	0.6	653	24	ABQ58440	Human colon cancer
257	17	0.6	383	21	AAK80883	Human breast tumou	c 330	17	0.6	656	21	AAF13116	Aspergillus oryzae
258	17	0.6	383	24	ABK46773	Human breast tumou	c 331	17	0.6	661	20	AAZ22439	Internal Transcrib
259	17	0.6	383	24	AAK59729	Breast tumour-spec	c 332	17	0.6	702	22	AAI00961	Human reproductive
260	17	0.6	387	21	AAK29487	Human secreted pro	c 333	17	0.6	702	23	ABV196431	Human testicular a
261	17	0.6	390	23	ABV18991	Human prostate exp	c 334	17	0.6	714	22	AAI95590	Human neuroblastom
262	17	0.6	397	22	AAK59060	Human cancer relat	c 335	17	0.6	729	23	ABL06067	Drosophila melanog
263	17	0.6	399	23	AAK574509	Human prostate exp	c 336	17	0.6	734	22	AAH36020	Human colon cancer
264	17	0.6	403	22	AAK59048	DNA encoding novel	c 337	17	0.6	739	21	AAK34392	Arabidopsis thalia
265	17	0.6	406	23	AAK567082	Human cancer relat	c 338	17	0.6	739	23	AAK590653	DNA encoding novel
266	17	0.6	413	22	AAI92244	DNA encoding novel	c 339	17	0.6	745	21	AAK45988	Arabidopsis thalia
267	17	0.6	418	23	ABK41834	Human polynucleoti	c 340	17	0.6	759	23	ABV05050	Human prostate exp
268	17	0.6	422	23	ABV13941	cDNA encoding nove	c 341	17	0.6	762	22	AAI97375	Human neuroblastom
269	17	0.6	427	23	AAK74078	Human prostate exp	c 342	17	0.6	772	22	AAK22707	Human gastric canc
270	17	0.6	428	22	AAK14140	DNA encoding novel	c 343	17	0.6	804	21	AAK90125	Cytokine receptor-
271	17	0.6	432	21	AAI16337	Human nervous syst	c 344	17	0.6	816	24	ABQ88847	Human prostate exp
272	17	0.6	435	22	AAK46068	Human prostate can	c 345	17	0.6	816	24	ABN98971	Arabidopsis thalia
273	17	0.6	435	22	ABA56606	Human breast cell	c 346	17	0.6	832	23	ABL15671	Drosophila melanog
274	17	0.6	435	22	ABA56606	Human foetal liver	c 347	17	0.6	840	22	AAH04154	Human cDNA clone (
275	17	0.6	435	22	ABA26221	Probe #4867 for ge	c 348	17	0.6	843	20	AAK00643	Human secreted pro
276	17	0.6	435	22	AAK04750	Human brain expres	c 349	17	0.6	859	23	AAK84155	DNA encoding novel
277	17	0.6	435	22	AAI14872	Human bone marrow	c 350	17	0.6	878	22	AAO2587	Human ovarian and
278	17	0.6	435	22	AAI36228	Probe #4805 for ge	c 351	17	0.6	884	22	AAH06551	Human CDNA clone (
279	17	0.6	435	22	AAI04659	Probe #4914 used t	c 352	17	0.6	918	23	ABV11455	Human prostate exp
280	17	0.6	435	24	ABK04855	Human genome-deriv	c 353	17	0.6	927	21	AAZ53603	Neisseria meningit
281	17	0.6	437	22	AAK59365	Human immune/haema	c 354	17	0.6	927	22	AAH53526	S. epidermidis ope
282	17	0.6	439	23	ABV04772	Human prostate exp	c 355	17	0.6	931	22	AAH01836	Human reproductive
283	17	0.6	442	23	ABV48770	Human prostate exp	c 356	17	0.6	931	23	ABL97129	Human testicular a
284	17	0.6	460	23	ABV35050	Human prostate exp	c 357	17	0.6	939	24	ABN91158	Staphylococcus epi
285	17	0.6	460	23	ABV43897	Human prostate exp	c 358	17	0.6	945	21	AAK50863	Arabidopsis thalia
286	17	0.6	478	24	ABN63353	Human prostate exp	c 359	17	0.6	947	23	ABV23244	Human prostate exp
287	17	0.6	484	22	AAH13621	Human cancer relat	c 360	17	0.6	947	23	ABV29088	Human prostate exp
288	17	0.6	486	23	AAK571136	Human cDNA clone (	c 361	17	0.6	979	22	AAH32025	Human olfactory re
289	17	0.6	510	21	AAK38101	DNA encoding thalia	c 362	17	0.6	996	24	ABN67399	Streptococcus poly
290	17	0.6	522	22	AAH09564	Human cDNA clone (	c 363	17	0.6	1001	22	AAH75151	Nucleotide sequenc
291	17	0.6	522	24	ABN94816	Gene #1314 used to	c 364	17	0.6	1013	22	AAI17919	G-protein coupled
292	17	0.6	534	23	ABV18243	Human prostate exp	c 365	17	0.6	1076	22	AAZ29941	c albicans apoptos
293	17	0.6	539	22	AAI90518	Human polynucleoti	c 366	17	0.6	1094	22	AAK41250	cDNA encoding nove
294	17	0.6	541	22	ABA51181	Human breast cell	c 367	17	0.6	1094	22	AAK34981	cDNA encoding nove
295	17	0.6	541	22	ABA69181	Human foetal liver	c 368	17	0.6	1125	21	AAK43347	Arabidopsis thalia
296	17	0.6	541	22	ABA36107	Probe #14573 for g	c 369	17	0.6	1132	22	AAI68145	Human aggreganase-
297	17	0.6	541	22	AAK17482	Human brain expres	c 370	17	0.6	1147	22	AAK91200	Human digestive sy
298	17	0.6	541	22	AAK43293	Human bone marrow	c 371	17	0.6	1149	22	AAK91197	Human digestive sy
299	17	0.6	541	22	AAI24061	Probe #13994 for g	c 372	17	0.6	1149	22	AAK91197	Human digestive sy
300	17	0.6	541	22	AAI49358	Probe #18044 used	c 373	17	0.6	1173	21	AAK83110	DNA encoding a pro
301	17	0.6	541	22	AAI09644	Probe #9635 used t	c 374	17	0.6	1179	23	AAK564921	DNA encoding novel

375	17	0.6	1185	22	AAK53293	Human polynucleoti	448	17	0.6	2073	24	ABL68820	Kidney cancer rela
376	17	0.6	1188	22	AAK52309	Human polynucleoti	c 449	17	0.6	2095	20	AAK27331	Human secreted pro
377	17	0.6	1229	22	AAI92643	Human polynucleoti	450	17	0.6	2115	20	AAK44723	Novel protein kina
378	17	0.6	1232	21	AAI12158	Murine X5L DNA fra	451	17	0.6	2124	24	AAI45611	Human ATP dependen
379	17	0.6	1245	22	ABA08870	Human Fas-associat	452	17	0.6	2175	24	ABN68111	Streptococcus poly
380	17	0.6	1261	21	AAI44835	Arabidopsis thalia	c 453	17	0.6	2180	22	AAH24225	Human oxidoreducta
381	17	0.6	1263	22	AAI93369	Mammalian interleu	454	17	0.6	2180	22	AAH14968	Human cDNA sequenc
382	17	0.6	1278	21	AAI90124	Murine cytokine re	c 455	17	0.6	2188	22	AAI34842	cDNA encoding nove
383	17	0.6	1284	23	ABV21452	Human prostate exp	456	17	0.6	2190	23	AAI05961	Drosophila melanog
384	17	0.6	1284	23	ABV27270	Human prostate exp	c 457	17	0.6	2191	23	AAI45025	cDNA encoding nove
385	17	0.6	1302	24	ABN91365	Staphylococcus epi	c 458	17	0.6	2192	24	AAI94879	Human DNA sequenc
386	17	0.6	1306	22	AAI54477	Zcytor 10 cytokine	c 459	17	0.6	2210	21	AAI62077	Hydrophobic domain
387	17	0.6	1318	21	AAI47883	Arabidopsis thalia	c 460	17	0.6	2224	19	AAI35472	Rat RSK3 coding se
388	17	0.6	1332	24	ABO78009	Chlamydia polynucl	c 461	17	0.6	2309	22	AAI53255	Human polynucleoti
389	17	0.6	1343	23	ABL12475	Drosophila melanog	462	17	0.6	2322	23	ABL05435	Drosophila melanog
390	17	0.6	1359	22	AAI65491	C glutamicum codin	463	17	0.6	2328	23	ABL19593	Drosophila melanog
391	17	0.6	1360	23	ABV23029	Human prostate exp	464	17	0.6	2330	22	AAH14498	Human cDNA sequenc
392	17	0.6	1360	23	ABV28865	Human prostate exp	465	17	0.6	2375	23	ABL07241	Drosophila melanog
393	17	0.6	1371	24	ABN66153	Streptococcus poly	c 466	17	0.6	2447	23	AAI83213	DNA encoding novel
394	17	0.6	1381	21	AAI36170	Arabidopsis thalia	467	17	0.6	2450	23	ABL11997	Drosophila melanog
395	17	0.6	1404	20	AAK611424	DNA encoding a hum	468	17	0.6	2451	22	AAI26984	cDNA encoding nove
396	17	0.6	1409	24	ABK11149	Murine TSLPR (thym	469	17	0.6	2460	21	AAI98006	Human T gene cDNA
397	17	0.6	1409	24	ABK11530	Mouse thymic strom	c 470	17	0.6	2462	19	AAI35473	Human hSK3 coding
398	17	0.6	1410	23	ABL12471	Drosophila melanog	c 471	17	0.6	2464	22	AAI45213	cDNA encoding nove
399	17	0.6	1425	22	AAI54451	Zcytor 10 cytokine	c 472	17	0.6	2465	22	AAI23681	Human DKC1 cDNA
400	17	0.6	1428	23	ABL57930	Human VG51 coding	c 473	17	0.6	2466	23	AAI69887	DNA encoding novel
401	17	0.6	1452	13	AAQ29383	Mouse perforin C-t	474	17	0.6	2469	22	AAI78832	Human immune/haema
402	17	0.6	1456	22	AAI62706	Human DAPPI cDNA	475	17	0.6	2471	24	AAI72320	ISIGP-3 cDNA. Hom
403	17	0.6	1504	22	AAI15476	Human cDNA sequenc	476	17	0.6	2479	23	ABL23280	Drosophila melanog
404	17	0.6	1530	20	AAI22768	Human IUPAC versio	477	17	0.6	2488	23	ABL17627	Drosophila melanog
405	17	0.6	1530	20	AAI22766	Human refined SOCS	478	17	0.6	2504	22	AAI55869	Rat GLUTX2 coding
406	17	0.6	1532	20	AAI22767	Human IUPAC versio	c 479	17	0.6	2521	20	AAI08414	Human small conduc
407	17	0.6	1536	22	AAI20195	Human translation	480	17	0.6	2521	21	AAI16086	Human prostate can
408	17	0.6	1536	22	AAI86071	Human translation	481	17	0.6	2565	23	ABL14698	Drosophila melanog
409	17	0.6	1546	23	ABL20043	Drosophila melanog	c 482	17	0.6	2571	22	AAI52271	Human polynucleoti
410	17	0.6	1590	21	AAI48082	Zea mays DNA fragm	c 483	17	0.6	2658	12	AAI4772	SP6DNA polymerase
411	17	0.6	1604	22	AAI15435	Human cDNA sequenc	484	17	0.6	2675	23	ABL12171	Drosophila melanog
412	17	0.6	1635	23	AAI80572	DNA encoding novel	c 485	17	0.6	2698	22	AAI18540	Human cDNA sequenc
413	17	0.6	1638	21	AAI43024	Arabidopsis thalia	486	17	0.6	2729	23	ABL06066	Drosophila melanog
414	17	0.6	1653	21	AAI63457	Human secreted pro	487	17	0.6	2785	24	ABN59856	Novel human coding
415	17	0.6	1659	22	ABA21325	Human nervous syst	c 488	17	0.6	2849	24	ABK34712	Human cDNA for nov
416	17	0.6	1665	21	AAI62067	Hydrophobic domain	c 489	17	0.6	2852	24	ABO70918	Listeria monocytog
417	17	0.6	1680	24	ABA05623	Human protein tyro	c 490	17	0.6	2886	21	AAI70575	Antisense DRE Anta
418	17	0.6	1681	23	ABL10139	Drosophila melanog	491	17	0.6	2887	24	AAI93762	Human nucleic acid
419	17	0.6	1682	22	AAI20196	Human translation	492	17	0.6	2909	23	ABL26884	Drosophila melanog
420	17	0.6	1682	22	AAI86072	Human translation	493	17	0.6	2911	22	AAI525925	Human cDNA encodin
421	17	0.6	1682	24	ABK83618	Human cDNA differe	c 494	17	0.6	2925	23	ABL20028	Drosophila melanog
422	17	0.6	1700	24	ABK94908	Human novel polynu	c 495	17	0.6	2936	23	ABL15670	Human cDNA sequenc
423	17	0.6	1742	23	ABL09199	Drosophila melanog	496	17	0.6	2937	22	AAI18341	Human cDNA sequenc
424	17	0.6	1771	23	AAI90655	DNA encoding novel	c 497	17	0.6	2986	22	AAI55032	S. epidermidis gen
425	17	0.6	1779	23	AAI92315	DNA encoding novel	c 498	17	0.6	3005	24	ABL53693	Human ubiquitin de
426	17	0.6	1782	23	ABL12479	Drosophila melanog	499	17	0.6	3080	24	AAI37604	Human intracellula
427	17	0.6	1786	22	AAI02945	Human shear stress	c 500	17	0.6	3102	23	ABV25452	Human prostate exp
428	17	0.6	1857	24	AAI62551	cDNA sequence #338	c 501	17	0.6	3103	24	ABL55454	Human BAF57 protei
429	17	0.6	1879	21	AAI44557	Zea mays DNA fragm	502	17	0.6	3114	24	AAI44674	Human transporter
430	17	0.6	1911	22	AAI52679	Human polynucleoti	c 503	17	0.6	3180	24	ABN79868	Fungal ZBC gene se
431	17	0.6	1923	22	AAI05489	Human reproductive	c 504	17	0.6	3214	23	ABL22286	Drosophila melanog
432	17	0.6	1923	23	ABL98342	Human testicular a	c 505	17	0.6	3224	23	AAI82583	DNA encoding novel
433	17	0.6	1939	19	AAI32415	Homo sapiens clone	c 506	17	0.6	3224	21	AAI89304	DNA encoding novel
434	17	0.6	1939	22	AAI98431	Human cDNA clone B	c 507	17	0.6	3236	21	AAI98888	Human pancreatic c
435	17	0.6	1942	22	AAI51695	Human polynucleoti	c 508	17	0.6	3280	20	AAI23684	Human DKC1 DNA fra
436	17	0.6	1948	19	AAI26612	Homo sapiens gluta	509	17	0.6	3331	23	AAI20044	Drosophila melanog
437	17	0.6	1950	24	AAI24027	Human protein phos	c 510	17	0.6	3339	19	AAI61096	Mouse membrane typ
438	17	0.6	1955	22	AAI34915	Human colon cancer	511	17	0.6	3372	22	AAI59730	Human polynucleoti
439	17	0.6	1965	20	AAI60621	Polynucleotide seq	512	17	0.6	3378	24	AAI99410	DNA of APP related
440	17	0.6	1986	24	ABO69092	Listeria monocytog	513	17	0.6	3406	24	ABN95130	Gene #1628 used to
441	17	0.6	1991	24	ABI58952	Human tumour marke	514	17	0.6	3406	24	ABK64397	Human benign prosc
442	17	0.6	2035	19	AAI30292	Bacillus thuringie	515	17	0.6	3406	24	AAI66479	Lung cancer relate
443	17	0.6	2050	22	AAI15461	Human cDNA sequenc	516	17	0.6	3458	24	AAI95018	Human DNA sequenc
444	17	0.6	2066	22	AAI15865	Human cDNA sequenc	c 517	17	0.6	3572	21	AAI18261	Lung cancer associ
445	17	0.6	2073	24	ABN83594	Human cDNA differe	518	17	0.6	3582	23	ABL17962	Drosophila melanog
446	17	0.6	2073	24	ABN95103	Gene #1601 used to	519	17	0.6	3600	21	AAI98971	S. xylosus mprF DN
447	17	0.6	2073	24	ABL68352	Kidney cancer rela	520	17	0.6	3626	22	AAI17757	Human cDNA sequenc

521	17	0.6	3635	22	AAS32830	Human genomic DNA	c 594	17	0.6	7387	21	AAA97914	L. mesenteroides a
c 522	17	0.6	3638	23	ABV23199	Human prostate exp	595	17	0.6	7465	24	ABN96860	Gene #3358 used to
c 523	17	0.6	3638	23	ABV29036	Human prostate exp	596	17	0.6	7655	21	AAA07847	His-UNC-53/1 fragm
524	17	0.6	3643	24	ABK84074	Human cDNA differe	c 597	17	0.6	7669	22	AAS46597	Tumour suppressor
525	17	0.6	3715	23	ABL20042	Drosophila melanog	c 598	17	0.6	7669	24	ABL33846	Human immune syste
526	17	0.6	3717	21	AC489334	Arabidopsis thalia	c 599	17	0.6	8032	24	ABL70448	Chemically treated
c 527	17	0.6	3791	24	ABK52289	cDNA encoding memb	c 600	17	0.6	8032	24	AAS61409	Human gene regulat
c 528	17	0.6	3970	21	AAA97911	L. mesenteroides a	c 601	17	0.6	8032	24	ABK31479	Signal transductio
529	17	0.6	4003	23	ABL12470	Drosophila melanog	602	17	0.6	8052	23	ABL26661	Drosophila melanog
530	17	0.6	4071	23	ABL08828	Drosophila melanog	603	17	0.6	8316	23	ABL18094	Drosophila melanog
c 531	17	0.6	4099	22	ABL26637	Human breast cance	c 604	17	0.6	8395	24	ABL32175	Human immune syste
532	17	0.6	4126	22	AK80162	Human immune/haema	c 605	17	0.6	8605	23	ABL06307	Drosophila melanog
533	17	0.6	4126	22	AK89461	Human digestive sy	c 606	17	0.6	8705	22	ABAB2624	Human HBM gene reg
534	17	0.6	4134	23	AAS89154	DNA encoding novel	c 607	17	0.6	8805	20	AAZ23193	Mouse mammary tumo
c 535	17	0.6	4150	23	ABL07491	Drosophila melanog	608	17	0.6	9057	24	AAD26665	Human G-protein co
536	17	0.6	4157	24	ABL57463	Human protein phos	609	17	0.6	9057	24	AAD26722	Human G-protein co
c 537	17	0.6	4165	17	AT16483	cDNA encoding huma	c 610	17	0.6	9321	21	AA97904	L. mesenteroides a
c 538	17	0.6	4165	19	AAV13998	Human eps15 protei	611	17	0.6	9840	22	AAC85482	Murine neuropeptid
c 539	17	0.6	4165	20	AX04191	Human eps15 encodi	612	17	0.6	9862	24	ABA92593	Human kinase prote
540	17	0.6	4182	23	ABL26992	Drosophila melanog	c 613	17	0.6	10026	24	ABL33876	Human immune syste
541	17	0.6	4192	20	AX00725	Human aggregan deg	614	17	0.6	10195	22	AAS26626	Human genomic DNA
c 542	17	0.6	4226	22	ABA21324	Human nervous syst	c 615	17	0.6	10438	23	ABL14372	Drosophila melanog
c 543	17	0.6	4257	24	ABK84770	Human cDNA differe	c 616	17	0.6	10634	22	AA105488	Human reproductive
544	17	0.6	4275	23	ABL09776	Drosophila melanog	c 617	17	0.6	10634	23	ABL98341	Human testicular a
545	17	0.6	4277	23	ABL11776	Drosophila melanog	c 618	17	0.6	10710	24	ABL32893	Human immune syste
546	17	0.6	4301	22	AAI68146	Human aggreganase-	619	17	0.6	10736	22	AAK80161	Human immune/haema
547	17	0.6	4303	21	AA95826	Human metalloprote	620	17	0.6	10736	22	AAK89460	Human digestive sy
c 548	17	0.6	4355	21	AC75582	Human ORFX ORF1137	621	17	0.6	10769	23	ABL26660	Drosophila melanog
549	17	0.6	4359	23	ABL10138	Drosophila melanog	622	17	0.6	11500	23	ABL26680	Drosophila melanog
550	17	0.6	4364	24	AAD23658	Human 16051a cDNA	c 623	17	0.6	11964	24	ABQ67025	Human anglogenesis
551	17	0.6	4406	22	AAS47111	Human DNA encoding	c 624	17	0.6	11976	24	ABL32595	Human immune syste
552	17	0.6	4407	21	AAA37111	Human PRO1563 (UNQ	c 625	17	0.6	12144	22	AAS46260	DNA encoding novel
553	17	0.6	4407	22	AAF54426	Probe #46 used in	626	17	0.6	13273	22	AAS36849	Human cardiovascular
554	17	0.6	4432	23	ABL12478	Drosophila melanog	627	17	0.6	13563	23	ABL06306	Drosophila melanog
555	17	0.6	4434	18	AA793389	Bloom's syndrome B	c 628	17	0.6	14209	22	ABK89137	Human digestive sy
556	17	0.6	4437	18	AA767013	Bloom syndrome act	c 629	17	0.6	14307	24	ABL32728	Human immune syste
557	17	0.6	4437	18	AA793390	Bloom's syndrome B	c 630	17	0.6	14551	24	ABL34585	Human metastasis a
558	17	0.6	4437	18	AA793392	Bloom's syndrome B	c 631	17	0.6	14598	22	AAS27769	DNA encoding novel
559	17	0.6	4437	18	AA793394	Bloom's syndrome B	c 632	17	0.6	15054	22	AAS40425	DNA encoding human
560	17	0.6	4437	18	AA793395	Bloom's syndrome B	c 633	17	0.6	15054	22	AA104033	Human reproductive
561	17	0.6	4437	24	ABL67661	Oesophagus cancer	634	17	0.6	15372	23	ABL12192	Drosophila melanog
562	17	0.6	4438	18	AA793391	Bloom's syndrome B	c 635	17	0.6	15424	23	ABL27214	Drosophila melanog
563	17	0.6	4438	18	AA793393	Bloom's syndrome B	c 636	17	0.6	16869	21	ABN97976	Human retroviral s
564	17	0.6	4516	23	ABL09198	Drosophila melanog	637	17	0.6	16941	21	AAZ34737	Drosophila dissati
565	17	0.6	4551	23	AAS87023	DNA encoding novel	c 638	17	0.6	17047	22	AAK81251	Human immune/haema
566	17	0.6	4569	24	AAD23659	Human 16051b cDNA	c 639	17	0.6	17534	24	ABK40026	Human chemically p
567	17	0.6	4708	23	ABL17626	Drosophila melanog	c 640	17	0.6	17965	22	AA105510	Human reproductive
568	17	0.6	4893	23	ABL07240	Drosophila melanog	641	17	0.6	18559	23	ABL14336	Drosophila melanog
c 569	17	0.6	5319	23	ABL05960	Drosophila melanog	642	17	0.6	18559	23	ABL21012	Drosophila melanog
c 570	17	0.6	5388	24	ABL32245	Human immune syste	643	17	0.6	19142	20	AAZ20580	Polynucleotide seq
c 571	17	0.6	5429	23	ABL12170	Drosophila melanog	644	17	0.6	19385	23	ABL21130	Drosophila melanog
c 572	17	0.6	5491	23	AA885968	DNA encoding novel	c 645	17	0.6	20184	23	ABL12118	Drosophila melanog
c 573	17	0.6	5698	22	AAS32873	Human genomic DNA	c 646	17	0.6	20184	23	ABL18276	Drosophila melanog
c 574	17	0.6	5703	22	AAS32874	Human genomic DNA	c 647	17	0.6	24053	22	AAAD12308	Toxoplasma gondii
575	17	0.6	6004	21	AA07835	Human homologue of	648	17	0.6	24110	22	AAAD16628	Human novel protei
c 576	17	0.6	6065	24	ABL32504	Human immune syste	c 649	17	0.6	26329	22	AAS42041	Genomic sequence #
c 577	17	0.6	6079	24	ABL32258	Human immune syste	c 650	17	0.6	27884	22	AAK77781	Human immune/haema
c 578	17	0.6	6204	21	AA97917	L. mesenteroides a	c 651	17	0.6	28344	23	ABL21640	Drosophila melanog
579	17	0.6	6230	23	ABL12474	Drosophila melanog	c 652	17	0.6	31129	24	AAD36229	Human transporter
580	17	0.6	6242	22	AAS27776	DNA encoding novel	653	17	0.6	31474	22	AA105461	Human reproductive
c 581	17	0.6	6283	24	ABK39991	Human chemically p	654	17	0.6	31474	23	ABL98314	Human testicular a
c 582	17	0.6	6283	24	ABL32834	Human immune syste	c 655	17	0.6	31949	22	AA105410	Human reproductive
c 583	17	0.6	6328	23	ABL02594	Drosophila melanog	c 656	17	0.6	31949	22	ABL98269	Human testicular a
584	17	0.6	6468	23	ABL09816	Drosophila melanog	c 657	17	0.6	32186	22	AA105411	Human reproductive
585	17	0.6	6545	23	ABL14373	Drosophila melanog	c 658	17	0.6	32186	23	ABL98270	Human testicular a
c 586	17	0.6	6596	23	ABL08072	Drosophila melanog	c 659	17	0.6	32190	22	AA136479	Human musculoskele
587	17	0.6	6754	20	AAZ20602	Polynucleotide seq	660	17	0.6	32195	22	AA104180	Human reproductive
c 588	17	0.6	6754	24	ABL70346	Chemically treated	c 661	17	0.6	32780	22	AAH24652	Nucleotide sequenc
c 589	17	0.6	6754	24	AA561305	Human gene regulat	662	17	0.6	36305	24	ABK22783	Human high bone ma
c 590	17	0.6	6810	20	AAZ20267	Borrelia burgdorfe	c 663	17	0.6	38374	24	ABN96966	Gene #3464 used to
591	17	0.6	7117	23	ABL05434	Drosophila melanog	c 664	17	0.6	38374	24	ABL68363	Kidney cancer rela
592	17	0.6	7198	23	ABL19592	Drosophila melanog	c 665	17	0.6	38374	24	ABL68364	Kidney cancer rela
c 593	17	0.6	7273	23	ABL11996	Drosophila melanog	c 666	17	0.6	38374	24	ABL68824	Kidney cancer rela

c 667	17	0.6	44602	22	AAK77611	Human immune/haema	740	16	0.5	189	22	AAK47454	Human bone marrow
c 668	17	0.6	48727	22	AAK67375	Human immune/haema	741	16	0.5	189	22	AAI53288	Probe #21974 used
c 669	17	0.6	50849	24	ABN87883	Human glutathione	c 742	16	0.5	189	24	ABQ91274	M. capsulatus gene
c 670	17	0.6	56093	24	ABL61744	Colon adenocarcino	c 743	16	0.5	189	24	ABQ91492	M. capsulatus gene
c 671	17	0.6	73465	24	ABQ98161	Human osteoblast d	c 744	16	0.5	192	24	AAQ90518	Murine oligonucleo
c 672	17	0.6	99960	21	AAZ50905	Human TBC-1 partia	c 745	16	0.5	199	22	AAH45193	Human secreted pro
c 673	17	0.6	114793	22	AAAD08215	Human genome from	c 746	16	0.5	202	21	AAAC08465	Human colon cancer
c 674	17	0.6	129021	21	AAAF22296	BAC containing rep	c 747	16	0.5	208	21	AAAC98716	Human biallelic po
c 675	17	0.6	149671	24	ABK84797	Human cDNA differe	c 748	16	0.5	209	21	AAAC35717	Arabidopsis thalia
c 676	17	0.6	155074	24	ABN85735	Human genomic regi	c 749	16	0.5	216	19	AAAX12202	Human biallelic po
c 677	17	0.6	183999	22	AAAF92831	Human ABC1 genomic	c 750	16	0.5	216	19	AAAX12203	Human biallelic po
c 678	17	0.6	249487	24	ABN85733	Mouse genomic regi	c 751	16	0.5	220	22	ABA49663	Human foetal cell
c 679	17	0.6	349980	22	AAH68525	C glutamic codin	c 752	16	0.5	220	22	ABA67566	Human foetal liver
c 680	17	0.6	349980	22	AAH68529	C glutamic codin	c 753	16	0.5	220	22	ABA34644	Probe #13110 for g
c 681	17	0.6	640681	24	ABA92787	Buchnera sp. genom	c 754	16	0.5	220	22	AAK15988	Human brain expres
c 682	17	0.6	1038602	20	AAZ01425	Complete genome se	c 755	16	0.5	220	22	AAK41734	Human bone marrow
c 683	17	0.6	2365589	24	ABA90521	Genomic sequence o	c 756	16	0.5	220	22	AAI22490	Probe #12423 for g
c 684	17	0.6	4411529	22	AAI99682	Mycobacterium tube	c 757	16	0.5	220	22	AAI47782	Probe #16468 used
c 685	16	0.5	17	23	ABK03548	Human CD20 DNzyme	c 758	16	0.5	220	22	AAI08176	Probe #8167 used t
c 686	16	0.5	20	22	AAF24978	Nucleotide sequenc	c 759	16	0.5	220	24	ABSI5743	Human genome-deriv
c 687	16	0.5	33	24	ABQ77511	Human cytokine rec	c 760	16	0.5	222	24	ABQ91649	M. capsulatus gene
c 688	16	0.5	36	13	AAQ31346	IL-6R antibody pri	c 761	16	0.5	223	22	AAAS4332	DNA encoding novel
c 689	16	0.5	40	20	AAZ25261	M-Raf mitochondria	c 762	16	0.5	227	23	ABV21387	Human prostate exp
c 690	16	0.5	50	22	AAAL31666	Human SNP oligonuc	c 763	16	0.5	227	23	ABV27205	Human prostate exp
c 691	16	0.5	65	24	ABN27831	Rat spliced transc	c 764	16	0.5	247	21	AAAC30920	Human secreted pro
c 692	16	0.5	65	24	ABN50981	Mouse spliced tran	c 765	16	0.5	251	19	AAAX1014	Human biallelic po
c 693	16	0.5	65	24	ABN51063	Mouse spliced tran	c 766	16	0.5	251	23	ABV06336	Human prostate exp
c 694	16	0.5	84	22	AAAS21921	Human collagen gen	c 767	16	0.5	252	22	ABA49012	Human breast cell
c 695	16	0.5	109	22	ABA72173	Human foetal liver	c 768	16	0.5	252	22	ABA66925	Human foetal liver
c 696	16	0.5	109	22	AAK20597	Human brain expres	c 769	16	0.5	252	22	ABA34011	Probe #12477 for g
c 697	16	0.5	109	22	AAK46739	Human bone marrow	c 770	16	0.5	252	22	AAK15371	Human brain expres
c 698	16	0.5	112	22	AAI49206	Probe #17892 used	c 771	16	0.5	252	22	AAK41094	Human bone marrow
c 699	16	0.5	112	24	ABSI7203	Human genome-deriv	c 772	16	0.5	252	22	AAI21859	Probe #11792 for g
c 700	16	0.5	113	24	ABL74122	Corn tassell-derive	c 773	16	0.5	252	22	AAI47143	Probe #15829 used
c 701	16	0.5	132	15	AAQ53915	Partial sequence o	c 774	16	0.5	252	22	AAI07546	Probe #7537 used t
c 702	16	0.5	132	18	AAV03166	Partial RNA-2 sequ	c 775	16	0.5	252	24	ABSI5087	Human genome-deriv
c 703	16	0.5	132	20	AAV99299	Partial nucleotide	c 776	16	0.5	254	21	AAAC70683	Single nucleotide
c 704	16	0.5	133	24	ABL69090	Kidney cancer rela	c 777	16	0.5	254	21	AAAC70701	Single nucleotide
c 705	16	0.5	141	22	ABAA49960	Human breast cell	c 778	16	0.5	255	22	AAH82160	Rat differential t
c 706	16	0.5	141	22	ABA67879	Human foetal liver	c 779	16	0.5	257	20	AAZ20003	Spider venom parti
c 707	16	0.5	141	22	ABA34933	Probe #13399 for g	c 780	16	0.5	260	20	AAZ20004	Human secreted parti
c 708	16	0.5	141	22	AAK16283	Human brain expres	c 781	16	0.5	260	21	AAAC03558	Human secreted pro
c 709	16	0.5	141	22	AAI22792	Probe #12725 for g	c 782	16	0.5	261	16	AAAT20840	Human gene signatu
c 710	16	0.5	141	22	AAI48094	Probe #16780 used	c 783	16	0.5	261	24	ABN25398	Human ORFX polynuc
c 711	16	0.5	141	22	AAI08466	Probe #8457 used t	c 784	16	0.5	262	23	ABV02197	Human prostate exp
c 712	16	0.5	141	24	ABSI16061	Human genome-deriv	c 785	16	0.5	268	20	AAH87257	Human single nucle
c 713	16	0.5	143	23	AAAL42527	Exon 2 from a gene	c 786	16	0.5	269	23	ABV32511	Human prostate exp
c 714	16	0.5	143	24	ABA01108	Human DNA sequence	c 787	16	0.5	269	23	ABV41436	Human prostate exp
c 715	16	0.5	143	24	AAI99833	Human chromosome 2	c 788	16	0.5	270	24	ABL85716	Human ovarian canc
c 716	16	0.5	145	22	ABA73137	Human foetal liver	c 789	16	0.5	271	22	ABA48166	Human breast cell
c 717	16	0.5	145	22	AAK21573	Human brain expres	c 790	16	0.5	271	22	ABA66043	Human foetal liver
c 718	16	0.5	145	22	AAK47733	Human bone marrow	c 791	16	0.5	271	22	ABA33126	Probe #11592 for g
c 719	16	0.5	145	22	AAI53566	Probe #22252 used	c 792	16	0.5	271	22	AAK14466	Human brain expres
c 720	16	0.5	145	24	ABSI21764	Human genome-deriv	c 793	16	0.5	271	22	AAK40206	Human bone marrow
c 721	16	0.5	150	22	AAH21878	Mouse digital sequ	c 794	16	0.5	271	22	AAI20974	Probe #10907 for g
c 722	16	0.5	150	24	ABK71456	Central nervous sy	c 795	16	0.5	271	22	AAI46221	Probe #14907 used
c 723	16	0.5	152	22	AAAC89210	Human brain T calc	c 796	16	0.5	271	22	AAI06687	Probe #6678 used t
c 724	16	0.5	163	22	AAAC91735	Streptococcus pneu	c 797	16	0.5	271	24	ABSI4254	Human genome-deriv
c 725	16	0.5	165	22	AAI29052	Colon tumour relat	c 798	16	0.5	273	22	AAK56129	Human immune/haema
c 726	16	0.5	175	22	ABA76018	Human foetal liver	c 799	16	0.5	276	24	ABQ69697	Listeria innocua D
c 727	16	0.5	175	22	ABAA0581	Probe #19047 for g	c 800	16	0.5	276	22	AAAD02662	Human Wtl antisens
c 728	16	0.5	175	22	AAK24696	Human brain expres	c 801	16	0.5	277	23	ABV09136	Human prostate exp
c 729	16	0.5	175	22	AAK50695	Human bone marrow	c 802	16	0.5	277	23	ABV33726	Cellubrevin-1 part
c 730	16	0.5	175	22	AAI27708	Probe #17641 for g	c 803	16	0.5	284	17	AAAT33726	Human cellubrevin
c 731	16	0.5	175	22	AAI56673	Probe #25359 used	c 804	16	0.5	284	21	AAAX39872	M. capsulatus gene
c 732	16	0.5	175	24	ABSI24165	Human genome-deriv	c 805	16	0.5	285	24	ABQ91398	EST clone DF266.
c 733	16	0.5	181	16	AAAT25078	Human gene signatu	c 806	16	0.5	286	20	AAAX98389	Human cancer cell
c 734	16	0.5	183	24	ABQ91838	M. capsulatus gene	c 807	16	0.5	288	24	ABQ67341	Listeria innocua D
c 735	16	0.5	186	24	ABQ90654	M. capsulatus gene	c 808	16	0.5	288	24	ABQ69760	Listeria innocua D
c 736	16	0.5	186	24	AAZ20050	M. capsulatus gene	c 809	16	0.5	290	22	ABA07185	Human pancreatic c
c 737	16	0.5	187	20	AAZ20001	Spider venom parti	c 810	16	0.5	290	22	ABA07186	Human pancreatic c
c 738	16	0.5	187	22	ABA72865	Human foetal liver	c 811	16	0.5	290	22	ABA07188	Human pancreatic c
c 739	16	0.5	189	22	AAK21299	Human brain expres	c 812	16	0.5	290	22	AAK89817	Human digestive sy

813	16	0.5	290	22	AAK89818	Human digestive sy	c 886	16	0.5	376	23	ABV36296	Human prostate exp
814	16	0.5	290	22	AAK89820	Human digestive sy	c 887	16	0.5	376	23	ABV43117	Human prostate exp
815	16	0.5	291	23	ABL23291	Drosophila melanog	888	16	0.5	381	14	AAQ60422	Human brain Expres
816	16	0.5	291	24	ABQ67351	Listeria innocua D	889	16	0.5	383	22	ABA09434	Human tumour suppr
817	16	0.5	293	24	ABL72419	Corn tassell-derive	890	16	0.5	383	22	AA43407	DNA encoding novel
c 818	16	0.5	296	23	ABV34256	Human prostate exp	891	16	0.5	383	22	AAI88246	Human polynucleoti
819	16	0.5	298	24	ABL73833	Corn tassell-derive	c 892	16	0.5	383	22	AAI92187	Human polynucleoti
820	16	0.5	300	16	AAQ99392	Rat allograft infl	893	16	0.5	384	22	AAH53482	S. epidermidis ope
821	16	0.5	300	20	AAZ14620	Human gene express	894	16	0.5	384	23	ABV32066	Human prostate exp
c 822	16	0.5	300	20	AAZ12854	Human gene express	895	16	0.5	384	23	ABV41004	Human prostate exp
c 823	16	0.5	300	20	AAK98454	Human cancer cell	c 896	16	0.5	385	22	AAI91147	Human polynucleoti
824	16	0.5	300	21	AAK56612	Rat allograft infl	c 897	16	0.5	386	23	AAI91081	DNA encoding novel
825	16	0.5	300	21	AAA00860	Human colon cancer	c 898	16	0.5	388	22	AAI10681	Human breast cancer
c 826	16	0.5	300	22	AAH70472	Human cervical can	c 899	16	0.5	390	21	AAC41195	Arabidopsis thalia
c 827	16	0.5	300	22	AAH73162	Human cervical can	c 900	16	0.5	390	22	AAI09561	Human breast cancer
c 828	16	0.5	300	24	ABQ58483	Human colon cancer	c 901	16	0.5	391	20	AAV90050	EST clone CW922.
c 829	16	0.5	306	21	AAC23134	Human secreted pro	c 902	16	0.5	393	24	ABL78819	Human ovarian can
830	16	0.5	311	19	AAV19193	Human XAG growth f	903	16	0.5	394	21	AAK30052	Human secreted pro
831	16	0.5	311	22	AAK63352	HUXAG-3 related ES	904	16	0.5	394	21	AAZ42778	Human 5' EST isola
c 832	16	0.5	311	24	ABK09495	Human ovarian tumo	c 905	16	0.5	395	22	AAI23555	Human breast cancer
c 833	16	0.5	313	23	ABV15929	Human prostate exp	c 906	16	0.5	396	23	ABV00134	Human prostate exp
834	16	0.5	317	21	AAV10835	Fusarium venenatum	c 907	16	0.5	396	23	AAI01577	Human prostate exp
c 835	16	0.5	319	23	ABV01504	Human prostate exp	c 908	16	0.5	400	22	AAI87690	Human polynucleoti
836	16	0.5	320	22	ABA06885	Human pancreatic c	c 909	16	0.5	400	24	ABL83521	Human ovarian can
837	16	0.5	320	22	AAK87864	Human digestive sy	c 910	16	0.5	401	22	AAK95957	Human neuroguilin g
838	16	0.5	321	22	ABAL12027	Human nervous syst	c 911	16	0.5	401	22	AAK95958	Human neuroguilin g
c 839	16	0.5	322	22	AAI21198	Human breast cancer	c 912	16	0.5	401	22	AAK97450	Human neuroguilin g
c 840	16	0.5	324	24	ABQ91632	M. capsulatus gene	c 913	16	0.5	401	22	AAK97451	Human neuroguilin g
c 841	16	0.5	326	22	AAH69732	Human cervical can	c 914	16	0.5	401	24	ABL79404	Human ovarian can
842	16	0.5	330	24	ABL63443	Breast cancer rela	915	16	0.5	403	22	AAH99000	Human EST-derived
c 843	16	0.5	335	18	AAV78569	Staphylococcus aur	c 916	16	0.5	403	23	ABV04958	Human prostate exp
844	16	0.5	338	22	AAC84611	Human ZP13 protein	c 917	16	0.5	405	22	AAS37351	Novel human diagno
845	16	0.5	341	22	AAK28015	Novel cDNA encodin	c 918	16	0.5	405	22	AAI91149	Human polynucleoti
846	16	0.5	343	22	AAK60878	Human immune/haema	c 919	16	0.5	409	22	AAI14693	Human breast cancer
c 847	16	0.5	344	23	ABV01656	Human prostate exp	c 920	16	0.5	411	22	AAC27825	Human secreted pro
848	16	0.5	345	22	ABA74317	Human foetal liver	c 921	16	0.5	412	22	AAI31797	Human breast cancer
849	16	0.5	345	22	AAK22784	Human brain expres	922	16	0.5	412	23	ABV48088	Human prostate exp
850	16	0.5	345	22	AAK48953	Human bone marrow	c 923	16	0.5	413	21	AAH30495	Human colon cancer
851	16	0.5	345	22	AAI54781	Probe #23467 used	c 924	16	0.5	413	23	ABV15505	Human prostate exp
852	16	0.5	345	24	ABS22606	Human genome-deriv	925	16	0.5	413	24	ABL67631	Oesophagus cancer
853	16	0.5	346	23	ABV01745	Human prostate exp	926	16	0.5	413	24	ABL67913	Ovary cancer relat
854	16	0.5	347	23	ABV10914	Human prostate exp	c 927	16	0.5	415	20	AAZ20912	Polynucleotide seq
855	16	0.5	351	22	AAI09307	Human breast cancer	928	16	0.5	415	22	ABA44512	Human breast cell
856	16	0.5	351	22	AAI17196	Human breast cancer	929	16	0.5	415	22	ABA44954	Human foetal liver
c 857	16	0.5	352	24	ABN26569	Human ORFX polynuc	930	16	0.5	415	22	ABA24719	Probe #3185 for ge
c 858	16	0.5	353	22	AAI12322	Human breast cancer	931	16	0.5	415	22	AAK03225	Human brain expres
859	16	0.5	355	18	AAK83277	Breast cancer tumo	932	16	0.5	415	22	AAK28679	Human bone marrow
860	16	0.5	355	19	AAV69023	DNA molecule encod	933	16	0.5	415	22	AAK87305	Human immune/haema
861	16	0.5	355	19	AAV68999	DNA molecule encod	934	16	0.5	415	22	AAK87307	Human immune/haema
862	16	0.5	355	21	AAC80800	Human breast tumou	935	16	0.5	415	22	AAK87309	Human immune/haema
863	16	0.5	355	21	AAC80960	Human breast tumou	936	16	0.5	415	22	AAI13255	Probe #3188 for ge
864	16	0.5	355	24	ABN16600	Human ORFX polynuc	937	16	0.5	415	22	AAI34608	Probe #3294 used t
865	16	0.5	355	24	ABK46690	Human breast tumou	938	16	0.5	415	22	AAI03160	Probe #3151 used t
866	16	0.5	355	24	ABK46690	Human breast tumou	939	16	0.5	415	24	ABS03190	Human genome-deriv
867	16	0.5	355	24	AAV69646	Breast tumour-spec	c 940	16	0.5	417	21	AAC01953	Human secreted pro
868	16	0.5	355	24	AAV699806	Breast tumour-spec	c 941	16	0.5	418	21	AAC98493	Human colon cancer
c 869	16	0.5	356	18	AAV77300	Staphylococcus aur	942	16	0.5	420	21	AAA27071	Rat pPARalpha liga
c 870	16	0.5	356	24	ABN18021	Human ORFX polynuc	c 943	16	0.5	420	22	AAH81518	Human differential
c 871	16	0.5	357	21	AAK67422	Eucalyptus grandis	944	16	0.5	421	22	AAH81518	Human differential
c 872	16	0.5	360	22	AAK64881	Novel human polynu	c 945	16	0.5	421	23	ABV31983	Human prostate exp
c 873	16	0.5	360	24	ABL77407	Human ovarian can	946	16	0.5	423	21	AAC08059	Human secreted pro
874	16	0.5	362	24	ABK45352	cDNA encoding colo	c 947	16	0.5	423	23	ABV10825	Human prostate exp
875	16	0.5	366	21	AAA31622	Plant microsatelli	c 948	16	0.5	425	21	AAC74755	Human ORFX ORF310
c 876	16	0.5	367	18	AAV78420	Staphylococcus aur	c 949	16	0.5	425	23	ABV10673	Human prostate exp
c 877	16	0.5	367	23	ABV31457	Human prostate exp	c 950	16	0.5	425	24	ABN25491	Human ORFX polynuc
c 878	16	0.5	367	23	ABV40436	Human prostate exp	c 951	16	0.5	426	22	AAS28019	Novel cDNA encodin
c 879	16	0.5	370	21	AAH82128	N. meningitidis pa	c 952	16	0.5	427	24	ABL80950	Human ovarian can
880	16	0.5	371	22	AAH81429	Human polynucleoti	c 953	16	0.5	429	23	ABL21719	Drosophila melanog
c 881	16	0.5	372	21	AAH30196	Human colon cancer	954	16	0.5	431	22	AAI02285	Human reproductive
882	16	0.5	372	23	AAH70696	DNA encoding novel	c 955	16	0.5	432	24	ABL78814	Human ovarian can
c 883	16	0.5	374	22	AAI17453	Human breast cancer	956	16	0.5	434	22	AAS21895	Human collagen gen
884	16	0.5	374	22	AAI86024	Human polynucleoti	957	16	0.5	434	24	ABK35449	Human cDNA encodin
c 885	16	0.5	374	22	AAI91055	Human polynucleoti	c 958	16	0.5	435	23	ABV03967	Human prostate exp

c 959 16 0.5 435 23 ABV10296 Human prostate exp  
 c 960 16 0.5 435 24 ABL63193 Breast cancer rela  
 c 961 16 0.5 435 24 ABL81835 Human ovarian can  
 c 962 16 0.5 436 21 AAC33861 Arabidopsis thalia  
 c 963 16 0.5 436 23 ABV38797 Human prostate exp  
 c 964 16 0.5 437 22 AA193338 Human polynucleoti  
 c 965 16 0.5 437 23 ABV31911 Human polynucleoti  
 c 966 16 0.5 437 24 ABK62524 Rat sequence diffe  
 c 967 16 0.5 438 24 ABK44732 cDNA encoding colo  
 c 968 16 0.5 439 24 ABK63522 Human cancer relat  
 c 969 16 0.5 439 24 ABL89487 Human polynucleoti  
 c 970 16 0.5 440 22 AAK02565 Human brain expres  
 c 971 16 0.5 440 24 ABS02473 Human genome-deriv  
 c 972 16 0.5 442 23 ABV45729 Human prostate exp  
 c 973 16 0.5 444 21 AAC78302 Human cancer assoc  
 c 974 16 0.5 444 22 AAF67940 Corynebacterium gl  
 c 975 16 0.5 445 22 ABA43511 Human breast cell  
 c 976 16 0.5 445 22 ABA53961 Human foetal liver  
 c 977 16 0.5 445 22 ABA23711 Probe #2177 for ge  
 c 978 16 0.5 445 22 AAK02230 Human brain expres  
 c 979 16 0.5 445 22 AAK27676 Human bone marrow  
 c 980 16 0.5 445 22 AAL12258 Probe #2191 for ge  
 c 981 16 0.5 445 22 AAI33613 Probe #2299 used t  
 c 982 16 0.5 445 22 AAI02172 Probe #2163 used t  
 c 983 16 0.5 445 24 ABS02139 Human genome-deriv  
 c 984 16 0.5 446 24 ABN24305 Human OREX polynuc  
 c 985 16 0.5 446 24 ABL94016 Arabidopsis thalia  
 c 986 16 0.5 447 24 ABN91727 Staphylococcus epi  
 c 987 16 0.5 448 22 AAL11756 Human foetal liver  
 c 988 16 0.5 449 22 ABA58979 Human brain expres  
 c 989 16 0.5 449 22 AAK07143 Human bone marrow  
 c 990 16 0.5 449 22 AAK32887 Human bone marrow  
 c 991 16 0.5 449 22 AAI38696 Probe #7382 used t  
 c 992 16 0.5 449 23 ABV13136 Human prostate exp  
 c 993 16 0.5 449 23 ABV15356 Human prostate exp  
 c 994 16 0.5 449 23 ABV50494 Human prostate exp  
 c 995 16 0.5 449 24 ABS07691 Human genome-deriv  
 c 996 16 0.5 450 23 ABV31839 Human prostate exp  
 c 997 16 0.5 450 23 ABV40803 Human prostate exp  
 c 998 16 0.5 450 23 ABV40928 Human prostate exp  
 c 999 16 0.5 451 24 ABA61779 Lung small cell ca  
 1000 16 0.5 454 22 ABA57699 Human foetal liver

## ALIGNMENTS

RESULT 1  
 AAS03945  
 ID AAS03945 standard; cDNA; 3133 BP.

XX AAS03945;  
 AC  
 XX

DT 12-SEP-2001 (first entry)  
 XX

DE Human caspase recruitment domain 12 (CARD-12) cDNA.

KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
 KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
 KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
 KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
 KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
 KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
 KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;  
 KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
 KW excitotoxic brain damage; liver disease.

XX Homo sapiens.

OS  
 XX

FH Key Location/Qualifiers

FT CDS 36..3110  
 /\*tag= a

/product= "Human CARD-12"

WO200130971-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US29643.

27-OCT-1999; 99US-0161822.

(MILL-) MILLENNIUM PHARM INC.

Bertin J, Robison KE;

WPI: 2001-308628/32.

P-PSDB; AAU02880.

Isolated caspase recruitment domain-12 polypeptide and nucleic acids encoding them, useful for treating and diagnosing disorders associated with abnormal apoptosis such as cancer, arthritis and Alzheimer's disease -

Claim 2; Fig 1; 93pp; English.

The sequence represents a cDNA which encodes the human caspase recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a number of proteins that transmit signals that activate apoptosis and inflammatory pathways in response to stress and other stimuli. Therefore, CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include cancer, viral infections (e.g. caused by poxviruses, adenoviruses), autoimmune disorders (e.g. systemic lupus erythematosus, arthritis), neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial infarction, stroke), inflammatory and immune system disorders (e.g. Crohn's disease, insulin-dependent diabetes, contact dermatitis, psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, lepromatous leprosy), ischaemic and hypoxic brain injury, kidney ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial meningitis and liver disease.

Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

Query Match 100.0%; Score 3072; DB 22; Length 3133;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGAATGACTGTATA 60

Db 36 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGAATGACTGTATA 95

QY 61 AAGCAATACACAGATGACCTATTGTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATC 120

Db 96 AAGCAATACACAGATGACCTATTGTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATC 155

QY 121 ATTTGCTGCGAGAAGGTGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 180

Db 156 ATTTGCTGCGAGAAGGTGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 215

QY 181 AAGGGTTACAGATGCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 240

Db 216 AAGGGTTACAGATGCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 275

QY 241 TTTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 300

Db 276 TTTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 335

QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTATCCCTT 360

Db 336 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTATCCCTT 395





Db 2556 GCTCAGATCTTCACAAATTTGGTCAAACTGAGCATCTTCTGATTATCAGAAAAATTACCTG 2615  
QY 2581 GAAAAAGATGAAATGAAGCTCTTCATGAACATGATCGACAGATCAAGTCTCAGACAG 2640  
Db 2616 GAAAAAGATGAAATGAAGCTCTTCATGAACATGATCGACAGATCAAGTCTCAGACAG 2675  
QY 2641 CTCACCGACATGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCTGAGCAGCTGTG 2700  
Db 2676 CTCACCGACATGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCTGAGCAGCTGTG 2735  
QY 2701 AAACATTTGGAGGAGTCCCAACATCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2760  
Db 2736 AAACATTTGGAGGAGTCCCAACATCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2795  
QY 2761 GATACAGAGATAGNAATTTTAGTGCCATTTTGTGGAAGAACCCTCTGAAAAACTTCCAG 2820  
Db 2796 GATACAGAGATAGNAATTTTAGTGCCATTTTGTGGAAGAACCCTCTGAAAAACTTCCAG 2855  
QY 2821 CAGTTGAATTTGGGGGAAAATCGTGTGACAGTGTGATGGCTTGCCTTCATGGTGTA 2880  
Db 2856 CAGTTGAATTTGGGGGAAAATCGTGTGACAGTGTGATGGCTTGCCTTCATGGTGTA 2915  
QY 2881 TTTGAGAACTTAAGCAATTAAGTCTTTTGTGACTTTGTACTAAGAAATTTTACCTGAT 2940  
Db 2916 TTTGAGAACTTAAGCAATTAAGTCTTTTGTGACTTTGTACTAAGAAATTTTACCTGAT 2975  
QY 2941 CCAGCATTAAGCAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCT 3000  
Db 2976 CCAGCATTAAGCAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCT 3035  
QY 3001 AGGCTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGAGTGCTTTTAAA 3060  
Db 3036 AGGCTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGAGTGCTTTTAAA 3095  
QY 3061 CTAGTAAGTCT 3072  
Db 3096 CTAGTAAGTCT 3107  
RESULT 2  
AAH98254  
ID AAH98254 standard; cDNA; 3545 BP.  
XX AC AAH98254;  
XX DT 12-OCT-2001 (first entry)  
XX DE Murine EST-derived coding sequence SEQ ID NO: 111.  
XX DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition; ss.  
XX OS Mus musculus.  
XX OS WO200154477-A2.  
XX PN 02-AUG-2001.  
XX PD 25-JAN-2001; 2001WO-US02687.  
XX PF 25-JAN-2000; 2000US-0491404.  
XX PR 17-JUL-2000; 2000US-0617746.  
XX PR 03-AUG-2000; 2000US-0631451.  
XX PR 15-SEP-2000; 2000US-0663870.  
XX XX (HYSE-) HYSEQ INC.  
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werlman T;  
XX WPI; 2001-476164/51.  
DR

DR P-PSDB; AAM23595.  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use -  
XX Claim 1; Page 250-251; 1275pp; English.  
XX The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention.  
XX Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;  
SQ Query Match 95.0%; Score 2919; DB 22; Length 3545;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 60  
Db 232 ATGAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 291  
QY 61 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGGGAAGTAACATC 120  
Db 292 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGGGAAGTAACATC 351  
QY 121 ATTTGCTCGAGAAGGTGGAGCAGATGCTGCTAGAGGGATCATTCACATGATTTTGAAA 180  
Db 352 ATTTGCTCGAGAAGGTGGAGCAGATGCTGCTAGAGGGATCATTCACATGATTTTGAAA 411  
QY 181 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAAGGAGTGAATCTCTCTA 240  
Db 412 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAAGGAGTGAATCTCTCTA 471  
QY 241 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACCAT 300  
Db 472 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACCAT 531  
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT 360  
Db 532 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT 591  
QY 361 GGTGAAGATATGACATATTTTAACTTGAAGAGCCTTTCACAGAACCTGTCTGTGG 420  
Db 592 GGTGAAGATATGACATATTTTAACTTGAAGAGCCTTTCACAGAACCTGTCTGTGG 651  
QY 421 AGGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCTCTCGCAGGCT 480  
Db 652 AGGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCTCTCGCAGGCT 711  
QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGCAAGGCAAGTCCACATCTGTCGAG 540  
Db 712 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGCAAGGCAAGTCCACATCTGTCGAG 771  
QY 541 CGCATTTGCCATGCTCTCGGGGCTCCGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTC 600  
Db 772 CGCATTTGCCATGCTCTCGGGGCTCCGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTC 831  
QY 601 TTCTTCCTCCGCTCAGCAGGCCCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660  
Db 832 TTCTTCCTCCGCTCAGCAGGCCCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 891  
QY 661 CTGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 720  
Db 892 CTGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 951  
QY 721 CAGAGGTTCTTTTCTCTCTGATGGCTTACAAATGAATCAAGCCCCAGAACTGCCAGAA 780  
Db 952 CAGAGGTTCTTTTCTCTCTGATGGCTTACAAATGAATCAAGCCCCAGAACTGCCAGAA 1011

QY 781 ATCGAAGCCCTGATAAGGAAAAACCCGCTTCAAGAAATGCTCATCGTCACCACTACC 840  
Db 1012 ATCGAAGCCCTGATAAGGAAAAACCCGCTTCAAGAAATGCTCATCGTCACCACTACC 1071  
QY 841 ACTGAGTGCCCTGAGGCACATACACGCGAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 900  
Db 1072 ACTGAGTGCCCTGAGGCACATACACGCGAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 1131  
QY 901 ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGGCTTGCTGAAGGC 960  
Db 1132 ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGGCTTGCTGAAGGC 1191  
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Db 1192 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1251  
QY 1021 GTGGTCATCACTTGTCGAATCCAGATGGGTGAAAGTGAAGTTCACATCTCACACACAACA 1080  
Db 1252 GTGGTCATCACTTGTCGAATCCAGATGGGTGAAAGTGAAGTTCACATCTCACACACAACA 1311  
QY 1081 ACCTGTGTCATACCTTCTATGATCTGTGATACAGAAAAACAAACACAAACATAAAGGT 1140  
Db 1312 ACCTGTGTCATACCTTCTATGATCTGTGATACAGAAAAACAAACACAAACATAAAGGT 1371  
QY 1141 GTGGCTGCAAGTGACTTCAATTCGGAGCCTGGACCCTGTGGATACCTAGCTCTGGAGGT 1200  
Db 1372 GTGGCTGCAAGTGACTTCAATTCGGAGCCTGGACCCTGTGGATACCTAGCTCTGGAGGT 1431  
QY 1201 GTGTTCTCCCAAGTTTGATTTGCAACTGACAGATGTGTCAGCGTGGAATGAGGATGTC 1260  
Db 1432 GTGTTCTCCCAAGTTTGATTTGCAACTGACAGATGTGTCAGCGTGGAATGAGGATGTC 1491  
QY 1261 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1320  
Db 1492 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1551  
QY 1321 TTCTTTTCAAGTCATTTCCAGGAGTACACAGCAGGACGAGACTCAGCAGTTTATTGACG 1380  
Db 1552 TTCTTTTCAAGTCATTTCCAGGAGTACACAGCAGGACGAGACTCAGCAGTTTATTGACG 1611  
QY 1381 TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTTGCAGAAAATGGTTTCCATT 1440  
Db 1612 TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTTGCAGAAAATGGTTTCCATT 1671  
QY 1441 TCGGACATTTACATCCACTTATACAGCTGCTCCGGTACACCTGCGGTATCTGTGGAA 1500  
Db 1672 TCGGACATTTACATCCACTTATACAGCCTGCTCCGGTACACCTGCGGTATCTGTGGAA 1731  
QY 1501 GCCACCAAGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCCTCTCGGA 1560  
Db 1732 GCCACCAAGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCCTCTCGGA 1791  
QY 1561 CTTTCCATGCCCAAGAGGCTCTCTGGAGACAGAAATCTTTGCAAAAGTGTGAAAAACACC 1620  
Db 1792 CTTTCCATGCCCAAGAGGCTCTCTGGAGACAGAAATCTTTGCAAAAGTGTGAAAAACACC 1851  
QY 1621 ACTGAGCAGAANAATCTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1880  
Db 1852 ACTGAGCAGAANAATCTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1911  
QY 1681 TTATATCAAGAGAGTACATCCAATCAGCCCTCAGGCCAAGAAATTTGAAGCTTTCTTTCAA 1740  
Db 1912 TTATATCAAGAGAGTACATCCAATCAGCCCTCAGGCCAAGAAATTTGAAGCTTTCTTTCAA 1971  
QY 1741 GGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 1800  
Db 1972 GGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 2031  
QY 1801 CATTTGCCAATTTGCAAGTGTCTGGAGTTCATTAATACTGACATTTTATGGGGAGCT 1860  
Db 2032 CATTTGCCAATTTGCAAGTGTCTGGAGTTCATTAATACTGACATTTTATGGGGAGCT 2091

QY 1861 ATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
Db 2092 ATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 2151  
QY 1921 GAAAACCTACATTTCCAGCAGGCTGTATCTTTTCACTGGAAGCAGGAATTCAGG 1980  
Db 2152 GAAAACCTACATTTCCAGCAGGCTGTATCTTTTCACTGGAAGCAGGAATTCAGG 2211  
QY 1981 ACTCTGGAGTGCACACTCCCGGATTTTCAGCAAGTTGAATAGCAAGATATACATCTG 2040  
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Db 2272 GGAATAATPTCAGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGCTGTGGTG 2331  
QY 2101 GCTGGAGCCTCAGTTTGGTCCCTCAGCACCTGTAAGAACATTTATCTCTCATGGTGAA 2160  
Db 2332 GCTGGAGCCTCAGTTTGGTCCCTCAGCACCTGTAAGAACATTTATCTCTCATGGTGAA 2391  
QY 2161 GCCAGTCCCTCACCATAGAAAGATGAGAGCAGCATCACATCTGTAAACAACTGAAAC 2220  
Db 2392 GCCAGTCCCTCACCATAGAAAGATGAGAGCAGCATCACATCTGTAAACAACTGAAAC 2451  
QY 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGTGGTCTGACTGACAGTTGGGT 2280  
Db 2452 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGTGGTCTGACTGACAGTTGGGT 2511  
QY 2281 AACTTGAAGAACCTTACAAAGCTTCATAATGGATAACATAAAGATGAATGAAGAGTGT 2340  
Db 2512 AACTTGAAGAACCTTACAAAGCTTCATAATGGATAACATAAAGATGAATGAAGAGTGT 2571  
QY 2341 ATAAACTAGCTGAAGGCCGTGAAAAACCTGAAGAAGATGTTTATTTCAATTTGACCCAC 2400  
Db 2572 ATAAACTAGCTGAAGGCCGTGAAAAACCTGAAGAAGATGTTTATTTCAATTTGACCCAC 2631  
QY 2401 TTGCTGACATTTGGAGAGGAAATGGATACATAGTCAAGTCTCTGCAAGTGAACCTGT 2460  
Db 2632 TTGCTGACATTTGGAGAGGAAATGGATACATAGTCAAGTCTCTGCAAGTGAACCTGT 2691  
QY 2461 GACCTTGAAGAAATTCNAATTAGTCTCTGCTGCTGCTGCTGCAATGCAAGTGAANATCCTA 2520  
Db 2692 GACCTTGAAGAAATTCNAATTAGTCTCTGCTGCTGCTGCTGCAATGCAAGTGAANATCCTA 2751  
QY 2521 GCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTTCTGATTTATCAGAAAAATFACCTG 2580  
Db 2752 GCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTTCTGATTTATCAGAAAAATFACCTG 2811  
QY 2581 GAAAAAGATGGAATGAAGCTCTTCATGAACTGATCGACAGGATGAACGCTGCTAGAACAG 2640  
Db 2812 GAAAAAGATGGAATGAAGCTCTTCATGAACTGATCGACAGGATGAACGCTGCTAGAACAG 2871  
QY 2641 CTCACGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTTG 2700  
Db 2872 CTCACGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTTG 2931  
QY 2701 ABAATTTGAGAGGTTCCCAACCTGCTCAAGCTTGGGTTGAAAACTGAGACTCACA 2760  
Db 2932 ABAATTTGAGAGGTTCCCAACCTGCTCAAGCTTGGGTTGAAAACTGAGACTCACA 2991  
QY 2761 GATACAGAGATTAGAATTTTAGGTGCAATTTTGGAAAGAACCTCTGAAAACTTCCAG 2820  
Db 2992 GATACAGAGATTAGAATTTTAGGTGCAATTTTGGAAAGAACCTCTGAAAACTTCCAG 3051  
QY 2821 CAGTTGAAATTTGGCGGAAATCGTGAGCAGTGAATGGGTGGCTTGCCTTTCATGGGTGTA 2880  
Db 3052 CAGTTGAAATTTGGCGGAAATCGTGAGCAGTGAATGGGTGGCTTGCCTTTCATGGGTGTA 3111  
QY 2881 TTTGAGAACTTTAAGCAATTTAGTGTTTTTCAGCTTTAGTACTAAAGAAATTTCTACCTGAT 2940  
Db 3112 TTTGAGAACTTTAAGCAATTTAGTGTTTTTCAGCTTTAGTACTAAAGAAATTTCTACCTGAT 3171  
QY 2941 CCAGCATTTAGTCAGAAAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCT 3000



Db 980 CTGAGTGCCTGAGGCGACATACGCGAGTTTGGTGCCTCGACTGCTGAGGTGGGGGATATGA 1039  
QY 902 CAGAAGACAGCGCCCGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGCTGAAGGCT 961  
Db 1040 CAGAAGACAGCGCCCGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGCTGAAGGCT 1099  
QY 962 TGTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1021  
Db 1100 TGTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1159  
QY 1022 TGGTCATCACTTGTGAATCCAGATGGGTGAAGTGAAGTTCCTACTCTCACACACAACAA 1081  
Db 1160 TGGTCATCACTTGTGAATCCAGATGGGTGAAGTGAAGTTCCTACTCTCACACACAACAA 1219  
QY 1082 CGCTGTTCCATACCTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGTG 1141  
Db 1220 CGCTGTTCCATACCTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGTG 1279  
QY 1142 TGGCTGCAAGTGAATTCATTCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGGT 1201  
Db 1280 TGGCTGCAAGTGAATTCATTCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGGT 1339  
QY 1202 TGTTCCTCCACAAAGTTTGATTCGAACCTGCAGGATGTGCCACCGTGAATGAGGATGTCC 1361  
Db 1340 TGTTCCTCCACAAAGTTTGATTCGAACCTGCAGGATGTGCCACCGTGAATGAGGATGTCC 1399  
QY 1262 TGGTGCAACTGGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCCAAGTATAAAT 1321  
Db 1400 TGGTGCAACTGGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCCAAGTATAAAT 1459  
QY 1322 TCTTTCCAAAGTCAATTCAGGAGTACACAGCAGGAGGAGACATCAGCAGTTTATTCACGT 1381  
Db 1460 TCTTTCCAAAGTCAATTCAGGAGTACACAGCAGGAGGAGACATCAGCAGTTTATTCACGT 1519  
QY 1382 CTATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTTCCATTT 1441  
Db 1520 CTATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTTCCATTT 1579  
QY 1442 CGGACATTACATCCACTTATAGCAGCTGCTCCGGTACACCTCTGGGTCAATCTGTGGAAG 1501  
Db 1580 CGGACATTACATCCACTTATAGCAGGCTGCTCCGGTACACCTCTGGGTCAATCTGTGGAAG 1639  
QY 1502 CCACGAGGCTGTATGAAGCACCCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGAC 1561  
Db 1640 CCACGAGGCTGTATGAAGCACCCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGAC 1699  
QY 1562 TTTCCATCGCAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACACCA 1621  
Db 1700 TTTCCATCGCAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACACCA 1759  
QY 1622 CTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681  
Db 1760 CTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1819  
QY 1682 TATATCAAGAGTATACATCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAAG 1741  
Db 1820 TATATCAAGAGTATACATCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAAG 1879  
QY 1742 GTAAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTGAAAC 1801  
Db 1880 GTAAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTGAAAC 1939  
QY 1802 ATTTGCCCAATTCGCAAGTGTCTGAGCTTCATTAACCTGGAATTTATGGGGAGCTA 1861  
Db 1940 ATTTGCCCAATTCGCAAGTGTCTGAGCTTCATTAACCTGGAATTTATGGGGAGCTA 1999  
QY 1862 TGGCTTTCATGGGAAAAGGCTGCAGAGACACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921  
Db 2000 TGGCTTTCATGGGAAAAGGCTGCAGAGACACACAGGTGGAATCCACATGGAAGAGGCCCCAG 2059  
QY 1922 AAACCTTACATTCACAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGA 1981  
Db 2060 AAACCTTACATTCACAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGA 2119

QY 1982 CTCTGAGGCTCACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATATCACATATCTGG 2041  
Db 2120 CTCTGAGGCTCACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATATCACATATCTGG 2179  
QY 2042 GGAATAATTTACGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTCTGTGTGG 2101  
Db 2180 GGAATAATTTACGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTCTGTGTGG 2239  
QY 2102 CTGGAAGCCTCAGCTTTGGTCTCAGCACCTGTGAAGAACATTTATCTCTCATGGTGAAG 2161  
Db 2240 CTGGAAGCCTCAGCTTTGGTCTCAGCACCTGTGAAGAACATTTATCTCTCATGGTGAAG 2299  
QY 2162 CCAGTCCCTCACCATAGAAGATGAGAGCACATCACATCTGTAAACAACCTGAAAACCT 2221  
Db 2300 CCAGTCCCTCACCATAGAAGATGAGAGCACATCACATCTGTAAACAACCTGAAAACCT 2359  
QY 2222 TGAGTATTCATGACCTTACAGAAATCAACGGCTGCCGGTGTCTGACTGACAGCTTGGGTA 2281  
Db 2360 TGAGTATTCATGACCTTACAGAAATCAACGGCTGCCGGTGTCTGACTGACAGCTTGGGTA 2419  
QY 2282 ACTTGAAGAACCTTACAAAGCTCATATATGATTAACATAAAGATCAATGAAGAGATGCTA 2341  
Db 2420 ACTTGAAGAACCTTACAAAGCTCATATATGATTAACATAAAGATCAATGAAGAGATGCTA 2479  
QY 2342 TAAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTATTTTCATTTGACCCACT 2401  
Db 2480 TAAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTATTTTCATTTGACCCACT 2539  
QY 2402 TGCTGACATTTGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCGAAGTGAACCTGTG 2461  
Db 2540 TGCTGACATTTGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCGAAGTGAACCTGTG 2599  
QY 2462 ACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGCTGCTGCTGCAAAATGCAAGTGAACCTGTAG 2521  
Db 2600 ACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGCTGCTGCTGCAAAATGCAAGTGAACCTGTAG 2659  
QY 2522 CTGAGAAATCTTCAAAATTTGGTCAAACTGAGCATCTCTTGATTTTATCAGAAAAATTTACCTGG 2581  
Db 2660 CTGAGAAATCTTCAAAATTTGGTCAAACTGAGCATCTCTTGATTTTATCAGAAAAATTTACCTGG 2719  
QY 2582 AAAAAGATGGAATGAAGCTCTTCATGAATGATGACAGGATGAACGTGCTAGAACAAG 2641  
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QY 2702 AACATTTGGAGGAGTCCCAACACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACAG 2761  
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QY 2762 ATACAGAGATTAGAATTTTAGTGCATTTTTTTGGAAGAACCCTCTGAAAAACTTCCAGC 2821  
Db 2900 ATACAGAGATTAGAATTTTAGTGCATTTTTTTGGAAGAACCCTCTGAAAAACTTCCAGC 2959  
QY 2822 AGTTGAATTTGGCGGGAATTCGTGTGAGCAGTATGATGGCTTGCCTTCATGGGTGTAT 2881  
Db 2960 AGTTGAATTTGGCGGGAATTCGTGTGAGCAGTATGATGGCTTGCCTTCATGGGTGTAT 3019  
QY 2882 TTCAGAAATCTTAAGCAATTAAGTGTTTTTTTCACCTTTAGTACTTAAGAAATTTCTACCTGATC 2941  
Db 3020 TTCAGAAATCTTAAGCAATTAAGTGTTTTTTTCACCTTTAGTACTTAAGAAATTTCTACCTGATC 3079  
QY 2942 CAGCATTAGTCAGAAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTCAGAAAGCTA 3001  
Db 3080 CAGCATTAGTCAGAAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTCAGAAAGCTA 3139  
QY 3002 GGCTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTGTTTATACAGGTGCTTTTAAAC 3061  
Db 3140 GGCTTGTGGGTGGCAATTTGATGATGATGATGATCTCAGTGTGTTTATACAGGTGCTTTTAAAC 3199

Qy 3062 TAGTAACGTCT 3072  
|||||  
Db 3200 TAGTAACGTCT 3210

## RESULT 4

ABK22731  
ID ABK22731 standard; cDNA; 3396 BP.

XX AC ABK22731;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN A.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; cancer; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX OS WO200190156-A2.

XX PN 29-NOV-2001.

XX PD 24-MAY-2001; 2001WO-US17158.

XX PF 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNEAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX PI Oliveira VAM, Hayashi H, Pawlowski K;

XX DR WPI; 2002-083086/11.

XX DR P-PSDB; AAU80861.

XX PT New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke -

XX PS Claim 1; Page 166-171; 216pp; English.

XX CC The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a

CC cDNA encoding a CARD domain containing protein.

XX Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;

XX Query Match 93.4%; Score 2868; DB 24; Length 3396;  
XX Best Local Similarity 99.9%; Pred. No. 0;  
XX Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTCTTTATA 60  
Db |||||||

Qy 277 ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTCTTTATA 336  
Db |||||||

Qy 61 AAGCAATACAGATGACCTATTTCTATGGAATCTTCTGAATCGCGAAGAAAGTAACATC 120  
Db |||||||

Qy 337 AAGCAATACAGATGACCTATTTCTATGGAATCTTCTGAATCGCGAAGAAAGTAACATC 396  
Db |||||||

Qy 121 ATTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGA 180  
Db |||||||

Qy 397 ATTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGA 456  
Db |||||||

Qy 181 AAGGTTTCAGAGTCTCTTAACCTCTTTCTTAATCCCTTAAGGAGTGAACATCTCTCTA 240  
Db |||||||

Qy 457 AAGGTTTCAGAGTCTCTTAACCTCTTTCTTAATCCCTTAAGGAGTGAACATCTCTCTA 516  
Db |||||||

Qy 241 TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT 300  
Db |||||||

Qy 517 TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT 576  
Db |||||||

Qy 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGCACTTTTATCCCTT 360  
Db |||||||

Qy 577 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGCACTTTTATCCCTT 636  
Db |||||||

Qy 361 GGTGAAGATATTGACATTTATTTTAACTTGAAGGACCTTTCACAGAACTGCTCTGTGG 420  
Db |||||||

Qy 637 GGTGAAGATATTGACATTTATTTTAACTTGAAGGACCTTTCACAGAACTGCTCTGTGG 696  
Db |||||||

Qy 421 AGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGACAGCT 480  
Db |||||||

Qy 697 AGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGACAGCT 756  
Db |||||||

Qy 481 CTTCAGAGCCCTGCATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 540  
Db |||||||

Qy 757 CTTCAGAGCCCTGCATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 816  
Db |||||||

Qy 541 CGCATTCGCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAATTCCTC 600  
Db |||||||

Qy 817 CGCATTCGCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAATTCCTC 876  
Db |||||||

Qy 601 TTTCTCTCTCTCAGCAGGGCCCGAGGTGGACTTTTGAAGCCCTCTGTGATCAATC 660  
Db |||||||

Qy 877 TTTCTCTCTCTCAGCAGGGCCCGAGGTGGACTTTTGAAGCCCTCTGTGATCAATC 936  
Db |||||||

Qy 661 CTGATATACCTGGCACAAATCAGNAGCAGACATTCATGGCCATGCTGCTGAGTGGG 720  
Db |||||||

Qy 937 CTGATATACCTGGCACAAATCAGNAGCAGACATTCATGGCCATGCTGCTGAGTGGG 996  
Db |||||||

Qy 721 CAGAGGTTCTTTCTCTTCTTGTGGCTTACAAATGAATCAAGCCCAAGTCCAGGAG 780  
Db |||||||

Qy 997 CAGAGGTTCTTTCTCTTCTTGTGGCTTACAAATGAATCAAGCCCAAGTCCAGGAG 1056  
Db |||||||

Qy 781 ATCAAGCCCTGATAAAGAAACACCGCTTCAAGAACATGGTCTGCTCACCCTACC 840  
Db |||||||

Qy 1057 ATCAAGCCCTGATAAAGAAACACCGCTTCAAGAACATGGTCTGCTCACCCTACC 1116  
Db |||||||

Qy 841 ACTGAGTGCCTGAGCAGACATACGGCAGTTTGGTCCCTGACTGCTGAGGTGGGATATG 900  
Db |||||||

Qy 1117 ACTGAGTGCCTGAGCAGACATACGGCAGTTTGGTCCCTGACTGCTGAGGTGGGATATG 1176  
Db |||||||

Qy 901 ACAGAACACACGCCCGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGTCTGAAGGC 960  
Db |||||||

Qy 1177 ACAGAACACACGCCCGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGTCTGAAGGC 1236  
Db |||||||

Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGAGTGTGAGGAATCTCATGAGACCCCTCTCTTT 1020  
Db |||||||









|||||  
Db 1814 AGTACAGCAGGACGAGAACTCAGCAGTTTATTGACGCTCATGAGCCAGAGAGGTGA 1873  
QY 1403 CCAAGGGGAATGTTACTTGCAGAAAATGGTTTCCATTTCGGGACATTACATCCACTTATA 1462  
Db 1874 CCAAGGGGAATGTTACTTGCAGAAAATGGTTTCCATTTCGGGACATTACATCCACTTATA 1933  
QY 1463 GCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAAGCCACCAGGGCTGTTTATGAAGC 1522  
Db 1934 GCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAAGCCACCAGGGCTGTTTATGAAGC 1993  
QY 1523 ACCTCGCAGAGGTATCAACACGGCTGCCCTTCCTCGGACTTTCCATCGCCAAAGAGGCCCTC 1582  
Db 1994 ACCTCGCAGCAGTGTCAACACGGCTGCCCTTCCTCGGACTTTCCATCGCCAAAGAGGCCCTC 2053  
QY 1583 TCTGGGACAGAGGAATCTTTGCAAAAGTGTGAAAACACCACTGAGCAGAAAATTTCTGAAG 1642  
Db 2054 TCTGGGACAGAGGAATCTTTGCAAAAGTGTGAAAACACCACTGAGCAGAAAATTTCTGAAG 2113  
QY 1643 CCATAAACATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702  
Db 2114 CCATAAACATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 2173  
QY 1703 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762  
Db 2174 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 2233  
QY 1763 CAGGGAACATCCCGGATTAATTTGACTTCTTTGACATTTGCCCAATTTGCGAAGTG 1822  
Db 2234 CAGGGAACATCCCGGATTAATTTGACTTCTTTGACATTTGCCCAATTTGCGAAGTG 2293  
QY 1823 CTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882  
Db 2294 CCCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 2353  
QY 1883 CAGAAGACAGAGTGGAAATCCATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCAGGG 1942  
Db 2354 CAGAAGACACAGTGGAAATCCATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCAGGG 2413  
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTACACACTCCGG 2002  
Db 2414 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTACACACTCCGG 2473  
QY 2003 ATTTACAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTCAGCTCTGCCA 2062  
Db 2474 ATTTACAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGAAAATATTCAGCTCTGCCA 2533  
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCTCAGTTTGGTCC 2122  
Db 2534 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCTCAGTTTGGTCC 2593  
QY 2123 TCAGCACCTCTAAGAACATTTATTTCTCATGTGTGGAAGCCAGTCCCTCACCATTAGAAG 2182  
Db 2594 TCAGCACCTCTAAGAACATTTATTTCTCATGTGTGGAAGCCAGTCCCTCACCATTAGAAG 2653  
QY 2183 ATGAGGGCACATCACATCTGTAACAAACCTGAAAACCTTTGAGTATTCATGACTACAGA 2242  
Db 2654 ATGAGGGCACATCACATCTGTAACAAACCTGAAAACCTTTGAGTATTCATGACTACAGA 2713  
QY 2243 ATCAAGGCTGCCGGTGGTCTGACTGACAGCTTTGGGTAACTTGAAGAACCTTTACAAAGC 2302  
Db 2714 ATCAAGGCTGCCGGTGGTCTGACTGACAGCTTTGGGTAACTTGAAGAACCTTTACAAAGC 2773  
QY 2303 TCATAATGGATAACATAAAGATCAATGAAGATCTATAAATAGCTGAAGGCCCTGA 2362  
Db 2774 TCATAATGGATAACATAAAGATCAATGAAGATCTATAAATAGCTGAAGGCCCTGA 2833  
QY 2363 AAAACCTGAAGAGATGTGTTTATTTTCAATTTGACCCACTTGTCTGACATTTGGAGAGGAA 2422  
Db 2834 AAAACCTGAAGAGATGTGTTTATTTTCAATTTGACCCACTTGTCTGACATTTGGAGAGGAA 2893  
QY 2423 TGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAAGAAAATTTCAATTAG 2482  
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Db 2894 TGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAAGAAAATTTCAATTAG 2953  
QY 2483 TCTCCTGCTGCTTGTCTGCAAAATGCAGTGAATAATCTAGCTCAGAATCTTCAAAATTTGG 2542  
Db 2954 TCTCCTGCTGCTTGTCTGCAAAATGCAGTGAATAATCTAGCTCAGAATCTTCAAAATTTGG 3013  
QY 2543 TCAAACTGAGCATCTCTTTGATTTATCAGAAAATTTACCTGGAAAAGATGGAATGAAGCTC 2602  
Db 3014 TCAAACTGAGCATCTCTTTGATTTATCAGAAAATTTACCTGGAAAAGATGGAATGAAGCTC 3073  
QY 2603 TTTCATGAACCTGATGCGACAGATGAACGTGCTAGAACAGCTCACCGCAGCTGATGCTGCCCT 2662  
Db 3074 TTTCATGAACCTGATGCGACAGATGAACGTGCTAGAACAGCTCACCGCAGCTGATGCTGCCCT 3133  
QY 2663 GGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCAC 2722  
Db 3134 GGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCAC 3193  
QY 2723 AACTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAAATTTTAG 2782  
Db 3194 AACTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAAATTTTAG 3253  
QY 2783 GTGCATTTTTTGGAAAAGACCCCTCTGAAAACCTTCCAGCAGTTGAAATTTGGCGGGAATC 2842  
Db 3254 GTGCATTTTTTGGAAAAGACCCCTCTGAAAACCTTCCAGCAGTTGAAATTTGGCGGGAATC 3313  
QY 2843 GTGTGAGCAGTGTGATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAG 2902  
Db 3314 GTGTGAGCAGTGTGATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAG 3373  
QY 2903 TGTGTTTTTGTACTTTAGTACTTAAAGAAATTTCTACTGATCCAGCATTAGTCAGAAAACCTTA 2962  
Db 3374 TGTGTTTTTGTACTTTAGTACTTAAAGAAATTTCTACTGATCCAGCATTAGTCAGAAAACCTTA 3433  
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACAGTGGCTTGTGGTGGCAATTTG 3022  
Db 3434 GCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACAGTGGCTTGTGGTGGCAATTTG 3493  
QY 3023 ATCATCATGATCTCAGTGTATTATACAG 3049  
Db 3494 ATGATGATGATCTCAGTGTATTATACAG 3520  
RESULT 6  
AAH78218  
ID AAH78218 standard; DNA; 2215 Bp.  
XX  
AC AAH78218;  
XX  
DT 26-NOV-2001 (first entry)  
XX Nucleotide sequence of a human secreted polypeptide.  
DE Human; secreted polypeptide; nervous disease; muscular disease; tumour;  
KW gastrointestinal ulceration; spinal cord disease; trachea disease;  
KW thyroid gland disease; ovary disease; prostate disease; heart disease;  
KW renal gland disease; small intestine disease; thymus disease;  
KW lymph node disease; muscular system disease; colon disease;  
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
KW myocardial infarction; angioplasty; liver disease; coagulation disorder;  
KW microbial disease; immune disorder; inflammation; transplant rejection;  
KW bone thickness; bone density; ferroxidase loss; apoptosis;  
KW vascular smooth cell proliferation; vaccine; ss.  
XX Homo sapiens.  
OS  
FH Key  
FT CDS  
FT 1..2214  
FT /tag- a  
FT /product= "secreted polypeptide"  
FT /note= "no termination codon given"  
XX  
PN WO200166690-A2.

XX 13-SEP-2001.  
XX 05-MAR-2001; 2001WO-US07143.  
XX 06-MAR-2000; 2000US-0187107.  
XX 03-MAR-2000; 2000US-0188916.  
XX 03-OCT-2000; 2000US-0236874.  
XX 03-OCT-2000; 2000US-0237846.  
XX (SMK ) SMITHKLINE BEECHAM CORP.  
XX (SMK ) SMITHKLINE BEECHAM PLC.  
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
XX WPI; 2001-570768/64.  
XX P-PSDB; AAG67526.  
XX Novel isolated secreted polypeptide useful for treating nervous and  
XX muscular diseases, gastrointestinal ulceration, coagulation and immune  
XX disorders, microbial diseases, inflammation and transplant rejection -  
XX Claim 2; Page 52-53; 102pp; English.  
XX The present sequence encodes a human secreted polypeptide. The  
XX secreted polypeptides and polynucleotides are useful for treating  
XX nervous and muscular diseases, for inhibiting tumour formation and  
XX metastasis, for treating gastrointestinal ulceration, for preventing  
XX and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
XX renal gland, small intestine, heart, trachea, thymus, lymph node,  
XX muscular system and colon, for treating lipase deficiency in cystic  
XX fibrosis and pancreatitis, for treating undesirable clot formation  
XX such as myocardial infarction, during angioplasty and all surgical  
XX procedures that require decreased blood clot formation, for treating  
XX liver diseases, coagulation disorders and microbial diseases, for  
XX treating immune disorders, for treating inflammation and transplant  
XX rejection, for enhancing bone thickness and increasing bone density,  
XX for reducing the loss of essential ferroxidases, for suppressing  
XX apoptosis, and for regulating vascular smooth cell proliferation. They  
XX may also be used as vaccines.  
XX Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;  
Query Match 67.1%; Score 2062; DB 22; Length 2215;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 43 ATGGGAATGACTGTATTAAGCAATACAGATGACCTATTGTATGAATGTTCTGAAT 102  
DB 1 ATGGGAATGACTGTATTAAGCAATACAGATGACCTATTGTATGAATGTTCTGAAT 60  
QY 103 CGCGAAGAAGTAACATCATTTGCTCGGAGAAGGTGGAGCAGGATGCTGTAGAGGGATC 162  
DB 61 CGCGAAGAAGTAACATCATTTGCTCGGAGAAGGTGGAGCAGGATGCTGTAGAGGGATC 120  
QY 163 ATTCACATGATTTTGAAGAGGTTCAGAGCCCTGTAAACCTCTTTCTTAAATCCCTTAAG 222  
DB 121 ATTCACATGATTTTGAAGAGGTTCAGAGCCCTGTAAACCTCTTTCTTAAATCCCTTAAG 180  
QY 223 GAGTGGAACTATCCCTATTTTCAGACTTGAATGGACAAGCTTTTTCATCAGACATCA 282  
DB 181 GAGTGGAACTATCCCTATTTTCAGACTTGAATGGACAAGCTTTTTCATCAGACATCA 240  
QY 283 GAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 342  
DB 241 GAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 300  
QY 343 CTGAACCTTTTATCCCTTGGTGAAGATATTGACATTTATTTTAACTTGAAGACACCTTC 402  
DB 301 CTGAACCTTTTATCCCTTGGTGAAGATATTGACATTTATTTTAACTTGAAGACACCTTC 360  
QY 403 ACAGAACCTGTCCCTGTGGAGGAGGACCAACACCATCACCGGTGAGCAGCTGACCTG 462  
DB 1441 TGTGGGTATCTGTGGAGGCCACCGAGGCTGTATGAAGACCTTCGCAGCAGTGTATCAA 1500

DB 361 ACAGAACCTGTCTGTGGAGGAAGGACCAACACCATACCCGCTGGAGCAGCTGACCCCTG 420  
QY 463 AATGCCCTCCCTGCAGGCTCTTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTCGCAAGGC 522  
DB 421 AATGCCCTCCCTGCAGGCTCTTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTCGCAAGGC 480  
QY 523 AAGTCCACTCTGCTGCAGCGCATTTGCCATGTCTCTGGGCTCCGGAAGTGCAGGCTCTG 582  
DB 481 AAGTCCACTCTGCTGCAGCGCAATTTGCCATGTCTCTGGGCTCCGGAAGTGCAGGCTCTG 540  
QY 583 ACCAAGTTCAAAATTCGTTCTTCTCTCGTCTCAGCAGGGCCCGAGGTTGGACTTTTGA 642  
DB 541 ACCAAGTTCAAAATTCGTTCTTCTCTCGTCTCAGCAGGGCCCGAGGTTGGACTTTTGA 600  
QY 643 ACCCTCTGTGATCAACTCTCGATATACCTGCACAATCAGGAAGCAGACATTCATGCCC 702  
DB 601 ACCCTCTGTGATCAACTCTCGATATACCTGCACAATCAGGAAGCAGACATTCATGCCC 660  
QY 703 ATGCTGTCTGAAGCTGCGCAGAGGGTTCTTTTCTCTTCTTGTATGGCTACAATGAATCAAG 762  
DB 661 ATGCTGTCTGAAGCTGCGCAGAGGGTTCTTTTCTCTTCTTGTATGGCTACAATGAATCAAG 720  
QY 763 CCCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAAACCCCGCTTCAAGAACATG 822  
DB 721 CCCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAAACCCCGCTTCAAGAACATG 780  
QY 823 GTCATCGTCACACTTACCCTGAGTGCTGAGGCACATACGSCAGTTTGGTCCCTGACT 882  
DB 781 GTCATCGTCACACTTACCCTGAGTGCTGAGGCACATACGSCAGTTTGGTCCCTGACT 840  
QY 883 GCTGAGTGGGGATATGACAGAGACAGCGCCAGGCTCTCATCCGAAAGTGTCTGATC 942  
DB 841 GCTGAGTGGGGATATGACAGAGACAGCGCCAGGCTCTCATCCGAAAGTGTCTGATC 900  
QY 943 AAGAGCTGTCTGAAGGCTTGTGCTCAAAATTCAGAAATCCAGTGTCTGAGGAAATCTC 1002  
DB 901 AAGAGCTGTCTGAAGGCTTGTGCTCAAAATTCAGAAATCCAGTGTCTGAGGAAATCTC 960  
QY 1003 ATGAAGACCCCTCTCTTTTGTGTATCATCTGTGCAATCCAGATGGTGAAGTCAAGTTC 1062  
DB 961 ATGAAGACCCCTCTCTTTTGTGTATCATCTGTGCAATCCAGATGGTGAAGTCAAGTTC 1020  
QY 1063 CACTCTCACACACAAACACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAAC 1122  
DB 1021 CACTCTCACACACAAACACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAAC 1080  
QY 1123 AAACACAAACATAAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 1182  
DB 1081 AAACACAAACATAAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 1140  
QY 1183 GACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTTTGAATTTTCAAGTGTGCTGCAAGTGTGCT 1242  
DB 1141 GACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTGTGTTGATTTTCAAGTGTGCTGCAAGTGTGCT 1200  
QY 1243 AGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATATACAGCTCAAGG 1302  
DB 1201 AGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATATACAGCTCAAGG 1260  
QY 1303 TTCAAGCCAAAGTATAAATTTCTTCAAGTCAATTTCCAGAGGTACACAGCAGGAGGAAGA 1362  
DB 1261 TTCAAGCCAAAGTATAAATTTCTTCAAGTCAATTTCCAGAGGTACACAGCAGGAGGAAGA 1320  
QY 1363 CTCAGCAGTTTATTTGACGCTCTCATGAGCAGAGGAGGTGACCAAGGGGAATGGTTACTT 1422  
DB 1321 CTCAGCAGTTTATTTGACGCTCTCATGAGCAGAGGAGGTGACCAAGGGGAATGGTTACTT 1380  
QY 1423 CAGAAATGGTTTCCATTTCCGACATTCATCCACTTATAGAGCCTGCTCCGGTACACC 1482  
DB 1381 CAGAAATGGTTTCCATTTCCGACATTCATCCACTTATAGAGCCTGCTCCGGTACACC 1440  
QY 1483 TGTGGGTATCTGTGGAGGCCACCGAGGCTGTATGAAGACCTTCGCAGCAGTGTATCAA 1542  
DB 1441 TGTGGGTATCTGTGGAGGCCACCGAGGCTGTATGAAGACCTTCGCAGCAGTGTATCAA 1500

QY 1543 CACGGCTGCTTCTCGGACTTTCCATGCCAAGAGGCTCTCTGGAGACAGGAATCTTTG 1602  
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Db 1501 CACGGCTGCTTCTCGGACTTTCCATGCCAAGAGGCTCTCTGGAGACAGGAATCTTTG 1560  
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QY 1603 CAAAGTGTGAAAAACACCACCTGAGCAAGAAATCTGAAAGCCATAAAACATCAATTCCTTT 1662  
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Db 1561 CAAAGTGTGAAAAACACCACCTGAGCAAGAAATCTGAAAGCCATAAAACATCAATTCCTTT 1620  
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QY 1663 GTAGAGTGTGCATCCATTTATATACAGAGAGTACATCCAAATCAGCCCTGAGCCAGAA 1722  
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Db 1621 GTAGAGTGTGCATCCATTTATATACAGAGAGTACATCCAAATCAGCCCTGAGCCAGAA 1680  
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QY 1723 TTTCAAGCTTCTTCTCAAGGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTAC 1782  
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Db 1681 TTTCAAGCTTCTTCTCAAGGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTAC 1740  
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QY 1783 TTATTTGACTTCTTTGAAACATTTGCCAAATTTGCAAGTGTCTTGGACTTCATTTAAACTG 1842  
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Db 1741 TTATTTGACTTCTTTGAAACATTTGCCAAATTTGCAAGTGTCTTGGACTTCATTTAAACTG 1800  
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QY 1843 GACTTTTATGGGAGCTATGGCTTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGATC 1902  
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Db 1801 GACTTTTATGGGAGCTATGGCTTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGATC 1860  
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QY 1903 CACATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCAGGCGTGTATCTTTGTTCTTCAAC 1962  
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Db 1861 CACATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCAGGCGTGTATCTTTGTTCTTCAAC 1920  
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QY 1963 TGGAGCAGGAATTCAGGACTCTGGAGGTCACTCTCGGGGATTTTCAGCAAGTTGAATAAG 2022  
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Db 1921 TGGAGCAGGAATTCAGGACTCTGGAGGTCACTCTCGGGGATTTTCAGCAAGTTGAATAAG 1980  
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QY 2023 CAAGATATCATATCTTGGGAAAATATTGAGTCTGCCACAAGCCTCAGGCTCAATA 2082  
|||||  
Db 1981 CAAGATATCATATCTTGGGAAAATATTGAGTCTGCCACAAGCCTCAGGCTCAATA 2040  
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QY 2083 AAGAGATGTGCTGTGGTGGGAAAGCTCAGTTTGTGCTCAGCACCTGTGAAGAACATT 2142  
|||||  
Db 2041 AAGAGATGTGCTGTGGTGGGAAAGCTCAGTTTGTGCTCAGCACCTGTGAAGAACATT 2100  
|||||  
QY 2143 TATTCTCTCATGTGGGAGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATCT 2202  
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Db 2101 TATTCTCTCATGTGGGAGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATCT 2160  
|||||  
QY 2203 GTACAACACCTGAACCTTGAGTATTTCATGACCTACAGATCAACGGCTGCCGG 2257  
|||||  
Db 2161 GTACAACACCTGAACACCTTGAGTATTTCATGACCTACAGATCAACGGCTGCCGG 2215  
|||||

RESULT 7

AAH9581

ID AAH9581 standard; cDNA; 2950 BP.

XX

AC AAH9581;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein encoding cDNA sequence SEQ ID NO:416.

XX

KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiac; central nervous system; virucide;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
KW antiaggregant; haemostatic; antidiabetic; antiulcer; osteopathic; eczema;  
KW dermatological; antiallergic; antisthmatic; antidiabetic; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;

KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.  
XX Homo sapiens.

XX WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000WO-US35017.

XX 23-DEC-1999; 99US-04711275.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.

DR P-PSDB; AAM25640.

XX

PT Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX Claim 1; Page 511-512; 1217pp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and  
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;  
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;  
CC antiulcer; osteopathic; dermatological; antiallergic; antisthmatic;  
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis of  
CC disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders.

XX Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;  
SQ

Query Match 58.0%; Score 1781; DB 22; Length 2950;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1881; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1190 CTCTGGAGGTGTGTTCTTCCCAAGTTTGATTTTTCGAAGTCTGAGGATCTGCCAGCTGA 1249  
|||||  
Db 45 CTCTGGAGGTGTGTTCTTCCCAAGTTTGATTTTTCGAAGTCTGAGGATCTGCCAGCTGA 104  
|||||

QY 1250 ATGAGGATGTCTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGGTTTCAAGC 1309  
|||||  
Db 105 ATGAGGATGTCTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGGTTTCAAGC 164  
|||||

QY 1310 CAAAGTATAAATTTCTTTCACAAAGTATTCACAGGAGTACACAGGAGGAGAGACTCAGCA 1369  
|||||  
Db 165 CAAAGTATAAATTTCTTTCACAAAGTATTCACAGGAGTACACAGGAGGAGAGACTCAGCA 224  
|||||

QY 1370 GTTTATTGACGTCTCATGAGCCAGGAGGTGACCAAGGGAATGGTTACTTTCAGAAAA 1429  
|||||  
Db 225 GTTTATTGACGTCTCATGAGCCAGGAGGTGACCAAGGGAATGGTTACTTTCAGAAAA 284  
|||||

QY 1430 TGGTTTTCATTTTCGAGCATTTACATTCACAGCTCTCCGGTACACCTGTGGGT 1489  
|||||



XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
DR WPI: 2002-083086/11.  
DR P-PSDB; AAU80872.  
XX  
PT New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX  
PS Claim 1: Page 200-201; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
SQ Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other;

Query Match 27.3%; Score 840; DB 24; Length 891;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCCAGTCCACTCTGCTGCAG 540  
DB 1 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCCAGTCCACTCTGCTGCAG 60  
QY 541 CGCATTGCCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCGTC 600  
DB 61 CGCATTGCCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCGTC 120  
QY 601 TTCTTCTCCGCTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660  
DB 121 TTCTTCTCCGCTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTC 180  
QY 661 CTGGATATACCTGGCAATCAGAGAGCAGACATTCATGCGCCATGCTGCTGAAGCTGCGG 720  
DB 181 CTGGATATACCTGGCAATCAGAGAGCAGACATTCATGCGCCATGCTGCTGAAGCTGCGG 240  
QY 721 CAGAGGGTCTTTTCCCTTCTTGTGCTCAATGAATTCAGCCCGCAGAACTGCCAGAA 780  
DB 241 CAGAGGGTCTTTTCCCTTCTTGTGCTCAATGAATTCAGCCCGCAGAACTGCCAGAA 300  
QY 781 ATCGAAGCCCTGTATAAGGAAACCCACCGGTTCAAGAACATGGTCTATCGTCACCACTACC 840  
DB 301 ATCGAAGCCCTGTATAAGGAAACCCACCGGTTCAAGAACATGGTCTATCGTCACCACTACC 360  
QY 841 ACTGAGTGCTGAGGCACATACGCGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 900  
DB 361 ACTGAGTGCTGAGGCACATACGCGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 420  
QY 901 ACAGAGACAGCCGCCAGGCTCTCATCCGAGAAAGTCTGATCAAGGAGCTTGTCTGAAGGC 960  
DB 421 ACAGAGACAGCCGCCAGGCTCTCATCCGAGAAAGTCTGATCAAGGAGCTTGTCTGAAGGC 480

QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
DB 481 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 540  
QY 1021 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAGTCAGTTCCACTCTCACACACAACA 1080  
DB 541 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAGTCAGTTCCACTCTCACACACAACA 600  
QY 1081 ACGTGTTCATCACTTGTGCAATCCAGATGGGTGAAGTCAGTTCCACTCTCACACACAACA 1140  
DB 601 ACGTGTTCATCACTTGTGCAATCCAGATGGGTGAAGTCAGTTCCACTCTCACACACAACA 660  
QY 1141 GTGGTCGCAAGTGACTTCATTCGGAGCCTGGACACATGTCGGAGACCTAGTCTGGAGGT 1200  
DB 661 GTGGTCGCAAGTGACTTCATTCGGAGCCTGGACACATGTCGGAGACCTAGTCTGGAGGT 720  
QY 1201 GTGTTCTCCACAAAGTTTGAATTCGAACTCGAGATGTGTCAGCGTGAATGAGGATGTC 1260  
DB 721 GTGTTCTCCACAAAGTTTGAATTCGAACTCGAGATGTGTCAGCGTGAATGAGGATGTC 780  
QY 1261 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCCAAGATATAA 1320  
DB 781 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCCAAGATATAA 840  
QY 1321 TTCTTTTCAAAAGTCAATTCAGGAGTACACAGCAGGACGAAAGACTCAGCACT 1371  
DB 841 TTCTTTTCAAAAGTCAATTCAGGAGTACACAGCAGGACGAAAGACTCAGCACT 891  
RESULT 9  
ABK22732  
ID ABK22732 standard; cDNA; 1395 BP.  
XX  
AC ABK22732;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human cDNA encoding CLAN B.  
XX  
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; cancer; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
OS Homo sapiens.  
XX  
XX WO200190156-A2.  
XX  
PD 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
XX  
PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURNHAM INST.  
XX  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
DR WPI: 2002-083086/11.  
DR P-PSDB; AAU80872.  
XX  
PT New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation

	or cell death, autoimmune diseases or inflammation, e.g. carcinomas, arthritis or stroke
Claim 1;	Page 174-176; 216pp; English.
The invention relates to an isolated caspase recruitment domain (CARD) -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain from it, and the polynucleotides encoding them. Also included are a recombinant vector comprising the polynucleotide, recombinant cells containing the vector (e.g. bacteria, yeast, plant, animal, mammalian CC and insect cells) and an anti-CARD antibody. The CARD-containing polypeptide and CARD-encoding nucleic acid are useful for treating a pathology characterised by abnormal cell proliferation (e.g. cancer), abnormal cell death (apoptosis), autoimmune diseases or inflammation. In particular, the polypeptide and nucleic acid are useful for treating keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias, allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, graft-versus-host disease, stroke, myocardial infarction, heart failure, neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's disease) or immunodeficiency associated disease (e.g. human immunodeficiency virus (HIV) infection). The nucleic acids are useful in a variety of diagnostic applications. The present sequence is a cDNA encoding a CARD domain containing protein.	
Query Match	26.5%; Score 815; DB 24; Length 1395; Best Local Similarity 100.0%; Pred. No. 0; Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 2258	GTGTCCTGCACATGGAGAACTTGAAGAACCCTTACAAGGCTCATAATGGATAACA 2317 
DB 539	GTGTCCTGCACATGGAGAACTTGAAGAACCCTTACAAGGCTCATAATGGATAACA 598 
QY 2318	TAAAGATGAATGAGAAGATGCTATAAACCCTTAGCGAAGGCCCTGAAAACCTGAAGAAGA 2377 
DB 599	TAAAGATGAATGAGAAGATGCTATAAACCCTTAGCGAAGGCCCTGAAAACCTGAAGAAGA 658 
QY 2378	TGTGTTATTTCATTTGACCCACTTGCTGCACATTTGGAGAGGGAATGATTACATAGTCA 2437 
DB 659	TGTGTTATTTCATTTGACCCACTTGCTGCACATTTGGAGAGGGAATGATTACATAGTCA 718 
QY 2438	AGTCTCTGTCAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAAGTCTCCTGCTGCTGT 2497 
DB 719	AGTCTCTGTCAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAAGTCTCCTGCTGCTGT 778 
QY 2498	CTGCAATGCAATGAAATCTTAGCTCAGAAATCTTACAAATTTGGTCAAACCTGACCATTC 2557 
DB 779	CTGCAATGCAATGAAATCTTAGCTCAGAAATCTTACAAATTTGGTCAAACCTGACCATTC 838 
QY 2558	TTGATTTATCAGAAATTAACCTGGAAGAAGATGGAATGAAGCTCTTATGNACTGATCG 2617 
DB 839	TTGATTTATCAGAAATTAACCTGGAAGAAGATGGAATGAAGCTCTTATGNACTGATCG 898 
QY 2618	ACAGGATGAACGCTCTAGAACAGCTCACCGCACATGATGCTGCCCTGGGGCTGTGACGTGC 2677 
DB 899	ACAGGATGAACGCTCTAGAACAGCTCACCGCACATGATGCTGCCCTGGGGCTGTGACGTGC 958 
QY 2678	AAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGAGGTCCTCCAACCTCGTCAAGCTTG 2737 
DB 959	AAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGAGGTCCTCCAACCTCGTCAAGCTTG 1018 
QY 2738	GTTTGA AAACTGAGACTACAGATACAGAGATTAGAATTTAGGTGCATTTTTTGAA 2797 
DB 1019	GTTTGA AAACTGAGACTACAGATACAGAGATTAGAATTTAGGTGCATTTTTTGAA 1078 
QY 2798	AGAACCTCTCGAAAACTTCACAGCATTTGAATTTGGCGGGAATCGCTGACAGCTGATG 2857 
DB 1079	AGAACCTCTCGAAAACTTCACAGCATTTGAATTTGGCGGGAATCGCTGACAGCTGATG 1138 
QY 2858	GATGGCTTGCCCTTCATGGGTGATTATTGAGAAATCTTAAGCAATTAAGTGTTTTTTGACTTAA 2917 









OS	Homo sapiens.		
XX	WO200155322-A2.		
PN			
XX	02-AUG-2001.		
PD			
XX			
PF	17-JAN-2001; 2001WO-US01341.		
XX			
31	JAN-2000; 2000US-0179065.		
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24	FEB-2000; 2000US-0180628.		
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02	MAR-2000; 2000US-0184664.		
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16	MAR-2000; 2000US-0186350.		
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17	MAR-2000; 2000US-0189874.		
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18	APR-2000; 2000US-0190076.		
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07	JUL-2000; 2000US-0215135.		
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11	DEC-2000; 2000US-0254097.		
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05	JAN-2001; 2001US-0259678.		
PR			
XX			
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		

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XX Rosen CA, Barash SC, Ruben SM;
PI WPI: 2001-488783/53.
DR P-PSDB; AAU16173.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
XX Claim 1: SEQ ID No 339; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunoassays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention.
XX
XX Query Match 13.7%; Score 420; DB 22; Length 608;
XX Best Local Similarity 99.6%; Pred. No. 9.7e-198;
XX Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1494 TGTGGAAGCCACCGGCTGTATGAGCAGCTCGCAGCATGATCAACACGGCTGCCT 1553
DB 87 TGTGGAAGCCACCGGCTGTATGAGCAGCTCGCAGCATGATCAACACGGCTGCCT 146
QY 1554 TCTCGGACTTCCATCGCCAGAGGCTCTCTGGAGCAGCAATCTTGCAAGTGTGAA 1613
DB 147 TCTCGGACTTCCATCGCCAGAGGCTCTCTGGAGCAGCAATCTTGCAAGTGTGAA 206
QY 1614 AAACACCACTGAGCAAGAAATCTGAAAGCCATAAACATCAATCTTGTAGAGTGTGG 1673
DB 207 AAACACCACTGAGCAAGAAATCTGAAAGCCATAAACATCAATCTTGTAGAGTGTGG 266
QY 1674 CATCATTTATATCAAGAGATGATCATCAATATGAGCCCTGAGCAAGATTTGAAGCTTT 1733
DB 267 CATCATTTATATCAAGAGATGATCATCAATATGAGCCCTGAGCAAGATTTGAAGCTTT 326
QY 1734 CTTTCAAGGTAAGGCTTATATATCACTCAGGGAACATCCCGATCTATTATTGACTT 1793
DB 327 CTTTCAAGGTAAGGCTTATATATCACTCAGGGAACATCCCGATCTATTATTGACTT 386
QY 1794 CTTTGAACATTTGCCAATTTGCAAGTCTCTGGACTTCATTAACTGGACTTTTATGG 1853
DB 387 CTTTGAACATTTGCCAATTTGCAAGTCTCTGGACTTCATTAACTGGACTTTTATGG 446
QY 1854 GGGAGCTATGCTTCATGGGAAAGGCTGAGAGACACAGCGTGGATCCACATGGAGA 1913
DB 447 GGGAGCTATGCTTCATGGGAAAGGCTGAGAGACACAGCGTGGATCCACATGGAGA 506
QY 1914 GGCCCCAGAAACCTACATTCACAGAGGCTGTATCTTTGTTCTCACTGGAAGCAGGA 1973
DB 507 GGCCCCAGAAACCTACATTCACAGAGGCTGTATCTTTGTTCTCACTGGAAGCAGGA 566
```

```
QY 1974 ATTACGAGCTCTGGAGGTCACTCCGCGATTTCAGCAAGTT 2015
DB 567 ATTACGAGCTCTGGAGGTCACTCCGCGATTTCAGCAAGTT 608
XX
XX RESULT 14
XX ID AAS26575
XX AAS26575 standard; cDNA; 522 BP.
XX AC AAS26575;
XX XX
XX 07-NOV-2001 (first entry)
XX DE Human cDNA encoding a novel secreted protein, Seq ID 754.
XX KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;
XX cytosolic; cardiac; vasotropic; cerebroprotective; nootropic;
XX neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
XX vulnery; secreted protein; rheumatoid arthritis;
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
XX cerebrovascular disorder; cerebral ischaemia; angiogenesis;
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;
XX corneal infection; wound healing; epithelial cell proliferation;
XX skin ageing; food additive; preservative; antiproliferative.
XX OS Homo sapiens.
XX PN W0200155322-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01341.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 14-AUG-2000; 2000US-0220964.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.
XX PR 14-AUG-2000; 2000US-0225213.
XX PR 14-AUG-2000; 2000US-0225214.
XX PR 14-AUG-2000; 2000US-0225266.
XX PR 14-AUG-2000; 2000US-0225267.
XX PR 14-AUG-2000; 2000US-0225268.
XX PR 14-AUG-2000; 2000US-0225270.
XX PR 14-AUG-2000; 2000US-0225447.
XX PR 14-AUG-2000; 2000US-0225757.
XX PR 14-AUG-2000; 2000US-0225758.
XX PR 14-AUG-2000; 2000US-0225759.
XX PR 18-AUG-2000; 2000US-0226279.
XX PR 22-AUG-2000; 2000US-0226681.
XX PR 22-AUG-2000; 2000US-0226868.
XX PR 22-AUG-2000; 2000US-0227182.
XX PR 23-AUG-2000; 2000US-0227009.
XX PR 30-AUG-2000; 2000US-0228924.
XX PR 01-SEP-2000; 2000US-0229287.
XX PR 01-SEP-2000; 2000US-0229343.
XX PR 01-SEP-2000; 2000US-0229344.
XX PR 01-SEP-2000; 2000US-0229345.
```

	Query Match	9.9%	Score 304;	DB 22;	Length 522;
	Best Local Similarity	99.7%;	Pred. No. 3.7e-140;		
	Matches 354;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	236	CTCTATTTCAGGACTTGAATCGACAAAGCTCTTTTTCATCAGACATCAGAAGGAGACTTGG	295		
Db	1	CTCTATTTCAGGACTTGAATCGACAAAGCTCTTTTTCATCAGACATCAGAAGGAGACTTGG	60		
Qy	296	ACGATTTGGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATC	355		
Db	61	ACGATTTGGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATC	120		

QY 356 CCCTTGGTGAAGATATTGACATTATTTTAACTTCAAAAGCACCTTCACAGAACCTGTCC 415  
|||||  
Db 121 CCCTTGGTGAAGATATTGACATTATTTTAACTTCAAAAGCACCTTCACAGAACCTGTCC 180  
QY 416 TGTGGAGGAGGACCAACACCATCATCCCGTGGAGCAGCTGACCCCTGAATGCCCTTCCTGC 475  
Db 181 TGTGGAGGAGGACCAACACCATCATCCCGTGGAGCAGCTGACCCCTGAATGCCCTTCCTGC 240  
QY 476 AGGCTCTTCAGAGCCCTTCATCATTTGAAGGGATCTGGCAAGCAAGTCCACTCTGC 535  
Db 241 AGGCTCTTCAGAGCCCTTCATCATTTGAAGGGATCTGGCAAGCAAGTCCACTCTGC 300  
QY 536 TGCAGCGCATTCGCCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTT 590  
Db 301 TGCAGCGCATTCGCCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTT 355

RESULT 15  
ABK22733  
ID ABK22733 standard; cDNA; 578 BP.  
AC ABK22733;  
DT 26-MAR-2002 (first entry)  
DE Human cDNA encoding CLAN C.  
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.

OS Homo sapiens.  
XX WO200190156-A2.  
PN 29-NOV-2001.  
PD 24-MAY-2001; 2001WO-US17158.  
PF 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX (BURN-) BURNHAM INST.  
PA Reed JC, Pio PF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX WPI; 2002-083086/11.  
DR P-PSDB; AAU80863.  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX Claim 1; Page 177; 216pp; English.  
PS The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer), in  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX  
SQ Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;

Query Match 8.8%; Score 269; DB 24; Length 578;

Best Local Similarity 100.0%; Pred. No. 8.8e-123;

Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACAATAGCGGAGCCCTTATTCAAAGAATGGGAATGACTTTATA 60  
|||||  
Db 277 ATGAATTTTCATAAAGGACAATAGCGGAGCCCTTATTCAAAGAATGGGAATGACTTTATA 336  
QY 61 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGGAAAGTAACATC 120  
|||||  
Db 337 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGGAAAGTAACATC 396  
QY 121 ATTGTCTCGAGAAGGTGGAGCAGGATCTGCTAGAGGATCATTCACATGATTTTGA 180  
Db 397 ATTTGCTCGAGAAGGTGGAGCAGGATCTGCTAGAGGATCATTCACATGATTTTGA 456  
QY 181 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTCTTA 240  
Db 457 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTCTTA 516  
QY 241 TTTCAGGACTTGAATGGACAAGTCTTTT 269  
|||||  
Db 517 TTTCAGGACTTGAATGGACAAGTCTTTT 545

RESULT 16

ABK22765

ID ABK22765 standard; cDNA; 261 BP.

XX AC ABK22765;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN CARD.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX Homo sapiens.  
XX WO200190156-A2.  
PN 29-NOV-2001.  
PD 24-MAY-2001; 2001WO-US17158.  
PF 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX (BURN-) BURNHAM INST.  
PA Reed JC, Pio PF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX WPI; 2002-083086/11.  
DR P-PSDB; AAU80863.  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX Claim 1; Page 177; 216pp; English.  
PS The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing

```
PR 14-MAR-2001; 2001US-275980P.
XX 23-MAY-2001; 2001US-0864921.
PA (BURN-) BURNHAM INST.
PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI; 2002-083086/11.
DR DR P-PSDB; AAU80871.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Claim 1; Page 199; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
XX Sequence 261 BP; 86 A; 44 C; 59 G; 72 T; 0 other;
SQ
Query Match 8.5%; Score 261; DB 24; Length 261;
Best Local Similarity 100.0%; Pred. No. 8e-119;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTTCTAAGGACATAGCCGACCCCTTATTCAAGATGGGAATGACTGTATTA 60
DB 1 ATGAATTTCTAAGGACATAGCCGACCCCTTATTCAAGATGGGAATGACTGTATTA 60
QY 61 AAGCAATATCAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGTAACATC 120
DB 61 AAGCAATATCAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGTAACATC 120
QY 121 ATTTGTCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTGAAA 180
DB 121 ATTTGTCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTGAAA 180
QY 181 AAGGGTTCAGAGTCCTGTACCTCTTTCTTAATCCCTTAAGAGTGGAACTATCCTCTA 240
DB 181 AAGGGTTCAGAGTCCTGTACCTCTTTCTTAAATCCCTTAAGAGTGGAACTATCCTCTA 240
QY 241 TTTTCAGGACTTGAATGACAA 261
DB 241 TTTTCAGGACTTGAATGACAA 261
RESULT 17
ID ABA45612
XX ABA45612 standard; DNA; 421 BP.
XX
AC ABA45612;
XX
XX 01-FEB-2002 (first entry)
DT
```

```
XX Human breast cell single exon nucleic acid probe #4307.
XX
XX Human: microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
XX Homo sapiens.
OS
PN WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US006662.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 1; SEQ ID NO 4307; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
SQ
Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAATCTCCAGCAGTTGAATTTGGCGGAAA 2840
DB 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAATCTCCAGCAGTTGAATTTGGCGGAAA 239
QY 2841 TCCTGTGAGCAGTGATGGATGGCTTGCCTTCATCGGGTGTATTTGAGAACTTGAACAAT 2900
DB 240 TCCTGTGAGCAGTGATGGATGGCTTGCCTTCATCGGGTGTATTTGAGAACTTGAACAAT 299
QY 2901 AGTGTGTTTGTGACTTTAGTAGTAAAGAAATTTCTACCTGATCCAGCAGTATAGTCAAGAACT 2960
DB 300 AGTGTGTTTGTGACTTTAGTAGTAAAGAAATTTCTACCTGATCCAGCAGTATAGTCAAGAACT 359
QY 2961 TAGCCAAGTGTTATCCAAGTTAACTTTTCTGCAAGAGCTAGGCTTGTGTTGGTGGCAAT 3020
DB
```

Db 360 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419  
QY 3021 TG 3022  
II  
Db 420 TG 421

RESULT 18  
ABA56119  
ID ABA56119 standard; DNA; 421 BP.  
XX ABA56119;  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Human foetal liver single exon nucleic acid probe #4424.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00669.  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
XX  
DR Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
PS Claim 1; SEQ ID NO 4424; 639pp + sequence listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a single exon nucleic acid  
CC probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 22; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAA 2840  
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAA 239

QY 2841 TCGTGTGACAGTGTGATGGCTTCCCTCATGGTGTATTGAGAACTCTTAAGCAATT 2900  
Db 240 TCGTGTGACAGTGTGATGGCTTCCCTCATGGTGTATTGAGAACTCTTAAGCAATT 299

QY 2901 AGTGTGTGTGACTTTAGTACTAAAGAAATTTCTACTGATCCAGCATTAGTCAGAAAACT 2960  
Db 300 AGTGTGTGTGACTTTAGTACTAAAGAAATTTCTACTGATCCAGCATTAGTCAGAAAACT 359

QY 2961 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020  
Db 360 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419

QY 3021 TG 3022  
II  
Db 420 TG 421

RESULT 19  
ABA25770  
ID ABA25770 standard; DNA; 421 BP.  
XX ABA25770;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Probe #4236 for gene expression analysis in human heart cell sample.  
XX  
KW Human; gene expression; heart; microarray; vascular system; probe;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00666.  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488899/53.  
XX  
DR Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX  
PS Claim 1; SEQ ID No 4236; 530pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 22; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAA 2840  
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAA 239

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QY 2841 TCGGTGAGCAGTGATGGTGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATT 2900
    |||||||
Db 240 TCGGTGAGCAGTGATGGTGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATT 299
QY 2901 AGTGTGTTTGGACCTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAC 2960
    |||||||
Db 300 AGTGTGTTTGGACCTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAC 359
QY 2961 TAGCCAAGTGTATCCCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
    |||||||
Db 360 TAGCCAAGTGTATCCCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419
QY 3021 TG 3022
    ||
Db 420 TG 421

RESULT 20
AAK04305
ID AAK04305 standard; DNA; 421 BP.
XX
AC AAK04305;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 4296.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 4296; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system,
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
```

Query Match 7.9%; Score 242; DB 22; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAACTTCAGCAGTTGAATTTGGCGGGAAA 2840
    |||||||
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAACTTCAGCAGTTGAATTTGGCGGGAAA 239
QY 2841 TCGGTGAGCAGTGATGGTGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATT 2900
    |||||||
Db 240 TCGGTGAGCAGTGATGGTGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATT 299
QY 2901 AGTGTGTTTGGACCTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAC 2960
    |||||||
Db 300 AGTGTGTTTGGACCTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAC 359
QY 2961 TAGCCAAGTGTATCCCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
    |||||||
Db 360 TAGCCAAGTGTATCCCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419
QY 3021 TG 3022
    ||
Db 420 TG 421

RESULT 21
AAK29801
ID AAK29801 standard; DNA; 421 BP.
XX
AC AAK29801;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 4358.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 4358; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
```

Query Match 7.9%; Score 242; DB 22; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAAGTTCAGCAGTTGAATTTGGCGGGAAA 2840
|||||
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAAGTTCAGCAGTTGAATTTGGCGGGAAA 239
|||||
QY 2841 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 2900
|||||
Db 240 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 299
|||||
QY 2901 AGTGTGTTTGGTGTGATGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 2960
|||||
Db 300 AGTGTGTTTGGTGTGATGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 359
|||||
QY 2961 TAGCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
|||||
Db 360 TAGCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419
|||||
QY 3021 TG 3022
||
Db 420 TG 421

RESULT 22
AAI14389
ID AAI14389 standard; DNA; 421 BP.
XX
AC AAI14389;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #4322 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PS WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 4322; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
```

```
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAAGTTCAGCAGTTGAATTTGGCGGGAAA 2840
|||||
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAAGTTCAGCAGTTGAATTTGGCGGGAAA 239
|||||
QY 2841 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 2900
|||||
Db 240 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 299
|||||
QY 2901 AGTGTGTTTGGTGTGATGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 2960
|||||
Db 300 AGTGTGTTTGGTGTGATGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 359
|||||
QY 2961 TAGCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
|||||
Db 360 TAGCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419
|||||
QY 3021 TG 3022
||
Db 420 TG 421

RESULT 23
AAI35764
ID AAI35764 standard; DNA; 421 BP.
XX
AC AAI35764;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #4450 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PS WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 4450; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
```



SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 22; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGGAAGAACCTCTGAAAACCTCCAGCAGTGAATTTGGCGGGA 2840  
|||||  
DB 180 AGGTGCATTTTGGGAAGAACCTCTGAAAACCTCCAGCAGTGAATTTGGCGGGA 239

QY 2841 TCGTGTGAGCAGTGAATTTGGCGTTCATGGGTGATTTGAGAACTTTAAGCAATT 2900  
|||||  
DB 240 TCGTGTGAGCAGTGAATTTGGCGTTCATGGGTGATTTGAGAACTTTAAGCAATT 299

QY 2901 AGTGTGTTTGGACCTTTAGTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 2960  
|||||  
DB 300 AGTGTGTTTGGACCTTTAGTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 359

QY 2961 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATT 3020  
|||||  
DB 360 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATT 419

QY 3021 TG 3022  
||  
DB 420 TG 421

RESULT 24  
AAI04213  
ID AAI04213 standard; DNA; 421 BP.

XX AC AAI04213;  
XX DT 09-OCT-2001 (first entry)  
XX DE Probe #4204 used to measure gene expression in human breast sample.  
XX KW Probe; human; breast disease; breast cancer; development disorder; ss;  
XX KW Inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
XX OS Homo sapiens.  
XX PN WO200157270-A2.  
XX PD 09-AUG-2001.  
XX PF 29-JAN-2001; 2001WO-US00661.  
XX PR 04-FEB-2000; 2000US-0180312.  
XX PR 26-MAY-2000; 2000US-0207456.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-0234687.  
XX PR 27-SEP-2000; 2000US-0236359.  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX XX WPI; 2001-476286/51.  
XX DR Novel single exon nucleic acid probe used to measuring gene expression in a human breast -  
XX PS Claim 25; SEQ ID No 4204; 322pp; English.  
XX CC The present invention relates to novel single exon nucleic acid probes.  
XX CC The present sequence is one such probe. The probes are useful for  
XX CC measuring human gene expression in a human breast sample, where the probe  
XX CC hybridises at high stringency to a nucleic acid expressed in the human  
XX CC breast. The probes are useful for predicting, diagnosing, grading,  
XX CC staging, monitoring and prognosing diseases of the human breast,

CC particularly those diseases with polygenic aetiology. The diseases  
CC include: breast cancer, disorders of development, inflammatory diseases  
CC of the breast, fibrocystic changes, proliferative breast disease and  
CC non-carcinoma tumours.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 22; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGGAAGAACCTCTGAAAACCTCCAGCAGTGAATTTGGCGGGA 2840  
|||||  
DB 180 AGGTGCATTTTGGGAAGAACCTCTGAAAACCTCCAGCAGTGAATTTGGCGGGA 239

QY 2841 TCGTGTGAGCAGTGAATTTGGCGTTCATGGGTGATTTGAGAACTTTAAGCAATT 2900  
|||||  
DB 240 TCGTGTGAGCAGTGAATTTGGCGTTCATGGGTGATTTGAGAACTTTAAGCAATT 299

QY 2901 AGTGTGTTTGGACCTTTAGTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 2960  
|||||  
DB 300 AGTGTGTTTGGACCTTTAGTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 359

QY 2961 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATT 3020  
|||||  
DB 360 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATT 419

QY 3021 TG 3022  
||  
DB 420 TG 421

RESULT 25  
ABS04362  
ID ABS04362 standard; DNA; 421 BP.

XX AC ABS04362;  
XX XX 19-AUG-2002 (first entry)  
XX DE Human genome-derived single exon probe from lung SEQ ID No 4353.  
XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
XX KW chronic obstructive pulmonary disease; interstitial lung disease;  
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
XX KW primary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
XX KW hyaline membrane disease.  
XX OS Homo sapiens.  
XX PN WO200186003-A2.  
XX XX 15-NOV-2001.  
XX PD 30-JAN-2001; 2001WO-US00665.  
XX PF 04-FEB-2000; 2000US-180312P.  
XX PR 26-MAY-2000; 2000US-0207456P.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0236359P.  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2002-114183/15.  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
PT measure gene expression in human lung samples -  
PS Claim 1; SEQ ID NO 4353; 634pp; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614  
CC probes. Also included are a microarray comprising the novel set of  
CC probes; the novel set of probes which hybridise at high stringency to a  
CC nucleic acid expressed in the human lung; measuring gene expression in a  
CC sample derived from human lung, comprising (a) contacting the array with  
CC a collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of  
CC the array; identifying exons in a eukaryotic genome, comprising  
CC (a) algorithmically predicting at least one exon from genomic sequences  
CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene  
CC expression analysis, and for identifying exons in a gene, particularly  
CC using human lung derived mRNA and for the study of lung diseases  
CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
CC and hyaline membrane disease. The present sequence is a single exon  
CC probe of the invention.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;  
  
Query Match 7.9%; Score 242; DB 24; Length 421;  
Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2781 AGTGTCATTTTGGGAAGAACCCCTCTGAAAACCTCCAGCAGTTGAATTTGGCGGAA 2840  
DB 180 AGGTGCATTTTGGGAAGAACCCCTGAAAACCTCCAGCAGTTGAATTTGGCGGAA 239  
QY 2841 TCGTGTGACAGTGTGATGGCTTCCCTTCATGGGTGATTTTGAGAAATCTTAAGCAAT 2900  
DB 240 TCGTGTGACAGTGTGATGGCTTCCCTTCATGGGTGATTTTGAGAAATCTTAAGCAAT 299  
QY 2901 AGTGTTTTTGTACTTAGTACTTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAT 2960  
DB 300 AGTGTTTTTGTACTTAGTACTTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAT 359  
QY 2961 TAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAAT 3020  
DB 360 TAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAAT 419  
QY 3021 TG 3022

Db 420 TG 421  
II  
RESULT 26  
ABA50734  
ID ABA50734 standard; DNA; 220 BP.  
XX  
XX ABA50734;  
XX  
XX 01-FEB-2002 (first entry)  
XX Human breast cell single exon nucleic acid probe #9429.  
XX Human; microarray; single exon probe; gene expression; breast;  
XX disease; cancer; ss.  
XX Homo sapiens.  
XX WO200157271-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00662.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0608408.  
XX 03-AUG-2000; 2000US-0632366.  
XX 21-SEP-2000; 2000US-0234687.  
XX 27-SEP-2000; 2000US-0236359.  
XX 04-OCT-2000; 2000GB-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-496933/54.  
XX  
XX New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -  
XX Claim 4; SEQ ID NO 9429; 327pp + sequence listing; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting  
CC the probes with a collection of detectably labelled nucleic acids  
CC derived from mRNA of human breast, and then measuring the label  
CC bound to each probe of the microarray. The probes are useful for  
CC verifying the expression of regions of genomic DNA predicted to  
CC encode proteins. They are useful for gene discovery, and for  
CC determining predisposition and/or prognosing breast disease. Gene  
CC expression analysis is useful for assessing the toxicity of chemical  
CC agents on cells. The microarray of this invention presents a far greater  
CC diversity of probes for measuring gene expression, with far less bias  
CC than expressed sequence tag microarrays. The method is suitable for  
CC rapid production of functional information from genomic sequence. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;  
  
Query Match 7.2%; Score 220; DB 22; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2830 TTGGCGGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 2889  
DB 1 TTGGCGGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949  
|||||  
Db 61 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120  
QY 2950 GTCAGAAACTTACCCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 3009  
|||||  
Db 121 GTCAGAAACTTACCCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 180  
QY 3010 GGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAG 3049  
|||||  
Db 181 GGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 27  
ABA68704  
ID ABA68704 standard; DNA; 220 BP.  
XX ABA68704;  
AC  
XX  
DT  
XX  
XX  
DE  
XX  
DE Human foetal liver single exon nucleic acid probe #17009.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
KW  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD  
XX  
PF  
XX  
PF 30-JAN-2001; 2001WO-US00669.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
XX  
PS Claim 4; SEQ ID NO 17009; 639pp + sequence listing; English.  
XX

CC The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC foetal liver. The present sequence is a single exon nucleic acid  
CC probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

QY Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;  
Query Match 7.2%; Score 220; DB 22; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGCGCGGAAATCGTGTGACAGTGTGATGGCTTCCCTTCATGGGTGATTGAGAA 2889  
|||||  
Db 1 TTGCGCGGAAATCGTGTGACAGTGTGATGGCTTCCCTTCATGGGTGATTGAGAA 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949  
|||||  
Db 61 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120  
QY 2950 GTCAGAAACTTACCCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 3009  
|||||  
Db 121 GTCAGAAACTTACCCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 180  
QY 3010 GGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAG 3049  
|||||  
Db 181 GGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 28  
ABA35668  
ID ABA35668 standard; DNA; 220 BP.  
XX ABA35668;  
AC  
XX  
DT  
XX  
XX  
DE  
XX  
DE Probe #14134 for gene expression analysis in human heart cell sample.  
XX  
KW Human; gene expression; heart; microarray; vascular system; probe;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
KW congenital heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.  
XX  
PD  
XX  
PF  
XX  
PF 30-JAN-2001; 2001WO-US00666.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488899/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX  
XX  
PS Claim 4; SEQ ID NO 14134; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

QY Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;  
Query Match 7.2%; Score 220; DB 22; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGACGAGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 2889  
Db 1 TTGGCGGGAATCGTGTGACGAGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 60  
QY 2890 CTTAAGCAATTAGTGTGTTTTCGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTA 2949  
Db 61 CTTAAGCAATTAGTGTGTTTTCGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTA 120  
QY 2950 GTCCAGAAAACCTTAGCCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGT 3009  
Db 121 GTCCAGAAAACCTTAGCCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGT 180  
QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 3049  
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 29  
AAK17044  
ID AAK17044 standard; DNA; 220 BP.  
AC AAK17044;  
XX  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe SEQ ID NO: 17035.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe;  
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
KW epilepsy; cancer; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00667.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483446/52.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT brains -  
XX

Example 4; SEQ ID NO: 17035; 650pp + Sequence Listing; English.  
XX  
PS The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention.  
XX  
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 22; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGACGAGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 2889

Db 1 TTGGCGGGAATCGTGTGACGAGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 60  
QY 2890 CTTAAGCAATTAGTGTGTTTTCGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTA 2949  
Db 61 CTTAAGCAATTAGTGTGTTTTCGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTA 120  
QY 2950 GTCCAGAAAACCTTAGCCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGT 3009  
Db 121 GTCCAGAAAACCTTAGCCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGT 180  
QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 3049  
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 30  
AAK42828  
ID AAK42828 standard; DNA; 220 BP.  
XX  
AC AAK42828;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed single exon probe SEQ ID NO: 17385.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00668.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488900/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human bone marrow -  
XX  
PS Example 4; SEQ ID NO: 17385; 658pp + Sequence Listing; English.  
XX

The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention.  
XX  
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 22; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGACGAGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 2889  
Db 1 TTGGCGGGAATCGTGTGACGAGTGATGGCTTGCCTTCATGGGTGATTGAGAAT 60

```
QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120

QY 2950 GTCAGAAAACCTTAGCCCAAGTGTATCCAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 3009
|||||
Db 121 GTCAGAAAACCTTAGCCCAAGTGTATCCCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 180

QY 3010 GGGTGGCAATTTCGATGATGATGATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTTCGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 31
AAI23590
ID AAI23590 standard; DNA; 220 BP.
XX
AC AAI23590;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #13523 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
KW Homo sapiens.
OS
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US006070.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 13523; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGACGACGTGATGGCTTGCCTTCATGGTGTATTGAGAAT 2889
|||||
Db 1 TTGGCGGGAATCGTGTGACGACGTGATGGCTTGCCTTCATGGTGTATTGAGAAT 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120
```

```
QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120

QY 2950 GTCAGAAAACCTTAGCCCAAGTGTATCCAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 3009
|||||
Db 121 GTCAGAAAACCTTAGCCCAAGTGTATCCCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTT 180

QY 3010 GGGTGGCAATTTCGATGATGATGATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTTCGATGATGATGATCTCAGTGTATTATACAG 220
```

```
RESULT 32
AAI48904
ID AAI48904 standard; DNA; 220 BP.
XX
AC AAI48904;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #17590 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
KW Homo sapiens.
OS
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 17590; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
```

```
Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2830 TTGGCGGGAATCGTGTGACGACGTGATGGCTTGCCTTCATGGTGTATTGAGAAT 2889
|||||
Db 1 TTGGCGGGAATCGTGTGACGACGTGATGGCTTGCCTTCATGGTGTATTGAGAAT 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120
```

```
QY 2950 CTCAGAAACTTAGCCAGTGTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 3009
      |||||||
Db 121 CTCAGAAACTTAGCCAGTGTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 180

QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTCTATTACAG 3049
      |||||||
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTCTATTACAG 220

RESULT 33
AAI09206
ID AAI09206 standard; DNA; 220 BP.
XX
AC AAI09206;
XX
XX 09-OCT-2001 (first entry)
XX
XX Probe #9197 used to measure gene expression in human breast sample.
XX
XX Probe; human; breast disease; breast cancer; development disorder; ss;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX Homo sapiens.
XX
XX WO200157270-A2.
XX
XX 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US00661.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression
XX in a human breast -
XX
XX Claim 25; SEQ ID No 9197; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes.
XX The present sequence is one such probe. The probes are useful for
XX measuring human gene expression in a human breast sample, where the probe
XX hybridises at high stringency to a nucleic acid expressed in the human
XX breast. The probes are useful for predicting, diagnosing, grading,
XX staging, monitoring and prognosing diseases of the human breast,
XX particularly those diseases with polygenic aetiology. The diseases
XX include: breast cancer, disorders of development, inflammatory diseases
XX of the breast, fibrocystic changes, proliferative breast disease and
XX non-carcinoma tumours.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
XX
XX Query Match 7.2%; Score 220; DB 22; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-98;
XX Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTCATCGGGGTATTGAGAAAT 2889
      |||||||
Db 1 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTCATCGGGGTATTGAGAAAT 60
```

```
QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTTACCTGATCCAGCAATTA 2949
      |||||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTTACCTGATCCAGCAATTA 120

QY 2950 GTCAGAAACTTAGCCAGTGTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 3009
      |||||||
Db 121 GTCAGAAACTTAGCCAGTGTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 180

QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTCTATTACAG 3049
      |||||||
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTCTATTACAG 220

RESULT 34
ABS16884
ID ABS16884 standard; DNA; 220 BP.
XX
XX ABS16884;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human genome-derived single exon probe ORF from lung SEQ ID No 16875.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tubercous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US00665.
XX
XX 04-FEB-2000; 2000US-180312P.
XX
XX 26-MAY-2000; 2000US-207456P.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-234687P.
XX
XX 27-SEP-2000; 2000US-236359P.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -
XX
XX Claim 4; SEQ ID No 16875; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
```

CC (a) algorithmically predicting at least one exon from genomic sequences  
CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene  
CC expression analysis, and for identifying exons in a gene, particularly  
CC using human lung derived mRNA and for the study of lung diseases  
CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
CC and hyaline membrane disease. The present sequence is a single exon  
CC probe open reading frame of the invention.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 24; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2830 TTGGCGGAAATCGTGTGACGATGATGAGTTCCTTCAATGCTGATTTGAGAAAT 2889  
Db 1 TTGGCGGAAATCGTGTGACGATGATGAGTTCCTTCAATGCTGATTTGAGAAAT 60  
QY 2890 CTTAAGCAATAGTGTGTTGACTTTAGTACTAAGAAATTTCTACTGATCCAGCATTA 2949  
Db 61 CTTAAGCAATAGTGTGTTGACTTTAGTACTAAGAAATTTCTACTGATCCAGCATTA 120  
QY 2950 GTCAGAAAACCTTACCAAGTGTATCCAACTTAACTTTTCGCAAGAAGCTAGGCTTGT 3009  
Db 121 GTCAGAAAACCTTACCAAGTGTATCCAACTTAACTTTTCGCAAGAAGCTAGGCTTGT 180  
QY 3010 GGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3049  
Db 181 GGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 220

RESULT 35  
ABK22768  
ID ABK22768 standard; cDNA; 165 BP.

XX ABK22768;

DT 26-MAR-2002 (first entry)

XX Human cDNA encoding CLAN SAM.

KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; cancer; abnormal cell death; apoptosis;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Crohn's disease; stroke;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.

OS Homo sapiens.  
XX WO200190156-A2.  
PN 29-NOV-2001.  
XX 24-MAY-2001; 2001WO-US17158.  
XX 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX (BURN-) BURNHAM INST.  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX WPI; 2002-083086/11.  
DR P-PSDB; AAU0874.  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX Claim 1; Page 204; 216pp; English.  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing a  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Crohn's disease, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX Sequence 165 BP; 51 A; 37 C; 38 G; 39 T; 0 other;  
QY Query Match 3.7%; Score 114; DB 24; Length 165;  
Best Local Similarity 99.4%; Pred. NO. 7.3e-46;  
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1924 ACCTACATCCAGAGGGGCTGATCTTCTTCACTGAGGAGGAGGATTCAGGACT 1983  
Db 1 ACCTACATCCAGAGGGGCTGATCTTCTTCACTGAGGAGGAGGATTCAGGACT 60  
QY 1984 CTGGAGGTACACTCCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATCATCTCGGGG 2043  
Db 61 CTGGAGGTACACTCCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATCATCTCGGGG 120  
QY 2044 AAAATATTAGCTCTCCCAAGCCCTCAGGCTGCAATAAAGAGA 2088  
Db 121 AAAATATTAGCTCTCCCAAGCCCTCAGGCTGCAATAAAGAGA 165  
XX RESULT 36  
XX ABN40447  
XX ID ABN40447 standard; DNA; 60 BP.  
XX ABN40447;  
XX

```
XX 15-JUL-2002 (first entry)
XX Human spliced transcript detection oligonucleotide SEQ ID NO:13195.
DE Human; mouse; rat; splice transcript: detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss..
XX Homo sapiens.
OS WO200210449-A2.
PN WO200210449-A2.
XX 07-FEB-2002.
PD 20-JUL-2001; 2001WO-IB01903.
XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX (COMP-) COMPUGEN INC.
PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes.
PS Example 1; SEQ ID 13195; 47pp; English.
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, and was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 60 BP; 12 A; 7 C; 22 G; 19 T; 0 other;
SQ
Query Match 2.0%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.5e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2828 ATTTGGCGGGAATCGTGTGAGCACTGATGGATGCTTGCCTTCATGGTGTATTGTAGA 2887
DB 1 ATTTGGCGGGAATCGTGTGAGCACTGATGGATGCTTGCCTTCATGGTGTATTGTAGA 60
RESULT 37
ABK22753/c
ID ABK22753 standard; DNA; 29 BP.
XX
AC ABK22753;
```

```
XX 26-MAR-2002 (first entry)
XX Human CLAN A PCR primer #2.
DE Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
XX autoimmune disease; inflammation; keratinocyte hyperplasia;
XX inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
XX balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
XX leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
XX Crohn's disease; graft-versus-host disease; stroke; PCR primer;
XX myocardial infarction; heart failure; neurodegenerative disease;
XX Parkinson's disease; Alzheimer's disease; HIV;
XX human immunodeficiency virus infection.
XX Homo sapiens.
OS WO200190156-A2.
XX 29-NOV-2001.
PD 24-MAY-2001; 2001WO-US17158.
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX (BURN-) BURNHAM INST.
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
XX Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI; 2002-083086/11.
XX New caspase recruitment domain (CARD)-containing polypeptides and
XX encoding nucleic acids, useful for treating abnormal cell proliferation
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
XX arthritis or stroke.
XX Example 10; Page 115; 216pp; English.
XX The invention relates to an isolated caspase recruitment domain (CARD)
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
XX from it, and the polynucleotides encoding them. Also included are a
XX recombinant vector comprising the polynucleotide, recombinant cells
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
XX and insect cells) and an anti-CARD antibody. The CARD-containing
XX polypeptide and CARD-encoding nucleic acid are useful for treating a
XX pathology characterised by abnormal cell proliferation (e.g. cancer),
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
XX particular, the polypeptide and nucleic acid are useful for treating
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
XX muscle cell proliferation in arteries following balloon angioplasty
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
XX disease) or immunodeficiency associated disease (e.g. human
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful
XX in a variety of diagnostic applications. The present sequence is a
XX PCR primer used to amplify a nucleic acid encoding a CARD-containing
XX protein.
XX Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;
SQ
Query Match 0.9%; Score 29; DB 24; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1152 TGACTTCATTCGGACCTGGACCACCTGTG 1180
|||||
```



Db 29 TGACTTCATTCGGAGCCTGGACCACTGTG 1

RESULT 38  
ABK22754

ID ABK22754 standard; DNA; 25 BP.

AC ABK22754;

XX 26-MAR-2002 (first entry)

DT Human CLAN B PCR primer #1.

DE Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;

XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;

KW autoimmune disease; inflammation; keratinocyte hyperplasia;

KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;

KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;

KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;

KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;

KW myocardial infarction; heart failure; neurodegenerative disease;

KW Parkinson's disease; Alzheimer's disease; HIV;

XX human immunodeficiency virus infection.

XX Homo sapiens.

XX W0200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17158.

XX 24-MAY-2000; 2000US-0579240.

PR 10-OCT-2000; 2000US-0686347.

PR 14-MAR-2001; 2001US-275980P.

PR 23-MAY-2001; 2001US-0864921.

XX (BURN-) BURNHAM INST.

PA Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX Oliveira VAM, Hayashi H, Pawlowski K;

PI WPI; 2002-083086/11.

XX New caspase recruitment domain (CARD)-containing polypeptides and

PT encoding nucleic acids, useful for treating abnormal cell proliferation

PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

PT arthritis or stroke -

XX Example 10; Page 115; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)

CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain

CC from it, and the polynucleotides encoding them. Also included are a

CC recombinant vector comprising the polynucleotide, recombinant cells

CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian

CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a

CC pathology characterised by abnormal cell proliferation (e.g. cancer),

CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In

CC particular, the polypeptide and nucleic acid are useful for treating

CC graft-versus-host disease, stroke, myocardial infarction, heart failure,

CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's

CC disease) or immunodeficiency associated disease (e.g. human

CC immunodeficiency virus (HIV) infection). The nucleic acids are useful

CC in a variety of diagnostic applications. The present sequence is a

CC PCR primer used to amplify a nucleic acid encoding a CARD-containing

XX protein.

SQ Sequence 25 BP; 6 A; 4 C; 9 G; 6 T; 0 other;

Query Match 0.8%; Score 25; DB 24; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 CATCATTTGCTGGAGAGGTGGAG 141

DB 1 CATCATTTGCTGGAGAGGTGGAG 25

RESULT 39  
ABK22755/c

ID ABK22755 standard; DNA; 25 BP.

XX AC ABK22755;

XX 26-MAR-2002 (first entry)

DT Human CLAN B PCR primer #2.

DE Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;

XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;

KW autoimmune disease; inflammation; keratinocyte hyperplasia;

KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;

KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;

KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;

KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;

KW myocardial infarction; heart failure; neurodegenerative disease;

KW Parkinson's disease; Alzheimer's disease; HIV;

XX human immunodeficiency virus infection.

XX Homo sapiens.

XX W0200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17158.

XX 24-MAY-2000; 2000US-0579240.

PR 10-OCT-2000; 2000US-0686347.

PR 14-MAR-2001; 2001US-275980P.

PR 23-MAY-2001; 2001US-0864921.

XX (BURN-) BURNHAM INST.

PA Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX Oliveira VAM, Hayashi H, Pawlowski K;

PI WPI; 2002-083086/11.

XX New caspase recruitment domain (CARD)-containing polypeptides and

PT encoding nucleic acids, useful for treating abnormal cell proliferation

PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

PT arthritis or stroke -

XX Example 10; Page 115; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)

CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain

CC from it, and the polynucleotides encoding them. Also included are a

CC recombinant vector comprising the polynucleotide, recombinant cells

CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian

CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a

CC pathology characterised by abnormal cell proliferation (e.g. cancer),

CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In

CC particular, the polypeptide and nucleic acid are useful for treating

CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth

CC muscle cell proliferation in arteries following balloon angioplasty

CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,

CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,

CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's

CC disease) or immunodeficiency associated disease (e.g. human

CC immunodeficiency virus (HIV) infection). The nucleic acids are useful

CC in a variety of diagnostic applications. The present sequence is a

CC PCR primer used to amplify a nucleic acid encoding a CARD-containing

XX protein.

CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
 CC disease) or immunodeficiency associated disease (e.g. human  
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
 CC in a variety of diagnostic applications. The present sequence is a  
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing  
 CC protein.

XX Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 other;

Query Match 0.8%; Score 25; DB 24; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2959 CTTAGCCAAAGTGTATCCAAAGTTAA 2983

Db 25 CTTAGCCAAAGTGTATCCAAAGTTAA 1

RESULT 40

ABK22758

ID ABK22758 standard; DNA; 25 BP.

XX AC ABK22758;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN D PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX PI Oliveira VAM, Hayashi H, Pawlowski K;

XX DR WPI; 2002-083086/11.

XX PT New caspase recruitment domain (CARD)-containing polypeptides and

XX PT encoding nucleic acids, useful for treating abnormal cell proliferation

XX PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

XX PT arthritis or stroke

XX PS Example 10; Page 116; 216pp; English.

XX CC The invention relates to an isolated caspase recruitment domain (CARD)  
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
 CC from it, and the polynucleotides encoding them. Also included are a  
 CC recombinant vector comprising the polynucleotide, recombinant cells  
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
 CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
 CC particular, the polypeptide and nucleic acid are useful for treating  
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
 CC muscle cell proliferation in arteries following balloon angioplasty  
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
 CC disease) or immunodeficiency associated disease (e.g. human  
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
 CC in a variety of diagnostic applications. The present sequence is a  
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing  
 CC protein.

XX Sequence 25 BP; 11 A; 4 C; 5 G; 5 T; 0 other;

Query Match 0.8%; Score 25; DB 24; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AATTTTCATAAAGGACATAGCGGAG 28

Db 1 AATTTTCATAAAGGACATAGCGGAG 25

RESULT 41

ABK22752

ID ABK22752 standard; DNA; 24 BP.

XX AC ABK22752;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN A PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX PI Oliveira VAM, Hayashi H, Pawlowski K;

XX DR WPI; 2002-083086/11.

XX PT New caspase recruitment domain (CARD)-containing polypeptides and

XX PT encoding nucleic acids, useful for treating abnormal cell proliferation

XX PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

XX PT arthritis or stroke

PS Example 10; Page 115; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)  
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
 CC from it, and the polynucleotides encoding them. Also included are a  
 CC recombinant vector comprising the polynucleotide, recombinant cells  
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
 CC and insect cells) and an anti-CARD antibody. The CARD-containing  
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
 CC particular, the polypeptide and nucleic acid are useful for treating  
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
 CC muscle cell proliferation in arteries following balloon angioplasty  
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
 CC disease) or immunodeficiency associated disease (e.g. human  
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
 CC in a variety of diagnostic applications. The present sequence is a  
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing  
 CC protein.

XX SQ Sequence 24 BP; 5 A; 3 C; 12 G; 4 T; 0 other;

Query Match 0.8%; Score 24; DB 24; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.32;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 GGTGAGCAGGATGCTGTAGAGG 158  
 |||||  
 Db 1 GGTGAGCAGGATGCTGTAGAGG 24

RESULT 42

ABK22750

ID ABK22750 standard; DNA; 33 BP.

XX AC ABK22750;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN CARD domain PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX WO200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17158.

XX 24-MAY-2000; 2000US-0579240.

XX 10-OCT-2000; 2000US-0686347.

XX 14-MAR-2001; 2001US-275980P.

XX 23-MAY-2001; 2001US-0864921.

XX (BURN-) BURNHAM INST.

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
 PT arthritis or stroke -

XX Example 10; Page 117; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)  
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
 CC from it, and the polynucleotides encoding them. Also included are a  
 CC recombinant vector comprising the polynucleotide, recombinant cells  
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
 CC and insect cells) and an anti-CARD antibody. The CARD-containing  
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
 CC particular, the polypeptide and nucleic acid are useful for treating  
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
 CC muscle cell proliferation in arteries following balloon angioplasty  
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
 CC disease) or immunodeficiency associated disease (e.g. human  
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
 CC in a variety of diagnostic applications. The present sequence is a  
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing  
 CC protein.

XX SQ Sequence 33 BP; 12 A; 8 C; 6 G; 7 T; 0 other;

Query Match 0.8%; Score 24; DB 24; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.33;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATATAAGGACATAGC 24  
 |||||  
 Db 10 ATGAATTCATATAAGGACATAGC 33

RESULT 43

ABK22746/C

ID ABK22746 standard; DNA; 23 BP.

XX AC ABK22746;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN cDNA PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX WO200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17158.

XX 24-MAY-2000; 2000US-0579240.

```
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Example 10; Page 111; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
CC protein.
XX
XX Sequence 23 BP; 6 A; 6 C; 5 G; 6 T; 0 other;
SQ
Query Match 0.7%; Score 23; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 149 CTGCTAGAGGGATCATTCACATG 171
Db 23 CTGCTAGAGGGATCATTCACATG 1
RESULT 44
ABK22756
ID ABK22756 standard; DNA; 23 BP.
XX
XX AC ABK22756;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human CLAN C PCR primer #1.
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
```

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XX WO200190156-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17158.
XX
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Example 10; Page 115; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
CC protein.
XX
XX Sequence 23 BP; 8 A; 4 C; 5 G; 6 T; 0 other;
SQ
Query Match 0.7%; Score 23; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 GTAAACATCATTTGCTGCGAGAA 134
Db 1 GTAAACATCATTTGCTGCGAGAA 23
RESULT 45
ABK22749
ID ABK22749 standard; DNA; 21 BP.
XX
XX AC ABK22749;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human CLAN cDNA PCR primer #4.
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
```

KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
OS Homo sapiens.  
XX  
XX WO200190156-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
XX  
XX 24-MAY-2000; 2000US-0579240.  
XX 10-OCT-2000; 2000US-0686347.  
XX 14-MAR-2001; 2001US-275980P.  
XX 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURNHAM INST.  
XX  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
XX Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX WPI; 2002-083086/11.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
XX encoding nucleic acids, useful for treating abnormal cell proliferation  
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX arthritis or stroke -  
XX  
XX Example 10; Page 111; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
XX from it, and the polynucleotides encoding them. Also included are a  
XX recombinant vector comprising the polynucleotide, recombinant cells  
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
XX and insect cells) and an anti-CARD antibody. The CARD-containing  
XX polypeptide and CARD-encoding nucleic acid are useful for treating a  
XX pathology characterised by abnormal cell proliferation (e.g. cancer),  
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
XX particular, the polypeptide and nucleic acid are useful for treating  
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
XX muscle cell proliferation in arteries following balloon angioplasty  
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,  
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
XX disease) or immunodeficiency associated disease (e.g. human  
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful  
XX in a variety of diagnostic applications. The present sequence is a  
XX PCR primer used to amplify a nucleic acid encoding a CARD-containing  
XX protein.  
XX  
XX Sequence 21 BP; 5 A; 3 C; 6 G; 7 T; 0 other;  
XX  
XX Query Match 0.7%; Score 21; DB 24; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 9.9;  
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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XX 85 GTATGGAAATGTCCTGAATCGC 105  
XX ||||||  
XX 1 GTATGGAAATGTCCTGAATCGC 21  
XX  
XX Db  
XX  
XX RESULT 46  
XX ABK22751/c  
XX ID ABK22751 standard; DNA: 30 BP.  
XX  
XX AC ABK22751;  
XX  
XX

DT 26-MAR-2002 (first entry)  
XX  
XX Human CLAN CARD domain PCR primer #2.  
XX  
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
XX autoimmune disease; inflammation; keratinocyte hyperplasia;  
XX inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
XX balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
XX leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
XX Crohn's disease; graft-versus-host disease; stroke; PCR primer;  
XX myocardial infarction; heart failure; neurodegenerative disease;  
XX Parkinson's disease; Alzheimer's disease; HIV;  
XX human immunodeficiency virus infection.  
XX  
XX Homo sapiens.  
XX  
XX WO200190156-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
XX  
XX 24-MAY-2000; 2000US-0579240.  
XX 10-OCT-2000; 2000US-0686347.  
XX 14-MAR-2001; 2001US-275980P.  
XX 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURNHAM INST.  
XX  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
XX Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX WPI; 2002-083086/11.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
XX encoding nucleic acids, useful for treating abnormal cell proliferation  
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX arthritis or stroke -  
XX  
XX Example 10; Page 117; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
XX from it, and the polynucleotides encoding them. Also included are a  
XX recombinant vector comprising the polynucleotide, recombinant cells  
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
XX and insect cells) and an anti-CARD antibody. The CARD-containing  
XX polypeptide and CARD-encoding nucleic acid are useful for treating a  
XX pathology characterised by abnormal cell proliferation (e.g. cancer),  
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
XX particular, the polypeptide and nucleic acid are useful for treating  
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
XX muscle cell proliferation in arteries following balloon angioplasty  
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,  
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
XX disease) or immunodeficiency associated disease (e.g. human  
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful  
XX in a variety of diagnostic applications. The present sequence is a  
XX PCR primer used to amplify a nucleic acid encoding a CARD-containing  
XX protein.  
XX  
XX Sequence 30 BP; 11 A; 7 C; 6 G; 6 T; 0 other;  
XX  
XX Query Match 0.7%; Score 21; DB 24; Length 30;  
XX Best Local Similarity 100.0%; Pred. No. 10;  
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 232 TATCCTCTATTTCAGGACTTG 252  
XX ||||||  
XX 30 TATCCTCTATTTCAGGACTTG 10  
XX  
XX



OS Bacillus clausii.  
XX WO200229113-A2.  
PN  
XX  
PD 11-APR-2002.  
XX  
XX 05-OCT-2001; 2001WO-US311437.  
XX  
XX 06-OCT-2000; 2000US-0680598.  
PR 27-MAR-2001; 2001US-279526P.  
XX  
XX (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES AS.  
XX  
XX Berka R, Clausen IG;  
PI  
XX WPI; 2002-416684/44.  
DR  
XX  
XX Monitoring differential expression of several genes in first Bacillus  
PT cell relative to expression of same genes in one or more second  
PT Bacillus cells, by using substrate containing Bacillus genomic  
PT sequenced tag array  
XX  
XX Claim 11; SEQ ID NO 6263; 200pp; English.  
XX  
XX The invention describes a method of monitoring differential expression of  
CC genes in a first Bacillus cell relative to expression of the genes in  
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes  
CC isolated from Bacillus cells to a substrate containing array of Bacillus  
CC genomic sequenced tags (GST), examining the array, and determining  
CC relative gene expression by an observed hybridisation reporter signal of  
CC a spot in the array. The method is useful for measuring the expression of  
CC genes in a first Bacillus cell relative to expression of the same genes  
CC in one or more second Bacillus cells. The method is useful for monitoring  
CC global expression of several genes from a Bacillus cell, discovering new  
CC genes, identifying possible functions of unknown open reading frames and  
CC monitoring gene copy number variation and stability. Monitoring changes  
CC in expression of genes may be used to provide a representation of the way  
CC in which Bacillus cells adapt to changes in culture conditions,  
CC environmental stress or other physiological provocation. Extensive  
CC follow-up characterisation is unnecessary, when one spot on an array  
CC equals one gene or one open reading frame, since sequence information is  
CC available. This sequence represents a genomic sequence tag (GST) used in  
CC the method of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 475 BP; 132 A; 110 C; 144 G; 89 T; 0 other;  
Query Match 0.7%; Score 20; DB 24; Length 475;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1881 TGCAGAGACACACAGGTGGAA 1900  
|||||  
Db 378 TGCAGAGACACACAGGTGGAA 397  
RESULT 50  
ABK22734/c  
ID ABK22734 standard; cDNA; 768 BP.  
XX  
XX AC ABK22734;  
XX  
XX 26-MAR-2002 (first entry)  
DT  
XX Human cDNA encoding CLAN D.  
XX  
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;

KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
XX Homo sapiens.  
XX  
XX WO200190156-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US171158.  
XX  
XX 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURNHAM INST.  
PA  
XX  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX WPI; 2002-083086/11.  
XX p-PSDB; AAU80864.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX  
XX Claim 1; Page 178-179; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
XX SQ Sequence 768 BP; 218 A; 157 C; 180 G; 213 T; 0 other;  
Query Match 0.7%; Score 20; DB 24; Length 768;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2331 AGAAGATGCTATAAACTAG 2350  
|||||  
Db 755 AGAAGATGCTATAAACTAG 736  
Search completed: January 30, 2003, 23:02:21  
Job time : 680 secs





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:45:05 ; Search time 4070 Seconds  
(without alignments)  
12224.210 Million cell updates/sec

Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaattcataaaggacaa.....cttttaactagtaactgct 3072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 12

Total number of hits satisfying chosen parameters: 4061249

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
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4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
c 1	551	17.9	552	17	AQ309404
c 2	446	14.5	480	10	AV719179
c 3	342	11.1	364	9	A1263294
c 4	315	10.3	748	13	BI908869
c 5	291	9.5	371	10	AV656315
c 6	289	9.4	741	13	BI824482
c 7	551	17.9	552	17	AQ309404
c 8	446	14.5	480	10	AV719179
c 9	342	11.1	364	9	A1263294
c 10	315	10.3	748	13	BI908869
c 11	291	9.5	371	10	AV656315
c 12	289	9.4	741	13	BI824482
c 13	551	17.9	552	17	AQ309404
c 14	446	14.5	480	10	AV719179
c 15	342	11.1	364	9	A1263294
c 16	315	10.3	748	13	BI908869
c 17	291	9.5	371	10	AV656315
c 18	289	9.4	741	13	BI824482
c 19	551	17.9	552	17	AQ309404
c 20	446	14.5	480	10	AV719179
c 21	342	11.1	364	9	A1263294
c 22	315	10.3	748	13	BI908869
c 23	291	9.5	371	10	AV656315
c 24	289	9.4	741	13	BI824482
c 25	551	17.9	552	17	AQ309404
c 26	446	14.5	480	10	AV719179
c 27	342	11.1	364	9	A1263294
c 28	315	10.3	748	13	BI908869
c 29	291	9.5	371	10	AV656315
c 30	289	9.4	741	13	BI824482
c 31	551	17.9	552	17	AQ309404
c 32	446	14.5	480	10	AV719179
c 33	342	11.1	364	9	A1263294
c 34	315	10.3	748	13	BI908869
c 35	291	9.5	371	10	AV656315
c 36	289	9.4	741	13	BI824482
c 37	551	17.9	552	17	AQ309404
c 38	446	14.5	480	10	AV719179
c 39	342	11.1	364	9	A1263294
c 40	315	10.3	748	13	BI908869
c 41	291	9.5	371	10	AV656315
c 42	289	9.4	741	13	BI824482
c 43	551	17.9	552	17	AQ309404
c 44	446	14.5	480	10	AV719179
c 45	342	11.1	364	9	A1263294
c 46	315	10.3	748	13	BI908869
c 47	291	9.5	371	10	AV656315
c 48	289	9.4	741	13	BI824482
c 49	551	17.9	552	17	AQ309404
c 50	446	14.5	480	10	AV719179
c 51	342	11.1	364	9	A1263294
c 52	315	10.3	748	13	BI908869
c 53	291	9.5	371	10	AV656315
c 54	289	9.4	741	13	BI824482
c 55	551	17.9	552	17	AQ309404
c 56	446	14.5	480	10	AV719179
c 57	342	11.1	364	9	A1263294
c 58	315	10.3	748	13	BI908869
c 59	291	9.5	371	10	AV656315
c 60	289	9.4	741	13	BI824482
c 61	551	17.9	552	17	AQ309404
c 62	446	14.5	480	10	AV719179
c 63	342	11.1	364	9	A1263294
c 64	315	10.3	748	13	BI908869
c 65	291	9.5	371	10	AV656315
c 66	289	9.4	741	13	BI824482
c 67	551	17.9	552	17	AQ309404
c 68	446	14.5	480	10	AV719179
c 69	342	11.1	364	9	A1263294
c 70	315	10.3	748	13	BI908869
c 71	291	9.5	371	10	AV656315
c 72	289	9.4	741	13	BI824482
c 73	551	17.9	552	17	AQ309404
c 74	446	14.5	480	10	AV719179
c 75	342	11.1	364	9	A1263294
c 76	315	10.3	748	13	BI908869
c 77	291	9.5	371	10	AV656315
c 78	289	9.4	741	13	BI824482
c 79	551	17.9	552	17	AQ309404
c 80	446	14.5	480	10	AV719179
c 81	342	11.1	364	9	A1263294
c 82	315	10.3	748	13	BI908869
c 83	291	9.5	371	10	AV656315
c 84	289	9.4	741	13	BI824482
c 85	551	17.9	552	17	AQ309404
c 86	446	14.5	480	10	AV719179
c 87	342	11.1	364	9	A1263294
c 88	315	10.3	748	13	BI908869
c 89	291	9.5	371	10	AV656315
c 90	289	9.4	741	13	BI824482
c 91	551	17.9	552	17	AQ309404
c 92	446	14.5	480	10	AV719179
c 93	342	11.1	364	9	A1263294
c 94	315	10.3	748	13	BI908869
c 95	291	9.5	371	10	AV656315
c 96	289	9.4	741	13	BI824482
c 97	551	17.9	552	17	AQ309404
c 98	446	14.5	480	10	AV719179
c 99	342	11.1	364	9	A1263294
c 100	315	10.3	748	13	BI908869

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AQ320928 RPT11-93  
BG210375 RST29913  
AQ112439 CIT-HSP-2  
AW418826 ha21ell.x  
AQ624020 HS-5378\_B  
H25984 Y15607.r1  
AI023795 ox08d03.x  
AW283886 RPT11-78  
B58691 CIT-HSP-201  
BF207840 601862546  
AI224422 qh04f06.x  
BH348412 CH230-42F  
BF903662 IL2-MT018  
AQ889169 HS-2161\_B  
B1964738 ie55h09.y  
BF829853 MR3-HN005  
BQ627584 BB627584  
BQ204082 UI-R-DN1-  
BQ894786 AGENCOURT  
AV268403 AV268403  
AZ740007 RPT1-24-1  
BH861125 SALK\_0343  
AZ086396 RPT1-23-2  
AA784099 d1g08a1.f  
AA821339 VS68a01.r  
AI645009 VS68a01.y  
AZ223093 RPT1-23-9  
AQ555443 HS-5224\_A  
AL088892 Arabidops  
AZ360053 IM0103H11  
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B1854236 603381263  
BQ278245 AGENCOURT  
BG571228 602592168  
B1142462 SMOV3MCA8  
BE638399 SMOVL2CAS  
AQ069062 HS-2255\_B  
B1315256 dal96e06.  
AA493806 nh02f04.s  
AI366637 SMOV3MCA8  
AI603832 SMOV3MCA8  
AZ891870 RPT1-24-1  
B8786972 B8786972  
AQ357412 40862 MAR  
AQ952434 Sheared D  
AA670222 ad19h11.s  
AZ991565 2M0275B24  
AA294641 SMOV3MCA8  
AW838955 CM2-LT006  
AA294540 SMOV3MCA7  
T81898 YQ29a11.s1  
AA294143 SMOV3MCA1  
BJ174609 BJ174609  
AQ209355 HS-3240\_A  
AQ209355 2M0275B24  
BF601894 266990 MA  
AI643174 Y646909.y  
BF602580 267845 MA  
BG382487 298398 MA  
AI670486 SMOV3MCA8  
AL027875 Fuqu rubr  
B1394563 p9pln.pk0  
BG351255 088d06 Ma  
AZ221490 Gm\_UMB001  
BQ117309 EST602885  
AZ298434 RPT1-23-1  
B8386778 AG-ND-146  
AQ270247 HS-2045\_A  
BQ059717 BJ059717  
BJ070137 BJ070137  
BF258009 HVSMEF001  
BG385206 306845 MA

80	20	0.7	577	17	AQ570315	HS_5352_B	c 153	19	0.6	426	10	BE116426	BE116426
c 81	20	0.7	580	17	AZ987277	2M0269J15	154	19	0.6	428	12	BG084121	BG084121
82	20	0.7	603	13	BG936533	SS1-0911	c 155	19	0.6	429	10	AV836894	AV836894
c 83	20	0.7	605	12	BG098273	EST462792	156	19	0.6	435	10	AW002562	AW002562
84	20	0.7	605	13	BI537740	427953_MA	157	19	0.6	440	9	AI354218	AI354218
85	20	0.7	606	9	AL675250	AL675250	158	19	0.6	443	17	AQ646808	AQ646808
86	20	0.7	620	17	AZ802117	2M0061H04	c 159	19	0.6	444	17	AQ62794	AQ62794
87	20	0.7	627	9	AI511575	SMOVL3CAN	c 160	19	0.6	447	10	BE504198	BE504198
88	20	0.7	633	17	AZ510047	IM0354H14	c 161	19	0.6	448	10	BE348517	BE348517
89	20	0.7	633	17	BH769908	BMBAC368E	c 162	19	0.6	450	10	BE671155	BE671155
90	20	0.7	642	9	AL678336	AL678336	c 163	19	0.6	457	17	AZ862909	AZ862909
91	20	0.7	644	10	AW874886	SNOWMFCAR	c 164	19	0.6	459	17	AQ469016	AQ469016
92	20	0.7	651	13	BI627371	RH68662.5	c 165	19	0.6	461	17	AZ293884	AZ293884
93	20	0.7	652	10	BE346038	SMOVL2CAS	c 166	19	0.6	462	10	AW176753	AW176753
94	20	0.7	653	9	AI317901	SMOVL3CMAC	c 167	19	0.6	463	10	BB698639	BB698639
95	20	0.7	656	10	BE636495	SMOVL2CAS	c 168	19	0.6	479	14	H18652	H18652
96	20	0.7	660	12	BG310513	SMOVL3CMAC	c 169	19	0.6	483	9	AI988626	AI988626
97	20	0.7	677	17	BH794115	ME_MBA000	c 170	19	0.6	487	13	BJ431712	BJ431712
98	20	0.7	701	13	BJ004970	BJ004970	c 171	19	0.6	490	17	AZ799198	AZ799198
c 99	20	0.7	726	17	AL186746	Tetraodon	c 172	19	0.6	493	17	FR0022665	FR0022665
c 100	20	0.7	729	17	BG5395	CIT-HSP-202	c 173	19	0.6	494	10	AW174122	AW174122
c 101	20	0.7	731	12	BG250425	602362580	c 174	19	0.6	495	17	AZ857381	AZ857381
c 102	20	0.7	738	14	BM970986	UI-CF-EC1	c 175	19	0.6	500	9	AI319748	AI319748
c 103	20	0.7	742	17	AQ083585	Fan trogl	c 176	19	0.6	504	17	AZ650454	AZ650454
c 104	20	0.7	754	17	AQ329189	AG0329189	c 177	19	0.6	504	17	BH308171	BH308171
c 105	20	0.7	760	9	AI591096	tbxb0044F	c 178	19	0.6	505	9	AA956941	AA956941
c 106	20	0.7	760	13	BI918884	603180941	c 179	19	0.6	509	12	BF053859	BF053859
c 107	20	0.7	770	17	BH425589	BH425589	c 180	19	0.6	510	17	AZ159794	AZ159794
c 108	20	0.7	772	12	BG310534	SMOVL3CMAC	c 181	19	0.6	513	10	AW385224	AW385224
109	20	0.7	779	12	BG350988	099C11_Ma	c 182	19	0.6	514	9	AI325989	AI325989
110	20	0.7	783	13	BI184833	SNL-P-FN-	c 183	19	0.6	515	17	AQ204425	AQ204425
111	20	0.7	784	12	BF824698	SMOVL3CMAC	c 184	19	0.6	520	17	AI716507	AI716507
c 112	20	0.7	838	17	BH665093	BOMDY48TF	c 185	19	0.6	520	17	B27212	B27212
c 113	20	0.7	871	14	BO736366	AGENCOURT	c 186	19	0.6	520	17	AQ658864	AQ658864
114	20	0.7	891	12	BG248945	602361385	c 187	19	0.6	524	17	TA156A07Q	TA156A07Q
115	20	0.7	937	17	CNS02507	Tetraodon	c 188	19	0.6	525	10	AV836178	AV836178
c 116	20	0.7	939	17	CNS02105	Tetraodon	c 189	19	0.6	526	17	AZ219239	AZ219239
c 117	20	0.7	1036	12	BG176063	BM547558	c 190	19	0.6	529	17	AZ376550	AZ376550
c 118	20	0.7	1122	13	BM547558	AGENCOURT	c 191	19	0.6	531	10	BB175339	BB175339
c 119	20	0.7	1396	12	BG254706	602368693	c 192	19	0.6	532	9	AL730404	AL730404
c 120	19	0.6	207	10	AV365606	AV365606	c 193	19	0.6	535	17	FR0022682	FR0022682
c 121	19	0.6	209	9	AV144358	AV144358	c 194	19	0.6	538	10	AW659621	AW659621
c 122	19	0.6	238	10	AV371617	AV371617	c 195	19	0.6	539	14	BQ143315	BQ143315
c 123	19	0.6	254	14	BQ332700	RC6-ET006	c 196	19	0.6	543	10	AV605051	AV605051
c 124	19	0.6	256	9	AI340263	q866d01.x	c 197	19	0.6	544	10	BE666200	BE666200
c 125	19	0.6	272	12	BG381720	UI-R-CTO-	c 198	19	0.6	547	12	BE899936	BE899936
126	19	0.6	283	9	AV048726	AV048726	c 199	19	0.6	548	9	AI399038	AI399038
127	19	0.6	296	13	BJ428394	BJ428394	c 200	19	0.6	548	10	BB644885	BB644885
128	19	0.6	299	14	BQ509473	BQ509473	c 201	19	0.6	548	12	BF286023	BF286023
c 129	19	0.6	304	17	AQ094693	AQ094693	c 202	19	0.6	549	9	AI152272	AI152272
c 130	19	0.6	314	17	B62990	HS_3025_B	c 203	19	0.6	557	17	AQ962795	AQ962795
c 131	19	0.6	322	10	BB318669	BB318669	c 204	19	0.6	562	14	BQ561096	BQ561096
c 132	19	0.6	334	17	AQ285454	RPC111-90	c 205	19	0.6	570	14	BQ836529	BQ836529
c 133	19	0.6	350	14	BQ023747	UI-1-BB1p	c 206	19	0.6	571	14	BQ557338	BQ557338
c 134	19	0.6	351	17	AZ748488	RPC1-24-1	c 207	19	0.6	572	10	BE686715	BE686715
c 135	19	0.6	353	10	AW356070	AW356070	c 208	19	0.6	573	13	BI706154	BI706154
c 136	19	0.6	355	14	H88536	YW22902.sl	c 209	19	0.6	573	13	BI807257	BI807257
c 137	19	0.6	360	17	AQ039398	CIT-HSP-2	c 210	19	0.6	576	13	BI807257	BI807257
c 138	19	0.6	362	10	AW435221	UI-R-BJOp	c 211	19	0.6	579	17	BH311536	BH311536
c 139	19	0.6	368	17	AQ663225	HS_5463_B	c 212	19	0.6	580	17	AZ375867	AZ375867
140	19	0.6	369	9	AI082708	ox59f01.s	c 213	19	0.6	582	13	BJ341772	BJ341772
141	19	0.6	369	14	BQ909451	QHAL1D24.	c 214	19	0.6	588	13	BJ340962	BJ340962
c 142	19	0.6	382	10	AW233739	f41c01.x	c 215	19	0.6	591	13	BJ341826	BJ341826
c 143	19	0.6	383	14	N59369	yz87e09.sl	c 216	19	0.6	592	12	BG512024	BG512024
c 144	19	0.6	394	9	AO581814	AO581814	c 217	19	0.6	593	10	BE515396	BE515396
c 145	19	0.6	395	14	W83224	mf23q01.r1	c 218	19	0.6	598	13	BJ527326	BJ527326
c 146	19	0.6	397	14	H05527	yl70f08.sl	c 219	19	0.6	602	17	AQ435526	AQ435526
c 147	19	0.6	403	9	AI239575	q137a01.x	c 220	19	0.6	604	9	AA990951	AA990951
148	19	0.6	405	17	AQ645771	RPC193-EC	c 221	19	0.6	604	12	BE882860	BE882860
149	19	0.6	420	9	AI214067	ap29e06.x	c 222	19	0.6	605	17	FR0030367	FR0030367
c 150	19	0.6	422	14	R44768	YG23a04.sl	c 223	19	0.6	606	17	FR0030366	FR0030366
c 151	19	0.6	423	10	AW104704	xd44f06.x	c 224	19	0.6	609	13	BJ436302	BJ436302
152	19	0.6	423	14	H03699	yJ42e12.sl	c 225	19	0.6	612	12	BF519289	BF519289

c 226	19	0.6	614	14	BM890031	BM890031 fy64b04.y	299	19	0.6	896	17	BM135630	BM135630
c 227	19	0.6	615	13	BQ372342	BQ372342	c 300	19	0.6	898	17	AN935650	AN935650 ODG148 OI
c 228	19	0.6	616	17	AQ473825	AQ473825 CITBI-E1-	c 301	19	0.6	906	17	AL301591	Tetraodon
c 229	19	0.6	619	17	BH267158	BH267158 CH230-19B	c 302	19	0.6	909	14	BQ922514	AGENCOURT
c 230	19	0.6	621	17	AZ216149	AZ216149 Sheared D	c 303	19	0.6	929	17	CNS03RWG	AL257785 Tetraodon
c 231	19	0.6	625	10	BB626089	BB626089	c 304	19	0.6	937	17	BH151493	ENTQD75TF
c 232	19	0.6	628	17	AZ213893	AZ213893 Sheared D	c 305	19	0.6	956	12	BF233114	602023855
c 233	19	0.6	628	14	BQ625451	BQ625451 rdl5b11.y	c 306	19	0.6	962	14	BQ876117	AGENCOURT
c 234	19	0.6	629	13	BM120821	BM120821 L0944E07-	c 307	19	0.6	967	14	BQ226680	AGENCOURT
c 235	19	0.6	631	17	AZ941662	AZ941662 2M0201E02	c 308	19	0.6	982	14	BQ434528	AGENCOURT
c 236	19	0.6	641	10	BB604577	BB604577	c 309	19	0.6	1032	17	CNS03313	AL226164 Tetraodon
c 237	19	0.6	641	17	BE41128	BE41128 CIT-HSP-202	c 310	19	0.6	1051	12	BE274184	GA_EB002
c 238	19	0.6	646	17	AZ409793	AZ409793 LM0181C09	c 311	19	0.6	1066	12	BE887837	601511220
c 239	19	0.6	646	17	BH532779	BH532779 BOHNJ47TR	c 312	19	0.6	1079	17	CNS02J25	AL119670 Tetraodon
c 240	19	0.6	649	12	BG263181	BG263181 WHE2339.A	c 313	19	0.6	1080	17	CNS03DMX	AL332610 Tetraodon
c 241	19	0.6	651	12	BF917483	BF917483 IL3-UT011	c 314	19	0.6	1110	14	BM925342	BM925342 AGENCOURT
c 242	19	0.6	658	12	BG906258	BG906258 TALr1147H	c 315	19	0.6	1111	14	BQ720307	BM920307 AGENCOURT
c 243	19	0.6	664	13	BI271403	BI271403 NF050G10F	c 316	19	0.6	1152	14	BQ952091	AGENCOURT
c 244	19	0.6	665	14	BQ115180	BQ115180 EST600756	c 317	19	0.6	1162	17	CNS0450K	Tetraodon
c 245	19	0.6	667	10	BE387377	BE387377 601274417	c 318	19	0.6	1208	11	AK013250	Mus muscu
c 246	19	0.6	668	17	AZ273926	AZ273926 RPCI-23-1	c 319	0.6	1259	13	BI857106	BI857106 603383691	
c 247	19	0.6	669	17	AQ377545	AQ377545 RPCI11-14	c 320	19	0.6	1426	12	BG388238	602413232
c 248	19	0.6	671	17	AZ590971	AZ590971 LM0400P15	c 321	19	0.6	1658	12	BF346046	602018778
c 249	19	0.6	672	10	BB644884	BB644884	c 322	18	0.6	1117	12	BF885931	BF885931 PM3-TN010
c 250	19	0.6	674	14	BQ295048	BQ295048 WHE2857_F	c 323	18	0.6	117	17	BH407881	100705160
c 251	19	0.6	681	9	AI425341	AI425341 mf23q01.y	c 324	18	0.6	121	13	BM661260	952046C05
c 252	19	0.6	683	12	BG170358	BG170358 60233261	c 325	18	0.6	126	13	BI924452	EST544341
c 253	19	0.6	692	13	BJ017593	BJ017593	c 326	18	0.6	133	12	BF153251	BF153251 002D05 Ma
c 254	19	0.6	695	17	BH090963	BH090963 RPCI-24-2	c 327	18	0.6	148	10	AV388298	AV388298
c 255	19	0.6	697	17	AG168094	AG168094 Pan trogl	c 328	18	0.6	152	14	H40912	H40912 YO05004.s1
c 256	19	0.6	699	17	BH652451	BH652451 BOMBW90TF	c 329	18	0.6	162	10	AW096296	EST289476
c 257	19	0.6	701	17	BH032664	BH032664 RPCI-24-2	c 330	18	0.6	168	14	BQ286227	1k27e04.y
c 258	19	0.6	706	13	BJ023107	BJ023107	c 331	18	0.6	175	12	BG041172	BG041172 sv30e09.y
c 259	19	0.6	707	14	BQ864276	BQ864276 QG226E07.	c 332	18	0.6	180	17	AQ318179	RPCI111-97
c 260	19	0.6	708	13	BJ342238	BJ342238	c 333	18	0.6	181	12	BF062689	BF062689 7h64a04.x
c 261	19	0.6	709	9	AU075934	AU075934	c 334	18	0.6	182	12	BF070338	BF070338 st17f10.y
c 262	19	0.6	709	17	BH538954	BH538954 BOGIC42TF	c 335	18	0.6	184	14	W09743	W09743 ma56b06.r1
c 263	19	0.6	711	17	AG179888	AG179888 Pan trogl	c 336	18	0.6	185	17	BH314482	BH314482 CH230-52F
c 264	19	0.6	717	14	BQ865213	BQ865213 QGC2b11.y	c 337	18	0.6	186	17	TA92H01P	AL458772 T. brucei
c 265	19	0.6	719	12	BG701546	BG701546 602682794	c 338	18	0.6	187	17	AZ066340	RPCI-23-3
c 266	19	0.6	722	17	CNS02934	AL186745 Tetraodon	c 339	18	0.6	188	9	AV282016	AV282016 AV282016
c 267	19	0.6	723	13	BQ201505	BJ021505 BJ021505	c 340	18	0.6	190	13	BI230117	BI230117 GM15358.5
c 268	19	0.6	728	17	AZ720059	AZ720059 RPCI-24-8	c 341	18	0.6	191	17	AZ135773	AZ135773 BBS343Sp6
c 269	19	0.6	736	14	BQ990517	BQ990517 QGF20G06.	c 342	18	0.6	194	9	AV272497	AV272497 AV272497
c 270	19	0.6	743	10	AV700456	AV700456	c 343	18	0.6	194	13	BI212163	BI212163 RE17188.5
c 271	19	0.6	744	17	AQ268111	AQ268111 RPCI111-75	c 344	18	0.6	194	14	BQ102780	UUGC0167
c 272	19	0.6	745	14	BQ858470	BQ858470 QGC10F08.	c 345	18	0.6	196	14	BQ517490	BQ517490 EST624905
c 273	19	0.6	748	17	AQ688715	AQ688715 nbxb0078M	c 346	18	0.6	201	9	AA802323	AA802323 GM04203.5
c 274	19	0.6	750	13	BI177675	BI177675 EST518620	c 347	18	0.6	201	9	AI489897	EST248236
c 275	19	0.6	751	17	BH378950	BH378950 AG-ND-166	c 348	18	0.6	201	12	BE832522	CM3-MT011
c 276	19	0.6	756	17	AQ629359	AQ629359 RPCI-11-4	c 349	18	0.6	202	9	AA596746	AA596746 GM08323.5
c 277	19	0.6	759	17	AQ157206	AQ157206 nbxb0009I	c 350	18	0.6	205	9	AV284408	AV284408 AV284408
c 278	19	0.6	762	17	BH291495	BH291495 CH230-43P	c 351	18	0.6	206	12	BG636401	BG636401 SD4107.5
c 279	19	0.6	763	17	AQ326033	AQ326033 nbxb0024B	c 352	18	0.6	207	9	AV044609	AV044609 AV044609
c 280	19	0.6	767	13	BJ533906	BJ533906	c 353	18	0.6	207	13	BI610920	RH16938.5
c 281	19	0.6	775	14	BQ441308	BQ441308 AGENCOURT	c 354	18	0.6	208	12	BG099514	naq53b03.
c 282	19	0.6	786	17	AQ896016	AQ896016 HS_3072_B	c 355	18	0.6	208	12	BG099514	naq53b03.
c 283	19	0.6	792	17	BH525620	BH525620 BOGWX15TF	c 356	18	0.6	209	13	BI618208	RH48803.5
c 284	19	0.6	797	12	BG645081	BG645081 BOGWX15TF	c 357	18	0.6	212	12	BG642336	BG642336 SD4 Dros
c 285	19	0.6	804	12	BG749315	BG749315 603707966	c 358	18	0.6	213	9	AA419572	AA419572 zv03f07.r
c 286	19	0.6	809	17	AQ579476	AQ579476 nbxb0084B	c 359	18	0.6	215	13	BI588207	BI588207 RH29333.5
c 287	19	0.6	811	17	BH453059	BH453059 BOGV054TF	c 360	18	0.6	216	9	AI252945	AI252945 qv44h11.x
c 288	19	0.6	817	17	BH358172	BH358172 CH230-18E	c 361	18	0.6	216	10	AW086259	AW086259 KC70h02.x
c 289	19	0.6	822	17	AQ780828	AQ780828 HS_3104_B	c 362	18	0.6	216	10	BB545041	BB545041
c 290	19	0.6	834	12	BG368974	BG368974 HVSM1002	c 363	18	0.6	218	10	BE043197	BE043197 hk36e02.y
c 291	19	0.6	852	17	AZ754120	AZ754120 RPCI-24-1	c 364	18	0.6	219	13	BI573417	RH09057.5
c 292	19	0.6	854	17	AZ907362	AZ907362 RPCI-24-1	c 365	18	0.6	227	13	BI165019	BI165019 RE04818.5
c 293	19	0.6	857	17	CNS02UQB	AL214796 Tetraodon	c 366	18	0.6	228	10	BB019888	BB019888
c 294	19	0.6	862	17	CNS01ZLU	AL174459 Tetraodon	c 367	18	0.6	232	9	AL826520	AL826520 AL826520
c 295	19	0.6	872	17	AZ545701	AZ545701 ENTQ07TR	c 368	18	0.6	232	13	BI167680	RE08115.5
c 296	19	0.6	875	17	BH149586	BH149586 ENTQ023TF	c 369	18	0.6	233	9	AI345461	tb82e11.x
c 297	19	0.6	881	14	BQ930451	BQ930451 AGENCOURT	c 370	18	0.6	234	10	AV351508	AV351508
c 298	19	0.6	887	17	AZ532663	AZ532663 ENTBR74TR	c 371	18	0.6	235	9	AI345162	AI345162 tb80f10.x

372	18	0.6	235	10	BB068074	BB068074	BB068074	445	18	0.6	294	14	BQ102718	BQ102718	UUGC0102
373	18	0.6	237	10	AV347121	AV347121	AV347121	c 446	18	0.6	295	9	AA264935	AA264935	LD08560.5
374	18	0.6	237	17	AZ908204	RPCI-24-1	AZ908204	447	18	0.6	295	10	AV389602	AV389602	AV389602
375	18	0.6	241	10	BB563250	BB563250	BB563250	448	18	0.6	295	10	BB344311	BB344311	BB344311
376	18	0.6	242	9	AA032254	zk19h02.s	AA032254	c 449	18	0.6	295	13	BI573799	BI573799	RH09310.5
377	18	0.6	242	9	AI088395	qb1ic07.x	AI088395	c 450	18	0.6	296	10	AV910298	AV910298	AV910298
378	18	0.6	242	10	BB147654	BB147654	BB147654	c 451	18	0.6	298	9	AI032198	AI032198	or96e05.s
379	18	0.6	242	13	BI591860	RH07660.5	BI591860	c 452	18	0.6	298	13	BI358623	BI358623	GM27656.5
380	18	0.6	243	9	AV281427	AV281427	AV281427	c 453	18	0.6	299	10	BB190128	BB190128	BB190128
381	18	0.6	243	9	AA385910	EST99612	AA385910	c 454	18	0.6	301	14	HA9838	HA9838	yo24a09.s1
382	18	0.6	243	13	BI929718	EST549607	BI929718	c 455	18	0.6	302	13	BI634070	BI634070	SD27508.5
383	18	0.6	245	17	BH141519	TGDE69FH	BH141519	c 456	18	0.6	303	9	AI461872	AI461872	vw58f08.x
384	18	0.6	245	17	BH141801	TGDRH81FH	BH141801	c 457	18	0.6	303	9	AI164652	AI164652	AV164652
385	18	0.6	246	10	BE139683	xf71c09.x	BE139683	c 458	18	0.6	305	9	AI378775	AI378775	tc18h11.x
386	18	0.6	247	10	AV377125	AV377125	AV377125	c 459	18	0.6	305	12	BE935084	BE935084	PM4-MT010
387	18	0.6	249	10	BI170120	BB170120	BI170120	c 460	18	0.6	306	9	AA573480	AA573480	nm53q07.s
388	18	0.6	249	9	AI337698	qw86g04.x	AI337698	c 461	18	0.6	307	12	BF773497	BF773497	CM2-TT003
389	18	0.6	250	9	AV275662	AV275662	AV275662	c 462	18	0.6	308	9	AA264799	AA264799	LD08568.5
390	18	0.6	250	12	BG635500	SD12930.5	BG635500	c 463	18	0.6	309	10	AW836698	AW836698	QVI-LT003
391	18	0.6	251	9	AI345606	tb83e07.x	AI345606	c 464	18	0.6	309	17	AZ289805	AZ289805	RPCI-23-1
392	18	0.6	253	9	AI129848	AI129848	AI129848	c 465	18	0.6	310	13	BI584889	BI584889	RH24192.5
393	18	0.6	253	12	BF094446	BF094446	BF094446	c 466	18	0.6	312	13	BI641998	BI641998	SD20911.5
394	18	0.6	254	9	AL829350	AL829350	AL829350	c 467	18	0.6	312	17	AQ653919	AQ653919	Sheared D
395	18	0.6	255	9	AA033624	AA033624	AA033624	c 468	18	0.6	313	13	BI584801	BI584801	RH24082.5
396	18	0.6	255	10	AW268081	AW268081	AW268081	c 469	18	0.6	313	9	AA802281	AA802281	GM04133.5
397	18	0.6	255	12	BG358335	SD13334.5	BG358335	c 470	18	0.6	315	13	BI573058	BI573058	RH08751.5
398	18	0.6	255	13	BI611990	RH13257.5	BI611990	c 471	18	0.6	318	9	AL801032	AL801032	AL801032
399	18	0.6	257	12	BG096433	EST460952	BG096433	c 472	18	0.6	318	10	BE580906	BE580906	kp82h11.y
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401	18	0.6	259	9	AV039539	AV039539	AV039539	c 474	18	0.6	318	14	R34823	R34823	yh87h01.r1
402	18	0.6	260	17	AQ007535	AQ007535	AQ007535	c 475	18	0.6	321	17	AZ637772	AZ637772	LM0497P13
403	18	0.6	261	12	BG201929	RST21275	BG201929	c 476	18	0.6	322	13	BM136658	BM136658	WHE2615.F
404	18	0.6	261	17	AQ18504	AQ18504	AQ18504	c 477	18	0.6	327	13	AZ876003	AZ876003	2M0190P14
405	18	0.6	262	12	BG186550	RST5517.A	BG186550	c 478	18	0.6	337	13	BI072613	BI072613	C079P82U
406	18	0.6	262	13	BI634061	BI634061	BI634061	c 479	18	0.6	338	10	AW135716	AW135716	UI-H-B11-
407	18	0.6	264	9	AV237033	SD26425.5	AV237033	c 480	18	0.6	338	10	BE463993	BE463993	hy19406.x
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409	18	0.6	267	12	BF883299	QV3-ET020	BF883299	c 482	18	0.6	339	12	BG095557	BG095557	mac29b05.
410	18	0.6	268	10	BB055603	BB055603	BB055603	c 483	18	0.6	330	12	BE923694	BE923694	EST427463
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412	18	0.6	269	9	AI387652	GH18233.5	AI387652	c 485	18	0.6	330	17	AZ135757	AZ135757	bbs343Sp6
413	18	0.6	269	9	AA614253	np09h01.s	AA614253	c 486	18	0.6	331	13	BI584107	BI584107	RH22889.5
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416	18	0.6	271	13	BJ367810	BJ367810	BJ367810	c 489	18	0.6	333	9	AA699714	AA699714	z140f08.s
417	18	0.6	272	9	AV085453	AV085453	AV085453	c 490	18	0.6	333	13	BG941635	BG941635	ax15e01.x
418	18	0.6	272	10	AV389753	AV389753	AV389753	c 491	18	0.6	334	9	AI899683	AI899683	EST269126
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422	18	0.6	275	9	AV043383	AV043383	AV043383	c 495	18	0.6	336	9	AA391169	AA391169	LD09245.5
423	18	0.6	276	10	AW844415	RC2-CN005	AW844415	c 496	18	0.6	336	13	BI434682	BI434682	EST537443
424	18	0.6	276	13	BJ368140	BJ368140	BJ368140	c 497	18	0.6	338	9	AI432219	AI432219	th43a12.x
425	18	0.6	277	9	AV135656	AV135656	AV135656	c 498	18	0.6	339	17	AZ015723	AZ015723	RPCI-23-3
426	18	0.6	277	12	BG217734	RST37448	BG217734	c 499	18	0.6	340	10	AV389501	AV389501	AV389501
427	18	0.6	277	12	BF228702	EST00413	BF228702	c 500	18	0.6	340	12	BE816931	BE816931	RC2-BN024
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430	18	0.6	284	10	AV410655	AV410655	AV410655	c 503	18	0.6	344	12	BF719135	BF719135	meb33a12.
431	18	0.6	284	10	AV633039	AV633039	AV633039	c 504	18	0.6	344	13	BI476125	BI476125	fp52e06.y
432	18	0.6	284	10	AW072172	wz99b10.x	AW072172	c 505	18	0.6	345	14	U46399	U46399	HSU46399.Hu
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434	18	0.6	285	9	AV137197	AV137197	AV137197	c 507	18	0.6	350	12	BG630568	BG630568	cc-esflcL
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436	18	0.6	288	10	BB010023	BB010023	BB010023	c 509	18	0.6	354	10	AV655290	AV655290	AV655290
437	18	0.6	289	10	AV390026	AV390026	AV390026	c 510	18	0.6	356	17	AZ906192	AZ906192	RPCI-24-1
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439	18	0.6	289	10	BE678221	df84c06.x	BE678221	c 512	18	0.6	359	9	AI198996	AI198996	q145h12.x
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443	18	0.6	293	10	AV389491	AV389491	AV389491	c 516	18	0.6	361	14	R87705	R87705	yo44e09.s1
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665	18	0.6	413	10	BB790231	BB790231	BB790231	BB790231	18	0.6	431	14	H21827	H21827 yn78a09.s1
666	18	0.6	413	13	BI614289	BI614289	BI614289	BI614289	18	0.6	432	9	AI010212	AI010212 EST204663
667	18	0.6	414	9	AA926759	AA926759	AA926759	AA926759	18	0.6	432	10	AW661736	AW661736 h180b05.x
668	18	0.6	414	9	AI469498	AI469498	AI469498	AI469498	18	0.6	432	13	BI164246	BI164246 h03882.5
669	18	0.6	414	10	AV638557	AV638557	AV638557	AV638557	18	0.6	433	9	AA821014	AA821014 GM05408.5
670	18	0.6	414	10	AV934315	AV934315	AV934315	AV934315	18	0.6	433	9	AA573027	AA573027 nm42c03.s
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672	18	0.6	415	9	AI486464	AI486464	AI486464	AI486464	18	0.6	433	10	AW368131	AW368131 CM1-HT017
673	18	0.6	415	9	AA508379	AA508379	AA508379	AA508379	18	0.6	433	13	BI593626	BI593626 RH04434.5
674	18	0.6	415	12	BF662236	BF662236	BF662236	BF662236	18	0.6	433	14	H08408	H08408 Y192d09.s1
675	18	0.6	415	13	BI576125	BI576125	BI576125	BI576125	18	0.6	434	10	AW368113	AW368113 CM0-HT018
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678	18	0.6	416	17	AZ740668	AZ740668	AZ740668	AZ740668	18	0.6	435	9	AI242421	AI242421 q136e05.x
679	18	0.6	417	14	BQ464646	BQ464646	BQ464646	BQ464646	18	0.6	435	10	AV630299	AV630299 AV630299
680	18	0.6	417	10	AA803104	AA803104	AA803104	AA803104	18	0.6	435	10	AW368135	AW368135 CM1-HT017
681	18	0.6	418	9	AI050796	AI050796	AI050796	AI050796	18	0.6	435	10	BE556236	BE556236 sp99c01.y
682	18	0.6	418	9	AI468411	AI468411	AI468411	AI468411	18	0.6	435	14	W45427	W45427 zc83a05.s1
683	18	0.6	418	10	AW217349	AW217349	AW217349	AW217349	18	0.6	435	17	AZ159174	AZ159174 SP_0062.A
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685	18	0.6	419	9	AA808249	AA808249	AA808249	AA808249	18	0.6	436	10	BE552218	BE552218 hy04f01.x
686	18	0.6	419	10	BE691792	BE691792	BE691792	BE691792	18	0.6	436	10	BE634358	BE634358 uv66g02.y
687	18	0.6	419	14	W60356	W60356	W60356	W60356	18	0.6	437	13	BI778889	BI778889 EBR001.SQ
688	18	0.6	420	9	AI743438	AI743438	AI743438	AI743438	18	0.6	437	17	AQ386609	AQ386609 RPC111-14
689	18	0.6	420	10	BB784900	BB784900	BB784900	BB784900	18	0.6	438	17	AQ464184	AQ464184 HS_5098.A
690	18	0.6	420	12	BF877469	BF877469	BF877469	BF877469	18	0.6	439	9	AA696495	AA696495 GM07782.5
691	18	0.6	420	17	B79236	B79236	B79236	B79236	18	0.6	439	9	AI093465	AI093465 qb08d09.x
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REFERENCE 1 (bases 1 to 552)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Map Building
COMMENT Unpublished (1998)
Other GSSs: CITBI-EI-2528J13.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
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end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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DB 372 GTGTGAAAAACACACCTGAGCAGCAAGAAATCTGAAAGCCATAAATCAATCTTTGTAG 313
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QY 1667 AGTGTGSCATCCATTTATATCAAGAGAGTATCATCAAAATCAGCCCTGAGCCAAAGAAATTTG 1726
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DB 312 AGTGTGSCATCCATTTATATCAAGAGAGTATCATCAAAATCAGCCCTGAGCCAAAGAAATTTG 253
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QY 1727 AAGCTTTCTTCAAGGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTAT 1786
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DB 252 AAGCTTTCTTCAAGGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTAT 193
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QY 1787 TTGACTTCTTTGAACATTTGCCCAATTTGCAAGTGTCTGGACTTCATTAAACTGGACT 1846
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DB 192 TTGACTTCTTTGAACATTTGCCCAATTTGCAAGTGTCTGGACTTCATTAAACTGGACT 133
|||||
QY 1847 TTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAAATCCACA 1906
|||||
DB 132 TTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAAATCCACA 73
|||||
QY 1907 TGGAGAGGGCCCCAAGAACCTACATTTCCAGCAGGGCTGTATCTTTTCTTCAACTGGA 1966
|||||
DB 72 TGGAGAGGGCCCCAAGAACCTACATTTCCAGCAGGGCTGTATCTTTTCTTCAACTGGA 13
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QY 1967 AGCAGGAATTC 1977
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DB 12 AGCAGGAATTC 2
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RESULT 2
AV719179/c
LOCUS AV719179
DEFINITION AV719179 GLC Homo sapiens cDNA clone G1CEQA10 5', mRNA sequence.
ACCESSION AV719179
VERSION AV719179.1 GI:10816331
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KEYWORDS      EST.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               Qian,B., Wu,T., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,
               , Xu,X., Li,N., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,
               Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang
               , Y., Gu,Y., Chen,Z. and Han,Z.
TITLE          Homo sapiens cDNA GLC clones
JOURNAL        Unpublished (2000)
COMMENT        Contact: Zeguang Han
               Chinese National Human Genome Center at Shanghai
               351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
               201203, P. R. China
               Tel: 86-21-50801919(ex.45)
               Fax: 86-21-50801922
               Email: hanzgehc.sh.cn
               This clone is available at CHGC in Shanghai.
FEATURES       Location/Qualifiers
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               /db_xref="taxon:9606"
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               /clone_lib="GLC"
               /tissue_type="corresponding non cancerous liver tissue"
               /dev_stage="Adult"
               /lab_host="SOLR"
               /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
               XhoI"
BASE COUNT    138 a 120 c 85 g 137 t
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Query Match      14.5%; Score 446; DB 10; Length 480;
Best Local Similarity 100.0%; Pred. No. 4e-214;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2605 CATGAAGTATGACAGAGTGAACGCTGCTAGAACAGCTCACGCACTGATGCTGCCCTGG 2664
Db 480 CATGAAGTATGACAGAGTGAACGCTGCTAGAACAGCTCACGCACTGATGCTGCCCTGG 421
QY 2665 GCGTGTGACGTGAAGCGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCACAA 2724
Db 420 GCGTGTGACGTGAAGCGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCACAA 361
QY 2725 CTCGTCAAGCTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGATTAGT 2784
Db 360 CTCGTCAAGCTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGATTAGT 301
QY 2785 GCATTTTTTGGAAAGAACCCCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGGAATCGT 2844
Db 300 GCATTTTTTGGAAAGAACCCCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGGAATCGT 241
QY 2845 GTGAGCAGTGTGATGGCTTGCCTTCATPGGGTGATTTGAGAATCTTTAAGCAATTTAGTG 2904
Db 240 GTGAGCAGTGTGATGGCTTGCCTTCATPGGGTGATTTGAGAATCTTTAAGCAATTTAGTG 181
QY 2905 TTTTGTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAAACCTAGC 2964
Db 180 TTTTGTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAAACCTAGC 121
QY 2965 CAAGTGTATCAAGTTAACTTTCTTCGCAAGAGCTAGGCTTGTGGGTGGCAATTTGAT 3024
Db 120 CAAGTGTATCAAGTTAACTTTCTTCGCAAGAGAGCTAGGCTTGTGGGTGGCAATTTGAT 61
QY 3025 GATGATGATCTCAGTGTATTATACAGG 3050
Db 60 GATGATGATCTCAGTGTATTATACAGG 35
RESULT 3
AI263294/c

LOCUS      AI263294      364 bp      mRNA      linear      EST 03-FEB-1999
DEFINITION qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',
            mRNA sequence..
ACCESSION  AI263294
VERSION    AI263294.1  GI:3871497
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 364)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
COMMENT    Life Technologies catalog #: 11548-013
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/dbrrp/image/image.html
            Insert Length: 2146 Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 364.
FEATURES   Location/Qualifiers
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               /db_xref="taxon:9606"
               /clone="IMAGE:2005417"
               /clone_lib="NCI_CGAP_Pan1"
               /tissue_type="adenocarcinoma"
               /lab_host="DH10B"
               /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
               Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.72 kb. Life Technologies catalog #:
               11548-013"
BASE COUNT  117 a 84 c 55 g 108 t
ORIGIN
Query Match      11.1%; Score 342; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2731 AAGCTTGGTGTGAAAACCTGGAGACTCACAGATACAGAGATTAGAATTTAGTGCATTT 2790
Db 364 AAGCTTGGTGTGAAAACCTGGAGACTCACAGATACAGAGATTAGAATTTAGTGCATTT 305
QY 2791 TTTGGAAGAACCCCTCTGAAAACCTTCCAGCAGTTGAAATTTGGCGGGAATCGTGTGAGC 2850
Db 304 TTTGGAAGAACCCCTCTGAAAACCTTCCAGCAGTTGAAATTTGGCGGGAATCGTGTGAGC 245
QY 2851 AGTGATGGATGGCTTGCCTTCATGGGTGATTTTGAGAACTTTAAGCAATTTAGTGTTTT 2910
Db 244 AGTGATGGATGGCTTGCCTTCATGGGTGATTTTGAGAACTTTAAGCAATTTAGTGTTTT 185
QY 2911 GACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAAACCTTACCAAGTG 2970
Db 184 GACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAAACCTTACCAAGTG 135
QY 2971 TTATCCAAAGTTAACTTTCTTCGCAAGAGCTAGGCTTGTGGGTGGCAATTTGATGATGAT 3030
Db 124 TTATCCAAAGTTAACTTTCTTCGCAAGAGCTAGGCTTGTGGGTGGCAATTTGATGATGAT 65
QY 3031 GATCTCAGTGTATTATCAGGTGCTTTTAACTAGTAACTGCT 3072
Db 64 GATCTCAGTGTATTATCAGGTGCTTTTAACTAGTAACTGCT 23
RESULT 4
BI908869
LOCUS      BI908869      748 bp      mRNA      linear      EST 16-OCT-2001
DEFINITION 603066455F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215669 5',
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mRNA sequence.
ACCESSION BI908869
VERSION BI908869.1 GI:16171950
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: L14M11541 row: m column: 14
High quality sequence start: 7
High quality sequence stop: 744.
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/db_xref="taxon:9606"
/clone="IMAGE:5215669"
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/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 Kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT 236 a 148 c 166 g 198 t
ORIGIN
Query Match 10.3%; Score 315; DB 13; Length 748;
Best Local Similarity 100.0%; Pred. No. 1.1e-147;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTCATTAAGGACATAGCCGAGCCCTTATTCAGAAATGGGAATGACTGTTATA 60
DB 252 ATGAATTCATTAAGGACATAGCCGAGCCCTTATTCAGAAATGGGAATGACTGTTATA 311
QY 61 AAGCAATACAGATGACCTATTTGTATGGAATGCTCTAGATCGGAGAGTAACATC 120
DB 312 AAGCAATACAGATGACCTATTTGTATGGAATGCTCTAGATCGGAGAGTAACATC 371
QY 121 ATTTGCTCGGAGAGGCGGAGCAGGATGCTCTAGAGGATCATTCATGATTTTGA 180
DB 372 ATTTGCTCGGAGAGGCGGAGCAGGATGCTCTAGAGGATCATTCATGATTTTGA 431
QY 181 AAGGGTTCAGAGTCTCTTAACCTCTTTTAAATCCCTTAAGGAGTGAACATCCTCTA 240
DB 432 AAGGGTTCAGAGTCTCTTAACCTCTTTTAAATCCCTTAAGGAGTGAACATCCTCTA 491
QY 241 TTTGAGACTTGAATGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTCGAGCAT 300
DB 492 TTTGAGACTTGAATGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTCGAGCAT 551
QY 301 TTGCTCAGGATTTA 315
DB 552 TTGCTCAGGATTTA 566
us-09-697-089-3.olil2.rst
RESULT 5
AV656315 371 bp mRNA linear EST 16-JAN-2002
LOCUS AV656315 GLC Homo sapiens cDNA clone GLCEQA10 3', mRNA sequence.
DEFINITION AV656315
ACCESSION AV656315
VERSION AV656315.1 GI:9877329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
INSIGHT into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCEQA10"
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/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 112 a 85 c 91 g 82 t 1 others
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Query Match 9.5%; Score 291; DB 10; Length 371;
Best Local Similarity 99.7%; Pred. No. 1.2e-135;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 GAAAGGCTCGAAGACACAGGTGGATCCACATGGAGAGGCCCCAGAAACCTACATT 60
QY 1933 CCCAGCAGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGAGGTC 1992
DB 61 CCCAGCAGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGAGGTC 120
QY 1993 ACATCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTGGGAAAATATTC 2052
DB 121 ACATCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTGGGAAAATATTC 180
QY 2053 AGCTCTGCCACACGCCCTCAGGCTGCAATAAAGAGATGTGCTGTGTGGCTGGAAGCCTC 2112
DB 181 AGCTCTGCCACACGCCCTCAGGCTGCAATAAAGAGATGTGCTGTGTGGCTGGAAGCCTC 240
QY 2113 AGTTTGTCTCTCAGCAGCTGTGAAGAACATTTATTTCTCTCATGTGGAGCCAGTCCCTC 2172
DB 241 AGTTTGTCTCTCAGCAGCTGTGAAGAACATTTATTTCTCTCATGTGGAGCCAGTCCCTC 300
QY 2173 ACCATAGAAGATGAGAGGCACATCATCATCTGTGTAAACAAACCTG 2214
DB 301 ACCATAGAAGATGAGAGGCACATCATCATCTGTGTAAACAAACCTG 342
RESULT 6
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BI824482  
LOCUS 603038854F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5179909 5',  
DEFINITION mRNA sequence.  
ACCESSION BI824482  
VERSION BI824482.1 GI:15936032  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 741)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1448 row: k column: 14  
High quality sequence start: 3  
High quality sequence stop: 705.  
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/clone.lib="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/note="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."  
BASE COUNT 233 a 147 c 164 g 197 t  
ORIGIN  
Query Match 9.4%; Score 289; DB 13; Length 741;  
Best Local Similarity 100.0%; Pred. No. 1.6e-134;  
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 AGCCCTTATCAAGAAATGGGAATGACTGTTTATAAGCAAAATCACAGATGACCTATTGCT 86  
DB 256 AGCCCTTATCAAGAAATGGGAATGACTGTTTATAAGCAAAATCACAGATGACCTATTGCT 315  
QY 87 ATGGAAATGTTCTGAATCGCGAAGAGTAACATCATTTCTCGGAGAAGGTGGAGCAGGA 146  
DB 316 ATGGAAATGTTCTGAATCGCGAAGAGTAACATCATTTCTCGGAGAAGGTGGAGCAGGA 375  
QY 147 TGCTGCTAGAGGATCATTCACATGATTTTGAAGAAGGGTTCAGAGTCCCTGTAACCTCTT 206  
DB 376 TGCTGCTAGAGGATCATTCACATGATTTTGAAGAAGGGTTCAGAGTCCCTGTAACCTCTT 435  
QY 207 TCTTAAATCCCTTAGGAGTGAACATATCTCTATTTTCAGGACTTGAATGGACAAGTCT 266  
DB 436 TCTTAAATCCCTTAGGAGTGAACATATCTCTATTTTCAGGACTTGAATGGACAAGTCT 495  
QY 267 TTTTCATCAGACATCAGAGGAGAGCTTGGACGATTTGGCTCAGGATTTTA 315  
DB 496 TTTTCATCAGACATCAGAGGAGAGCTTGGACGATTTGGCTCAGGATTTTA 544  
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AW337918/c  
LOCUS AW337918 261 bp mRNA linear EST 31-JAN-2000  
DEFINITION he12h11.x1 NCI\_CGAP\_CML1 Homo sapiens cDNA clone IMAGE:2918853 3',  
mRNA sequence.  
ACCESSION AW337918  
VERSION AW337918.1 GI:6834544  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 261)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,  
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life  
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbrrp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 201.  
Location/Qualifiers  
1..261  
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/lab\_host="DH10B"  
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SalI; Site\_2: NotI; Cloned unidirectionally. Primer:  
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Query Match 7.3%; Score 223; DB 10; Length 261;  
Best Local Similarity 100.0%; Pred. No. 3.1e-101;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2850 CAGTGATGATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAGTGTGTTT 2909  
DB 261 CAGTGATGATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAGTGTGTTT 202  
QY 2910 TGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTTAGTCAGAAAACTTAGCCAACT 2969  
DB 201 TGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTTAGTCAGAAAACTTAGCCAACT 142  
QY 2970 GTATCCAGTTAACTTTTCTCGAAGAACTAGGCTTTGGTGGCAATTTGATGATCA 3029  
DB 141 GTATCCAGTTAACTTTTCTCGAAGAACTAGGCTTTGGTGGCAATTTGATGATCA 82  
QY 3030 TGATCTCAGTGTATTACAGGTGCTTTTAACTAGTAAGTCT 3072  
DB 81 TGATCTCAGTGTATTACAGGTGCTTTTAACTAGTAAGTCT 39  
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LOCUS AQ320928/c  
DEFINITION RPC111-93C9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-93C9, DNA  
sequence.  
ACCESSION AQ320928  
VERSION AQ320928.1 GI:4053662  
KEYWORDS GSS.

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 553)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building  
JOURNAL Unpublished (1998)  
COMMENT Other.GSSs: RPC11-93C9.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are derived from the human BAC library RPC1-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: T7  
Class: BAC ends.

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/db\_xref="GDB:7535384"  
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/clone="RPC1-11-93C9"  
/clone\_lib="RPC1-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: pBAC3.6; site\_1: EcoRI; site\_2: EcoRI;  
RPC11 Human Male BAC Library"  
BASE COUNT 170 a 107 c 114 g 162 t  
ORIGIN  
Query Match 5.5%; Score 170; DB 17; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.7e-74;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2615 TCGACAGATGAAGTGTAGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGACG 2674  
Db 258 TCGACAGATGAAGTGTAGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGACG 199  
Qy 2675 TCGAAGCAGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCAACTCGTCAAGC 2734  
Db 198 TCGAAGCAGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCAACTCGTCAAGC 139  
Qy 2735 TTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGT 2784  
Db 138 TTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGT 89  
RESULT 9  
BG210375  
LOCUS BG210375 476 bp mRNA linear EST 21-APR-2001  
DEFINITION RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG210375  
VERSION BG210375.1 GI:13732062  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 476)  
Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith  
, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher  
, J., Danzig,J. and Ducar,M.

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 553)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building  
JOURNAL Unpublished (1998)  
COMMENT Other.GSSs: RPC11-93C9.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are derived from the human BAC library RPC1-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: T7  
Class: BAC ends.

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/organism="Homo sapiens"  
/db\_xref="GDB:7535384"  
/db\_xref="taxon:9606"  
/clone="RPC1-11-93C9"  
/clone\_lib="RPC1-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: pBAC3.6; site\_1: EcoRI; site\_2: EcoRI;  
RPC11 Human Male BAC Library"  
BASE COUNT 170 a 107 c 114 g 162 t  
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Query Match 5.5%; Score 170; DB 17; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.7e-74;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2615 TCGACAGATGAAGTGTAGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGACG 2674  
Db 258 TCGACAGATGAAGTGTAGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGACG 199  
Qy 2675 TCGAAGCAGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCAACTCGTCAAGC 2734  
Db 198 TCGAAGCAGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCAACTCGTCAAGC 139  
Qy 2735 TTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGT 2784  
Db 138 TTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGT 89  
RESULT 9  
BG210375  
LOCUS BG210375 476 bp mRNA linear EST 21-APR-2001  
DEFINITION RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG210375  
VERSION BG210375.1 GI:13732062  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 476)  
Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith  
, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher  
, J., Danzig,J. and Ducar,M.

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 553)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building  
JOURNAL Unpublished (1998)  
COMMENT Other.GSSs: RPC11-93C9.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are derived from the human BAC library RPC1-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="GDB:7535384"  
/db\_xref="taxon:9606"  
/clone="RPC1-11-93C9"  
/clone\_lib="RPC1-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: pBAC3.6; site\_1: EcoRI; site\_2: EcoRI;  
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Query Match 5.5%; Score 170; DB 17; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.7e-74;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2615 TCGACAGATGAAGTGTAGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGACG 2674  
Db 258 TCGACAGATGAAGTGTAGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGACG 199  
Qy 2675 TCGAAGCAGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCAACTCGTCAAGC 2734  
Db 198 TCGAAGCAGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCAACTCGTCAAGC 139  
Qy 2735 TTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGT 2784  
Db 138 TTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGT 89  
RESULT 9  
BG210375  
LOCUS BG210375 476 bp mRNA linear EST 21-APR-2001  
DEFINITION RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG210375  
VERSION BG210375.1 GI:13732062  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 476)  
Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith  
, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher  
, J., Danzig,J. and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random  
activation of gene expression  
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
MEDLINE 21227151  
COMMENT Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atersys.com  
High quality sequence stop: 360.  
FEATURES  
source Location/Qualifiers  
1..476  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/notes="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."  
BASE COUNT 120 a 99 c 107 g 149 t 1 others  
ORIGIN  
Query Match 5.5%; Score 168; DB 12; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2.7e-73;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2873 TGGGTGATTGAGAATCTTAAGCAATAGTGTGTTTTGACTTTAGTACTAAGAATTC 2932  
Db 242 TGGGTGATTGAGAATCTTAAGCAATAGTGTGTTTTGACTTTAGTACTAAGAATTC 301  
Qy 2933 TACCTGATCCAGCATTAGTCAGAAACTTAGCCAACTGTTATCCAACTTACTTTCTGC 2992  
Db 302 TACCTGATCCAGCATTAGTCAGAAACTTAGCCAACTGTTATCCAACTTACTTTCTGC 361  
Qy 2993 AAGAAGCTAGGCTTGTGGTGCAATTTGATGATGATGATCTCAGTG 3040  
Db 362 AAGAAGCTAGGCTTGTGGTGCAATTTGATGATGATGATCTCAGTG 409  
RESULT 10  
AQ112439 630 bp DNA linear GSS 29-AUG-1998  
LOCUS CIT-HSP-2372C1.TR CIT-HSP Homo sapiens genomic clone 2372C1, DNA  
DEFINITION sequence.  
ACCESSION AQ112439  
VERSION AQ112439.1 GI:3484599  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 630)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and  
Venter,J.C.  
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1998)  
COMMENT Other.GSSs: CIT-HSP-2372C1.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC  
end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html).



EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites" 3 others

BASE COUNT 142 a 101 c 107 g 117 t Mismatches 0; Indels 0; Gaps 0;

Query Match 3.5%; Score 106; DB 17; Length 470;  
Best Local Similarity 100.0%; Pred. No. 6.8e-42;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 ATATCTGGGAAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTC 2093  
|||||  
Db 64 ATATCTGGGAAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTC 123  
|||||

QY 2094 TGGTGTGGCTGGAAGCCTCAGTTTGGTCTCAGCACCTGTAAAGAAC 2139  
|||||  
Db 124 TGGTGTGGCTGGAAGCCTCAGTTTGGTCTCAGCACCTGTAAAGAAC 169  
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RESULT 13  
H25984/c  
LOCUS 412 bp mRNA linear EST 10-JUL-1995  
DEFINITION IMAGE:162300 5', mRNA sequence.

ACCESSION H25984  
VERSION H25984.1 GI:895107  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 412)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Willson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 942  
High quality sequence stops: 347

Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 942 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 347.

FEATURES  
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/organism="Homo sapiens"  
/db\_xref="GDB:576544"  
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/clone\_lib="Soares breast 3NBHSt"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 129 a 84 c 73 g 124 t 2 others

Query Match 3.2%; Score 98; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 7.4e-38;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2975 CCAAGTTAACTTTTCTCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGC 3034  
|||||  
Db 340 CCAAGTTAACTTTTCTCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGC 281  
|||||

QY 3035 TCAGTGTATTACAGGTCGCTTTTAAACTAGTAAGTCT 3072  
|||||  
Db 280 TCAGTGTATTACAGGTCGCTTTTAAACTAGTAAGTCT 243  
|||||

RESULT 14  
AI023795  
LOCUS 499 bp mRNA linear EST 28-AUG-1998  
DEFINITION ox08d03.x1 Soares\_fetal\_liver\_spleen\_INFLS\_S1 Homo sapiens CDNA clone IMAGE:1655717 3', mRNA sequence.

ACCESSION AI023795  
VERSION AI023795.1 GI:3238839  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 499)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1179 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 439.

FEATURES  
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/clone\_lib="Soares\_fetal\_liver\_spleen\_INFLS\_S1"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; This is a subtracted version of the Original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 144 a 109 c 98 g 148 t

Query Match 3.0%; Score 93; DB 9; Length 499;  
Best Local Similarity 100.0%; Pred. No. 2.7e-35;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GTCTTTTTCATCAGACATCAGAGGAGACATTGGACGATTTGGCTCAGGATTTAAAGACT 322  
|||||  
Db 407 GTCTTTTTCATCAGACATCAGAGGAGACATTGGACGATTTGGCTCAGGATTTAAAGACT 466  
|||||

QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATC 355  
|||||  
Db 467 TGTACCATACCCCATCTTTTCTGAACCTTTATC 499  
|||||

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RESULT 15
A0283886
LOCUS
DEFINITION
  A0283886
  219 bp DNA linear GSS 27-APR-1999
  QY 2202 TGTACAAACCTGAAACCTTCAGTATTCATGACCTACAGATCAACGCTGCCGGT 2259
  Db 104 TGTACAAACCTGAAACCTTCAGTATTCATGACCTACAGATCAACGCTGCCGGT 161
  sequence.
  B58691
  B58691
  GSS
  SOURCE
  human.
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 219)
  Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
  Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
  Use of human BAC End Sequences for Sequence-Ready Map Building
  Unpublished (1998)
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: mdadams@tigr.org
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (info@resgen.com). BAC end search page:
  http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
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    /sex="Male"
    /cell_type="Lymphocytes"
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  /clone_lib="RPCI-11"
  /sex="Male"
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  Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2202 TGTACAAACCTGAAACCTTCAGTATTCATGACCTACAGATCAACGCTGCCGGT 2259
  Db 104 TGTACAAACCTGAAACCTTCAGTATTCATGACCTACAGATCAACGCTGCCGGT 161
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 635)
  Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden,
  K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M.
  and Venter, J.C.
  Use of a random BAC End Sequence Database for Sequence-Ready Map
  Building
  Unpublished (1997)
  Other_GSSs: CIT-HSP-2013L21.TR
  Contact: Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: mdadams@tigr.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
  Seq primer: M13-21
  Class: BAC ends.
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    /db_xref="taxon:9606"
    /clone="2013L21"
    /clone_lib="CIT-HSP"
    /sex="Male"
    /cell_type="Sperm"
    /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
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  /db_xref="taxon:9606"
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  /sex="Male"
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  Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2730 CAAGCTTGGTTCGAAAACCTGAGACTCACAGATCAGAGATTAGTATTTAGGT 2784
  Db 1 CAAGCTTGGTTCGAAAACCTGAGACTCACAGATCAGAGATTAGTATTTAGGT 55
  RESULT 17
  B587840/c
  LOCUS
  DEFINITION
    B587840
    840 bp mRNA linear EST 06-NOV-2000
    mRNA sequence.
    B587840
    B587840.1 GI:11101426
    EST.
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    ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 840)
    NIH-MGC http://mgc.hci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-remail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Preparation: CLONTECH Laboratories, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone Distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
    Plate: LLCM944 row: 1 column: 11
    High quality sequence stop: 636.
    Location/Qualifiers
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      /db_xref="taxon:9606"
      /clone="IMAGE:4082074"
      /clone_lib="NIH_MGC_53"
      /tissue_type="carcinoma, cell line"
      /lab_host="DH10B (T1 phage-resistant)"
      /note="Organ: bladder; Vector: pDNR-LIB (Clontech);
  JOURNAL
  COMMENT
  Building
  Unpublished (1997)
  Other_GSSs: CIT-HSP-2013L21.TR
  Contact: Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: mdadams@tigr.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
  Seq primer: M13-21
  Class: BAC ends.
  Location/Qualifiers
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    /db_xref="GDB:7042463"
    /db_xref="taxon:9606"
    /clone="2013L21"
    /clone_lib="CIT-HSP"
    /sex="Male"
    /cell_type="Sperm"
    /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
    HindIII"
  BASE COUNT 217 a 122 c 90 g 206 t
  ORIGIN
  1..635
  /organism="Homo sapiens"
  /db_xref="GDB:7042463"
  /db_xref="taxon:9606"
  /clone="2013L21"
  /clone_lib="CIT-HSP"
  /sex="Male"
  /cell_type="Sperm"
  /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
  HindIII"
  Query Match 1.8%; Score 55; DB 17; Length 635;
  Best Local Similarity 100.0%; Pred. No. 5.1e-16;
  Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2730 CAAGCTTGGTTCGAAAACCTGAGACTCACAGATCAGAGATTAGTATTTAGGT 2784
  Db 1 CAAGCTTGGTTCGAAAACCTGAGACTCACAGATCAGAGATTAGTATTTAGGT 55
  RESULT 17
  B587840/c
  LOCUS
  DEFINITION
    B587840
    840 bp mRNA linear EST 06-NOV-2000
    mRNA sequence.
    B587840
    B587840.1 GI:11101426
    EST.
    SOURCE
    human.
    ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 840)
    NIH-MGC http://mgc.hci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-remail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Preparation: CLONTECH Laboratories, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone Distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
    Plate: LLCM944 row: 1 column: 11
    High quality sequence stop: 636.
    Location/Qualifiers
      1..840
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:4082074"
      /clone_lib="NIH_MGC_53"
      /tissue_type="carcinoma, cell line"
      /lab_host="DH10B (T1 phage-resistant)"
      /note="Organ: bladder; Vector: pDNR-LIB (Clontech);
```

Site\_1: SfiI (ggcgcctggcc); Site\_2: SfiI (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGCGGCACATG-GT(30)BN-3', (where B = A, C, G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 276 a 143 c 165 g 256 t

ORIGIN

Query Match 1.8%; Score 55; DB 12; Length 840;  
Best Local Similarity 100.0%; Pred. No. 5.6e-16;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3018 ATTTCATGATGATCTCAGTGTATTACAGGTGCTTTTAACTAGTAAGTCT 3072  
|||||

Db 518 ATTTCATGATGATCTCAGTGTATTACAGGTGCTTTTAACTAGTAAGTCT 464  
|||||

RESULT 18  
AI222422 446 bp mRNA linear EST 30-NOV-1998  
LOCUS qn04f06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
DEFINITION IMAGE:1843715 3', mRNA sequence.  
ACCESSION AI222422  
VERSION AI222422.1 GI:3804625  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 446)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs@mail.nih.gov  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 546 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 437.

FEATURES  
source  
1..446  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1843715"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/lab\_host="DH108"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP\_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 128 a 95 c 86 g 137 t

ORIGIN

Query Match 1.0%; Score 32; DB 9; Length 446;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GTCCTTTTCATCAGACATCAGAGGAGACTTG 294

Db 415 GTCCTTTTCATCAGACATCAGAGGAGACTTG 446  
|||||

RESULT 19  
BH348412 518 bp DNA linear GSS 03-DEC-2001  
LOCUS CH230-42F7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
DEFINITION CH230-42F7, DNA sequence.  
ACCESSION BH348412  
VERSION BH348412.1 GI:17279146  
KEYWORDS GSS.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 518)  
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsagaye,G., Geer,K., Shvartsbeyn ,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.  
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
JOURNAL Unpublished (1999)  
COMMENT Other\_GSSs: CH230-42F7.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering\_information.htm). BAC end page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 42 row: F column: 7  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers  
1..518  
/organism="Rattus norvegicus"  
/strain="BN/SSNHsd/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230-42F7"  
/clone\_lib="CHORI-230 Segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: pTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"

BASE COUNT 133 a 124 c 146 g 115 t

ORIGIN

Query Match 1.0%; Score 32; DB 17; Length 518;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGTGTGTTCTCCACACAGTTTGATTTGCAACT 1229  
|||||

Db 420 GGTGTGTTCTCCACACAGTTTGATTTGCAACT 451  
|||||

RESULT 20  
BH293386 697 bp DNA linear GSS 30-NOV-2001  
LOCUS CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
DEFINITION CH230-44G15, DNA sequence.  
ACCESSION BH293386  
VERSION BH293386.1 GI:17205794  
KEYWORDS GSS.  
SOURCE Norway rat.



```

ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS      Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
              ,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
              Jong,P. and Fraser,C.M.
TITLE        Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL      Unpublished (1999)
COMMENT      Other_GSSs: CH230-44G15.TJ
              Contact: Shaying Zhao
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: szhao@tigr.org
              Clones are derived from the rat BAC library CHORI-230
              (http://www.chori.org/bacpac/rat230.htm). For BAC library
              availability, please contact Pieter de Jong (pdejong@email.cho.org).
              Clones may be purchased from BACPAC Resources
              (http://www.chori.org/bacpac/orering_information.htm). BAC end
              page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
              Plate: 44 row: G column: 15
              Seq primer: T7
              Class: BAC ends.
FEATURES
source       Location/Qualifiers
              1..597
              /organism="Rattus norvegicus"
              /strain="BN/SSNHsd/MCW"
              /db_xref="taxon:10116"
              /clone="CH230-44G15"
              /clone_lib="CHORI-230 Segment 1"
              /sex="Female"
              /cell_type="Brain"
              /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
              CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
              Pieter de Jong"
BASE COUNT   182 a 165 c 190 g 160 t
ORIGIN
Query Match      1.0%; Score 32; DB 17; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGTGTGTTCTCCACAGATTGATTCGAACT 1229
      |||||||||||||||||||||||||||||||
Db 412 GGTGTGTTCTCCACAGATTGATTCGAACT 443

RESULT 21
BF903662
LOCUS        BF903662                251 bp      mRNA      linear      EST 18-JAN-2001
DEFINITION   IL2-MT0180-181200-276-F03 MT0180 Homo sapiens cDNA, mRNA sequence.
ACCESSION    BF903662
VERSION      BF903662.1 GI:12295121
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
              ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663

ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS      Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
              ,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
              Jong,P. and Fraser,C.M.
TITLE        Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL      Unpublished (1999)
COMMENT      Other_GSSs: CH230-44G15.TJ
              Contact: Shaying Zhao
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: szhao@tigr.org
              Clones are derived from the rat BAC library CHORI-230
              (http://www.chori.org/bacpac/rat230.htm). For BAC library
              availability, please contact Pieter de Jong (pdejong@email.cho.org).
              Clones may be purchased from BACPAC Resources
              (http://www.chori.org/bacpac/orering_information.htm). BAC end
              page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
              Plate: 44 row: G column: 15
              Seq primer: T7
              Class: BAC ends.
FEATURES
source       Location/Qualifiers
              1..251
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_lib="MT0180"
              /dev_stage="Adult"
              /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
              SmaI; A mini-library was made by cloning products derived
              from ORESTES PCR (U.S. Letters Patent application No. 196
              ,716 - Ludwig Institute for Cancer Research) profiles
              into the pUC 18 vector. Reverse transcription of tissue
              mRNA and cDNA amplification were performed under low
              stringency conditions."
BASE COUNT   72 a 62 c 56 g 61 t
ORIGIN
Query Match      1.0%; Score 30; DB 12; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1057 GAGTTCACACTCTCACACAAACACAGCGTG 1086
      |||||||||||||||||||||||||||||||
Db 52 GAGTTCACACTCTCACACAAACACAGCGTG 81

RESULT 22
AQ889169/c
LOCUS        AQ889169                404 bp      DNA      linear      GSS 10-NOV-1999
DEFINITION   HS.2161_B1_A01_T7C CIT Approved Human Genomic Sperm Library D Homo
              sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.
ACCESSION    AQ889169
VERSION      AQ889169.1 GI:6345359
KEYWORDS     GSS.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
              Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
              Hood,L.
TITLE        Sequence-tagged connectors: A sequence approach to mapping and
              scanning the human genome
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE      99380589
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
              High Throughput Sequencing Center
              University of Washington
              401 Queen Anne Avenue North, Seattle, WA 98109, USA
              Tel: (206) 616-3618
              Fax: (206) 616-3887
              Email: jwallace@u.washington.edu
              Clones may be purchased from Research Genetics (info@resgen.com).
              BAC end Web Server: http://www.htsc.washington.edu
              Plate: 2161 row: B column: 1
              Seq primer: T7
              Class: BAC ends
              High quality sequence stop: 404.

```

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FEATURES
  source
    Location/Qualifiers
      1. .404
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="Plate=2161 Col=1 Row=B"
        /clone_lib="CIT Approved Human Genomic Sperm Library D"
        /sex="male"
        /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
          E-Coli DH10B"
BASE COUNT      119 a   93 c   70 g   122 t
ORIGIN

Query Match      0.9%; Score 28; DB 17; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 TAGAGGATCATTCACATGATTTTGAAA 180
|||||
Db 200 TAGAGGATCATTCACATGATTTTGAAA 173

RESULT 23
BF829853/c
LOCUS      BF829853      542 bp      mRNA      linear      EST 12-MAR-2002
DEFINITION 1c55H09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
            cDNA clone IMAGE:5671144 5' similar to TR:Q9VAF0 Q9VAF0 CG7816
            PROTEIN. ;, mRNA sequence.
ACCESSION  BF829853
VERSION     BI964738
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 542)
AUTHORS     Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Secearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
            , Jackson,Y. and Bowers,Y.
            Endocrine Pancreas Consortium
            Unpublished (2000)
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Douglas Melton DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Juliana Brown
            (brown@fas.harvard.edu) This sequence now available from the IMAGE
            consortium, for clone orders contact: info@image.llnl.gov
            High quality sequence stop: 456.
            Location/Qualifiers
              1. .542
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5671144"
                /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
                /sex="Both"
                /tissue_type="Islets of Langerhans"
                /dev_stage="Adult"
                /lab_host="DH10B"
            /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
              Site_2: Sal 1; Starting library constructed using
              SuperScript Plasmid Library kit (Life Technologies). cDNA
              made by oligo-dt priming. Size-selected by column
              fractionation; average insert size 1.08 kb. Library was
              amplified once on solid support and plasmid DNA from
FEATURES
  source
    Location/Qualifiers
      1. .606
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="HN0052"
        /dev_stage="Adult"
        /note="Organ: head_normal; Vector: puc18; Site_1: SmaI;
          Site_2: SmaI; A mini-library was made by cloning products
          derived from ORESTES PCR (U.S. Letters Patent application
          No. 196,716 - Ludwig Institute for Cancer Research)
          profiles into the pUC 18 vector. Reverse transcription of
          tissue mRNA and cDNA amplification were performed under
          low stringency conditions."
BASE COUNT      119 a   177 c   195 g   113 t
ORIGIN

library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
BASE COUNT      87 a   182 c   160 g   113 t
ORIGIN

Query Match      0.7%; Score 23; DB 13; Length 542;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1887 AGACACAGGTGGGAATCCACATGG 1909
|||||
Db 433 AGACACAGGTGGGAATCCACATGG 411

RESULT 24
BF829853
LOCUS      BF829853      606 bp      mRNA      linear      EST 13-JAN-2001
DEFINITION MR3-HN0052-261200-002-c12 HN0052 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF829853
VERSION     BF829853.1 GI:12175855
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 606)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-HN0052-
            261200-002-c12&t3=2000-12-26&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 24
            High quality sequence stop: 538.
            Location/Qualifiers
              1. .606
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="HN0052"
                /dev_stage="Adult"
                /note="Organ: head_normal; Vector: puc18; Site_1: SmaI;
          Site_2: SmaI; A mini-library was made by cloning products
          derived from ORESTES PCR (U.S. Letters Patent application
          No. 196,716 - Ludwig Institute for Cancer Research)
          profiles into the pUC 18 vector. Reverse transcription of
          tissue mRNA and cDNA amplification were performed under
          low stringency conditions."
BASE COUNT      119 a   177 c   195 g   113 t
ORIGIN

```



/db\_xref="taxon:10116"  
/clone="UI-R-DNI-cmv-e-08-0-UI"  
/clone\_lib="UI-R-DNI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"

/note=vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-DNI library is a normalized Rat Distal Colon library (nRDC) constructed in pT77 PAC vector according to the procedure described by Bonaldo, Lennon & Soares (Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag GAAGTGCTCC between the Not I cloning site and DT18 stretch. The Rat Distal Colon tissue was provided by Tom Freeman of the Sanger Center.

TAG\_LIB=UI-R-DNI  
TAG\_TISSUE=distal colon  
TAG\_SEQ=GAAGTGCTCC

BASE COUNT 184 a 185 c 146 g 203 t 1 others

Query Match 0.7% Score 23; DB 14; Length 719;

Best Local Similarity 100.0%; Pred. No. 8.6; Mismatches 0; Indels 0; Gaps 0;

Qy 2843 GTGTGACAGTGATGGTGGCTT 2865  
|||||  
Db 516 GTGTGACAGTGATGGTGGCTT 494

RESULT 27  
BQ894786/c

LOCUS BQ894786 914 bp mRNA linear EST 16-AUG-2002  
DEFINITION AGENCOURT 8119214 Lupski\_dorsal\_root\_ganglion Homo sapiens cDNA

clone IMAGE:6179738 5', mRNA sequence.  
ACCESSION BQ894786  
VERSION BQ894786.1 GI:22286800

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 914)

NTH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@email.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LENL at:

http://image.llnl.gov

Plate: L1AM13561 row: g column: 03

High quality sequence stop: 568.

Location/Qualifiers

FEATURES

source

1..914  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6179738"  
/clone\_lib="Lupski\_dorsal\_root\_ganglion"  
/sex="male"  
/tissue\_type="dorsal root ganglia"  
/dev\_stage="adult, 36 yr"  
/lab\_host="DH10B"

/note=vector: pCMV-SPORT6 (Life Technologies); Site\_1: NotI; Site\_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors:  
5'-TCGACCCACCGGTCG-3' and  
5'-GACTAGTCTAGATCGGCGGCCGCGCTT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT 132 a 321 c 249 g 212 t

ORIGIN

Query Match 0.7% Score 23; DB 14; Length 914;

Best Local Similarity 100.0%; Pred. No. 9.3; Mismatches 0; Indels 0; Gaps 0;

Qy 1887 AGACACAGTGGATCCACATGG 1909  
|||||

Db 476 AGACACAGTGGATCCACATGG 454

RESULT 28  
AV268403

LOCUS

DEFINITION AV268403 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930534P12 3', mRNA sequence.

ACCESSION AV268403

VERSION AV268403.1 GI:6256440

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 256)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,

Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,

Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai

C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,

Katsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata

Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H.,

Suzuki, H., Takahashi, F., Tatenomura, T., Tomimaga, N., Tsunoda, Y.,

Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,

Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,

Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki

Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh, M., Kitzunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki

Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

Location/Qualifiers

FEATURES

source

1..256  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="4930534P12"  
/clone\_lib="RIKEN full-length enriched, adult male testis





This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 336.  
Location/Qualifiers

#### FEATURES

1. .343  
Location/Qualifiers

/organism="Mus musculus"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1151400"  
/clone\_lib="Stratagene mouse skin (#937313)"  
/sex="females"  
/tissue\_type="whole skin"  
/dev\_stage="11 weeks old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo  
dt. Whole skin from 11 week old C57BL/6 female mice.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  
adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor  
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

84 a 103 c 95 g 61 t

BASE COUNT

#### ORIGIN

Query Match 0.7%; Score 21; DB 9; Length 343;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 ATGAATTCAGCCCGACGAACT 772

|||||

Db 319 ATGAATTCAGCCCGACGAACT 339

#### RESULT 34

##### LOCUS

AI645009 371 bp mRNA linear EST 29-APR-1999

DEFINITION IMAGE:1151400 5', mRNA sequence.

ACCESSION AI645009

VERSION AI645009.1 GI:4723484

KEYWORDS EST.

SOURCE house mouse.

#### ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 371)

REFERENCE Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter

, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

CONTACT: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:624608

This read is a RESEQUENCE of a previously sequenced mouse clone

correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 355.

Location/Qualifiers

1. .371

/organism="Mus musculus"

/strain="C57BL/6"

/db\_xref="taxon:10090"

FEATURES

source

/clone="IMAGE:1151400"  
/clone\_lib="Stratagene mouse skin (#937313)"  
/sex="females"  
/tissue\_type="whole skin"  
/dev\_stage="11 weeks old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo  
dt. Whole skin from 11 week old C57BL/6 female mice.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  
adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor  
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

92 a 109 c 101 g 59 t

BASE COUNT

#### ORIGIN

Query Match 0.7%; Score 21; DB 9; Length 371;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 ATGAATTCAGCCCGACGAACT 772

|||||

Db 321 ATGAATTCAGCCCGACGAACT 341

#### RESULT 35

##### LOCUS

AZ223093 432 bp DNA linear GSS 14-JUN-2000

DEFINITION RPCI-23-94H20-TV RPCI-23 Mus musculus genomic clone RPCI-23-94H20,

DNA sequence.

ACCESSION AZ223093

VERSION AZ223093.1 GI:8531142

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 432)

REFERENCE Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret

, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.

and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-94H20.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html

Plate: 94 row: H column: 20

Seq primer: 77

Class: BAC ends.

Location/Qualifiers

1. .432

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="RPCI-23-94H20"

/clone\_lib="RPCI-23"

/sex="Female"

/lab\_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site\_1:

EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACe3.6 vector at the

EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). \*

```

BASE COUNT      75 a   123 c   122 g   112 t
ORIGIN
Query Match      0.7%; Score 21; DB 17; Length 432;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 752 ATGAATTCACGCCAGAACT 772
      |||||||
Db 115 ATGAATTCACGCCAGAACT 95

RESULT 36
LOCUS      AQ555443/c      437 bp      DNA      linear      GSS 29-MAY-1999
DEFINITION HS_5224_A2_B05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=800 Col=10 Row=C, DNA sequence.
ACCESSION  AQ555443
VERSION     AQ555443.1 GI:4914996
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 437)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 800 row: C column: 10
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 437.
FEATURES             Location/Qualifiers
     source           1..437
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=800 Col=10 Row=C"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"
BASE COUNT      168 a   60 c   81 g   128 t
ORIGIN

Query Match      0.7%; Score 21; DB 17; Length 437;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GTGGCATCCATTATATCAAG 1690
      |||||||
Db 387 GTGGCATCCATTATATCAAG 367

EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). *
```

```

RESULT 37
LOCUS      CNS00SV2/c      462 bp      DNA      linear      GSS 28-JUN-1999
DEFINITION Arabidopsis thaliana genome survey sequence SP6 end of BAC T2N9 of
            TAMU library from strain Columbia of Arabidopsis thaliana, genomic
            survey sequence.
ACCESSION  AL088892
VERSION     AL088892.1 GI:5290032
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana.
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 462)
AUTHORS   Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
            Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 462)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL    Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source           1..462
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="T2N9"
                     /clone_lib="TAMU"
                     /note="end : SP6"
BASE COUNT      129 a   87 c   70 g   176 t
ORIGIN

Query Match      0.7%; Score 21; DB 17; Length 462;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 591 CAAATTCGTCTCTCTCTCCG 611
      |||||||
Db 239 CAAATTCGTCTCTCTCTCCG 219

RESULT 38
LOCUS      AZ360053/c      602 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION 1M0103H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0103H11 F, DNA sequence.
ACCESSION  AZ360053
VERSION     AZ360053.1 GI:10473753
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 602)
AUTHORS   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
```





```
RESULT 40
BI854236
LOCUS      603381263F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5389239 5',
DEFINITION mRNA sequence.
ACCESSION BI854236
VERSION   BI854236.1 GI:15994983
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 775)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: c9abps-r@mail.nih.gov
          Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
          Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM1991 row: m column: 16
          High quality sequence stop: 764.
FEATURES             source
    Location/Qualifiers
        1..775
            /organism="Mus musculus"
            /strain="NMRI"
            /db_xref="taxon:10090"
            /clone="IMAGE:5389239"
            /clone_lib="NCI_CGAP_Mam4"
            /tissue_type="tumor, gross tissue"
            /dev_stage="5 months"
            /lab_host="DH10B"
            /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
            Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigators
            providing samples: Lothar Hennighausen/Priscilla Furth,
            NIH Reference for transgenic model: Li et al., Cell Growth
            and Differentiation 7, 3-11 (1996)."
```

```
BASE COUNT      226 a 162 c 196 g 191 t
ORIGIN
Query Match      0.7%; Score 21; DB 13; Length 775;
Best Local Similarity 100.0%; Pred. NO. 91;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2965 CAAGTGTATCCAAAGTTAACT 2985
|||||
Db 386 CAAGTGTATCCAAAGTTAACT 406

RESULT 41
BQ278245
LOCUS      AGENCOURT_6838625 NIH_MGC_128 Homo sapiens cDNA clone IMAGE:5811028
DEFINITION 5', mRNA sequence.
ACCESSION BQ278245
VERSION   BQ278245.1 GI:20488453
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 950)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: c9abps-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

us-09-697-089-3.olil2.rst
```

```
CONTACT: Robert Strausberg, Ph.D.
Email: c9abps-r@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2059 row: d column: 05
High quality sequence stop: 447.
FEATURES             source
    Location/Qualifiers
        1..950
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5811028"
            /clone_lib="NIH_MGC_128"
            /tissue_type="mixed (pool of 40 RNAs)"
            /lab_host="DH10B (T1-phage-resistant)"
            /note="Vector: pDNR-LIB; Site.1: SfiI (ggccattatggcc);
            Site.2: SfiI (ggccgctcgcc); Double-stranded cDNA was
            prepared from a pool of 40 cell line polyA+ RNAs (bladder
            - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
            4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
            kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
            ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
            gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
            used in cloning as follows:
            5'-AACGAGTGTATCCAGCAGAGTGGCATTACGCCGGG-3' and
            5'-ATTCTAGAGCCGAGGCGCCGACATG-dt(30)NN-3'. Full-length
            enriched library was constructed using the Clontech
            Creator SMART kit and size-selected to contain the >2 kb
            size fraction (other fractions present in NIH_MGC_126 and
            NIH_MGC_127). Library created in the laboratory of T.
            Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
            Library."
BASE COUNT      286 a 297 c 140 g 218 t 9 others
ORIGIN
Query Match      0.7%; Score 21; DB 14; Length 950;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 AAAACAACAAACAAACATAAA 1137
|||||
Db 520 AAAACAACAAACAAACATAAA 540

RESULT 42
BG571228
LOCUS      602592168F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4719424 5',
DEFINITION mRNA sequence.
ACCESSION BG571228
VERSION   BG571228.1 GI:13578881
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1147)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: c9abps-r@mail.nih.gov
          Tissue Procurement: CLONTECH Laboratories, Inc.
          cDNA Library Preparation: CLONTECH Laboratories, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
```

Plate: LLCM1572 row: h column: 17  
High quality sequence stop: 240.

#### FEATURES

Location/Qualifiers  
1. .1147

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:4719424"

/clone\_lib="NIH\_MGC\_79"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: placenta; Vector: pDNR-LIB (Clontech);

Site\_1: Sfil (ggcgctcgcc); Site\_2: Sfil (ggccatagggc

); 5' and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CAGGCCATATGGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGGCGGCATG-dT(30)BN-3'

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC

Library."

BASE COUNT 477 a 135 c 499 g 36 t

ORIGIN

Query Match 0.7%; Score 21; DB 12; Length 1147;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1113 ACAGAAAAACAACACAAACA 1133

Db 298 ACAGAAAAACAACACAAACA 318

RESULT 43

LOCUS B1142462

DEFINITION SWOV3MCAM62G10SK Onchocerca volvulus molting L3 larva cDNA

(SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAM62G10 5',

mRNA sequence.

ACCESSION B1142462

VERSION B1142462.1 GI:14624172

KEYWORDS EST.

SOURCE Onchocerca volvulus.

ORGANISM Onchocerca volvulus

REFERENCE Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.

Genes expressed in molting L3 larvae of Onchocerca volvulus

Unpublished (1997)

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers

1. .64

/organism="Onchocerca volvulus"

/strain="Kumba, Cameroon"

/db\_xref="taxon:6282"

/clone="SWOV3MCAM62G10"

/clone\_lib="Onchocerca volvulus molting L3 larva cDNA

(SL96MLW-Ovml3)"

/dev\_stage="molting L3"

/lab\_host="xLi-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2:

Xho I; Filarial nematode parasite of humans. Third-stage

larvae, L3, were isolated from infected black flies in

Cameroon (forest strain). The L3 were cultured in 20% FCS

in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in

culture. L3 of *O. volvulus* molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustig@nycb.org)."

BASE COUNT 17 a 7 c 20 g 20 t

ORIGIN

Query Match 0.7%; Score 20; DB 13; Length 64;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2329 GAAGAAGATGCTATAAACT 2348

Db 42 GAAGAAGATGCTATAAACT 61

RESULT 44

LOCUS BE638399

DEFINITION SWOVLCAS15B03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OVL2)

Onchocerca volvulus cDNA clone SWOVLCAS15B03 5', mRNA sequence.

ACCESSION BE638399

VERSION BE638399.1 GI:9937018

KEYWORDS EST.

SOURCE Onchocerca volvulus.

ORGANISM Onchocerca volvulus

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

Onchocercidae; Onchocerca.

1 (bases 1 to 73)

Williams, S.A.

Genes expressed in L2 larvae of Onchocerca volvulus

Unpublished (1999)

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers

1. .73

/organism="Onchocerca volvulus"

/db\_xref="taxon:6282"

/clone="SWOVLCAS15B03"

/clone\_lib="Onchocerca volvulus L2 larvae cDNA

(SAW98MLW-OVL2)"

/dev\_stage="L2"

/lab\_host="xLi-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2:

Xho I; Filarial nematode parasite of humans. mRNA was

prepared from approximately 9,000 L2s isolated from

infected mosquitoes from Kumba, Cameroon and converted to

double-stranded cDNA using reverse transcriptase and

oligo(dT) followed by RNase H and DNA pol I. The library

has 7.3 x 10E4 independent recombinants and the average

insert size is approximately 1kb. The library was

constructed by Michelle Lizotte-Waniewski. The library is

available from Dr. S.A. Williams, email: genome@smith.edu."

BASE COUNT 22 a 11 c 19 g 21 t

ORIGIN

Query Match 0.7%; Score 20; DB 10; Length 73;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2329 GAAGAAGATGCTATAAAACT 2348  
|||||  
Db 27 GAAGAAGATGCTATAAAACT 46

RESULT 45  
LOCUS AQ069062/c  
DEFINITION HS\_2255\_B2\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=6 Row=P, DNA sequence.  
ACCESSION AQ069062  
VERSION AQ069062.1 GI:3384261  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 205)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2255 row: P column: 6  
Class: BAC ends  
High quality sequence stop: 205.  
Location/Qualifiers  
1..205  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 54 a 41 c 52 g 57 t 1 others  
ORIGIN

Query Match 0.7%; Score 20; DB 17; Length 205;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1112 TACAGAAAACAAACACAAA 1131  
|||||  
Db 134 TACAGAAAACAAACACAAA 115

RESULT 46  
LOCUS BI315256  
DEFINITION dah9606.y1 NICHD XGC Emb4 Xenopus laevis cdna clone IMAGE:4957906 5', mRNA sequence.  
ACCESSION BI315256  
VERSION BI315256.1 GI:14989583  
KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus.  
REFERENCE 1 (bases 1 to 215)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: [info@image.llnl.gov](mailto:info@image.llnl.gov)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 197.  
Location/Qualifiers  
1..215  
/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone="IMAGE:4957906"  
/clone\_lib="NICHD XGC Emb4"  
/dev\_stage="embryo, stage 31-32"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: whole embryo; Vector: PCMV-SPORT6; Site\_1: Noti; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 72 a 32 c 37 g 74 t  
ORIGIN

Query Match 0.7%; Score 20; DB 13; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2790 TTTTGGAAAGAACCTCTGA 2809  
|||||  
Db 196 TTTTGGAAAGAACCTCTGA 215

RESULT 47  
LOCUS AA493806  
DEFINITION nh02f04.s1 NCI-CGAP\_Thy1 Homo sapiens cdna clone IMAGE:943135, mRNA sequence.  
ACCESSION AA493806  
VERSION AA493806.1 GI:2223647  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 216)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 294 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham.  
Location/Qualifiers  
1..216  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:943135"

BASE COUNT 216 bp mRNA linear EST 19-AUG-1997  
ORIGIN

Query Match 0.7%; Score 20; DB 13; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2790 TTTTGGAAAGAACCTCTGA 2809  
|||||  
Db 196 TTTTGGAAAGAACCTCTGA 215

```

/clone_lib="NCI_CGAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH10B"
/notes="Vector: pAMP10; mRNA made from invasive thyroid
tumor, cDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert size
600 bp. Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
BASE COUNT      57 a      65 c      37 g      57 t
ORIGIN

Query Match      0.7%; Score 20; DB 9; Length 216;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GCACATCACATCTGTAACAA 2209
|||||
Db 92 GCACATCACATCTGTAACAA 111

RESULT 48
LOCUS      AI366637      225 bp      mRNA      linear      EST 08-JAN-1999
DEFINITION SWOV3MCAM11C04SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAM11C04 5',
mRNA sequence.
ACCESSION  AI366637
VERSION     AI366637.1 GI:4136382
KEYWORDS   EST.
SOURCE     Onchocerca volvulus.
ORGANISM   Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
REFERENCE  1 (bases 1 to 225)
AUTHORS   Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
TITLE     Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL   Unpublished (1997)
COMMENT   Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pbluescript SK.
Location/Qualifiers
1..225
/organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone_lib="SWOV3MCAM11C04"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3)"
/dev_stage="molting L3"
/lab_host="XLI-Blue MRF"
/notes="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigm@nyc.org)."

FEATURES
source

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BASE COUNT      65 a      39 c      57 g      64 t
ORIGIN

Query Match      0.7%; Score 20; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2329 GAAGAAGATGCTATAAAACT 2348
|||||
Db 30 GAAGAAGATGCTATAAAACT 49

RESULT 49
LOCUS      AI603832      248 bp      mRNA      linear      EST 21-APR-1999
DEFINITION SWOV3MCAM27A08SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAM27A08 5',
mRNA sequence.
ACCESSION  AI603832
VERSION     AI603832.1 GI:4612981
KEYWORDS   EST.
SOURCE     Onchocerca volvulus.
ORGANISM   Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
REFERENCE  1 (bases 1 to 248)
AUTHORS   Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
TITLE     Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL   Unpublished (1997)
COMMENT   Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pbluescript SK.
Location/Qualifiers
1..248
/organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone_lib="SWOV3MCAM27A08"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3)"
/dev_stage="molting L3"
/lab_host="XLI-Blue MRF"
/notes="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigm@nyc.org)."

BASE COUNT      71 a      47 c      58 g      69 t
ORIGIN

Query Match      0.7%; Score 20; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2329 GAAGAAGATGCTATAAAACT 2348

```

```
|||||
Db 14 GAAGAAATGCTATAAACT 33

RESULT 50
AZ891870
LOCUS
DEFINITION RPCI-24-180D14.TJ RPCI-24 Mus musculus genomic clone RPCI-24-180D14
, DNA sequence.
ACCESSION AZ891870
VERSION AZ891870.1 GI:13210815
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 299)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-180D14.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html
Plate: 180 row: D column: 14
Seq primer: SP6
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..299
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-180D14"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pFARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pFARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
BASE COUNT 103 a 57 c 85 g 54 t
ORIGIN

Query Match 0.7%; Score 20; DB 17; Length 299;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 954 TGAAGGCTGTGTGCTCCAAA 973
|||||
Db 202 TGAAGGCTGTGTGCTCCAAA 221

Search completed: January 31, 2003, 00:11:01
Job time : 4188 secs
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GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:51:05 ; Search time 102 Seconds  
(without alignments)  
9236.382 Million cell updates/sec

Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaatttcataaaggacaa.....cttttaaacactagtaactgct 3072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 12

Total number of hits satisfying chosen parameters: 47916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_NA:\*1: /cgn2.6/ptodata/2/ina/5A\_COMB.seq:\*2: /cgn2.6/ptodata/2/ina/5B\_COMB.seq:\*3: /cgn2.6/ptodata/2/ina/6A\_COMB.seq:\*4: /cgn2.6/ptodata/2/ina/6B\_COMB.seq:\*5: /cgn2.6/ptodata/2/ina/PCTUS\_COMB.seq:\*6: /cgn2.6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	0.6	888	4	US-09-071-035-425
2	18	0.6	1094	2	US-08-870-518-34
3	18	0.6	1515	3	US-08-747-221B-16
4	18	0.6	1515	3	US-08-747-221B-17
5	18	0.6	1515	4	US-09-005-051-16
6	18	0.6	1515	4	US-09-005-051-17
7	18	0.6	1611	6	5213972-6
8	18	0.6	1650	3	US-08-747-221B-60
9	18	0.6	1650	3	US-08-747-221B-61
10	18	0.6	1650	4	US-09-005-051-60
11	18	0.6	1650	4	US-09-005-051-61
12	18	0.6	1721	3	US-08-857-213-2
13	18	0.6	1800	1	US-08-139-937-11
14	18	0.6	1800	5	PCT-US93-11310-11
15	18	0.6	1926	4	US-09-079-955-10
16	18	0.6	1982	3	US-08-747-221B-13
17	18	0.6	1982	3	US-08-747-221B-15
18	18	0.6	1982	4	US-09-005-051-13
19	18	0.6	1982	4	US-09-005-051-15
20	18	0.6	2144	3	US-08-747-221B-57
21	18	0.6	2144	3	US-08-747-221B-59
22	18	0.6	2144	4	US-09-005-051-57
23	18	0.6	2144	4	US-09-005-051-59
24	18	0.6	3000	4	US-09-192-104-1
25	18	0.6	3000	4	US-09-543-446-1
26	18	0.6	3969	4	US-09-518-386B-4
27	18	0.6	4982	3	US-08-699-103B-1
					Sequence 425, App
					Sequence 34, Appl
					Sequence 16, Appl
					Sequence 17, Appl
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					Sequence 17, Appl
					Patent No. 5213972
					Sequence 60, Appl
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					Sequence 60, Appl
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					Sequence 61, Appl
					Sequence 2, Appl
					Sequence 11, Appl
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 10, Appl
					Sequence 13, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 13, Appl
					Sequence 15, Appl
					Sequence 57, Appl
					Sequence 59, Appl
					Sequence 1, Appl
					Sequence 4, Appl
					Sequence 1, Appl

101	16	0.5	733	1	US-08-461-360A-3	Sequence 3, Appli	c 174	16	0.5	1824	4	US-09-616-990-1	Sequence 1, Appli
102	16	0.5	733	1	US-08-461-359-3	Sequence 3, Appli	c 175	16	0.5	1828	4	US-09-280-116-108	Sequence 108, App
103	16	0.5	733	1	PCT-US94-12904-3	Sequence 3, Appli	c 176	16	0.5	1857	4	US-08-456-200B-13	Sequence 13, Appl
104	16	0.5	795	2	US-08-822-028-11	Sequence 11, Appl	c 177	16	0.5	1927	4	US-08-837-199A-9	Sequence 9, Appli
105	16	0.5	795	2	US-08-479-285-11	Sequence 11, Appl	c 178	16	0.5	1927	4	US-08-837-199A-40	Sequence 40, Appl
c 106	16	0.5	803	3	US-08-454-928-9	Sequence 9, Appli	c 179	16	0.5	1929	4	US-08-837-199A-11	Sequence 11, Appl
107	16	0.5	803	4	US-09-221-017B-684	Sequence 684, App	c 180	16	0.5	1929	4	US-08-837-199A-41	Sequence 41, Appl
c 108	16	0.5	843	4	US-09-296-284-24	Sequence 24, Appl	c 181	16	0.5	1964	4	US-09-117-853-1	Sequence 1, Appli
c 109	16	0.5	897	5	PCT-US96-05320A-303	Sequence 303, App	c 182	16	0.5	2157	4	US-08-837-199A-15	Sequence 15, Appl
c 110	16	0.5	921	4	US-09-296-284-3	Sequence 3, Appli	c 183	16	0.5	2158	4	US-08-837-199A-43	Sequence 43, Appl
111	16	0.5	1001	4	US-09-641-638-370	Sequence 370, App	c 184	16	0.5	2222	3	US-09-197-380-1	Sequence 1, Appli
112	16	0.5	1001	4	US-09-641-638-371	Sequence 371, App	c 185	16	0.5	2224	4	US-09-261-855-1	Sequence 1, Appli
113	16	0.5	1001	4	US-09-641-638-372	Sequence 372, App	c 186	16	0.5	2356	1	US-08-105-483-222	Sequence 222, App
114	16	0.5	1047	2	US-08-535-276-7	Sequence 7, Appli	c 187	16	0.5	2356	1	US-08-220-151-75	Sequence 75, Appl
115	16	0.5	1047	4	US-09-335-234-7	Sequence 7, Appli	c 188	16	0.5	2356	1	US-08-413-118-75	Sequence 75, Appl
116	16	0.5	1054	1	US-08-152-485-1	Sequence 1, Appli	c 189	16	0.5	2356	1	US-08-224-657-51	Sequence 51, Appl
117	16	0.5	1054	1	US-08-463-089-1	Sequence 1, Appli	c 190	16	0.5	2356	1	US-08-709-209-222	Sequence 222, App
118	16	0.5	1054	1	US-08-461-360A-1	Sequence 1, Appli	c 191	16	0.5	2356	1	US-08-458-101-222	Sequence 22, App
119	16	0.5	1054	1	US-08-461-359-1	Sequence 1, Appli	c 192	16	0.5	2356	2	US-08-184-009-78	Sequence 78, Appl
120	16	0.5	1054	5	PCT-US94-12904-1	Sequence 1, Appli	c 193	16	0.5	2356	2	US-08-417-210A-68	Sequence 68, Appl
c 121	16	0.5	1059	4	US-08-837-199A-23	Sequence 23, Appl	c 194	16	0.5	2356	2	US-08-458-356-78	Sequence 78, Appl
c 122	16	0.5	1059	4	US-08-837-199A-47	Sequence 47, Appl	c 195	16	0.5	2356	2	US-08-473-446-75	Sequence 75, Appl
c 123	16	0.5	1073	4	US-08-476-102A-1	Sequence 1, Appli	c 196	16	0.5	2356	4	US-08-460-736-78	Sequence 78, Appl
c 124	16	0.5	1075	4	US-08-837-199A-21	Sequence 21, Appl	c 197	16	0.5	2356	4	US-09-354-138-51	Sequence 51, Appl
c 125	16	0.5	1076	4	US-08-837-199A-46	Sequence 46, Appl	c 198	16	0.5	2413	4	US-09-367-206-2	Sequence 2, Appli
126	16	0.5	1081	2	US-08-832-883-57	Sequence 57, Appl	c 199	16	0.5	2429	4	US-09-360-545-68	Sequence 68, Appl
127	16	0.5	1081	2	US-08-832-877-57	Sequence 57, Appl	c 200	16	0.5	2453	5	PCT-US95-07180-1	Sequence 1, Appli
c 128	16	0.5	1103	3	US-08-899-786-13	Sequence 13, Appl	c 201	16	0.5	2465	1	US-08-421-661-5	Sequence 5, Appli
c 129	16	0.5	1104	4	US-08-423-399B-36	Sequence 36, Appl	c 202	16	0.5	2545	1	US-07-869-933-22	Sequence 22, Appl
c 130	16	0.5	1113	4	US-09-134-001C-566	Sequence 566, App	c 203	16	0.5	2545	1	US-09-103-663-22	Sequence 22, Appl
c 131	16	0.5	1134	4	US-08-432-999A-9	Sequence 9, Appli	c 204	16	0.5	2568	4	US-08-837-199A-1	Sequence 1, Appli
c 132	16	0.5	1162	1	US-08-423-399B-34	Sequence 34, Appl	c 205	16	0.5	2608	4	US-09-404-879A-386	Sequence 386, App
c 133	16	0.5	1166	5	PCT-US96-12129B-1	Sequence 1, Appli	c 206	16	0.5	2652	1	US-08-318-831-1	Sequence 1, Appli
c 134	16	0.5	1168	4	US-08-858-207A-182	Sequence 182, App	c 207	16	0.5	2675	1	US-08-232-079-1	Sequence 1, Appli
c 135	16	0.5	1173	3	US-08-740-644-1	Sequence 1, Appli	c 208	16	0.5	2700	4	US-09-236-284-8	Sequence 8, Appli
c 136	16	0.5	1178	2	US-08-933-750C-88	Sequence 88, Appl	c 209	16	0.5	2916	4	US-08-976-259-22	Sequence 22, Appl
c 137	16	0.5	1178	3	US-09-234-613-88	Sequence 88, Appl	c 210	16	0.5	2943	4	US-09-404-879A-385	Sequence 385, App
c 138	16	0.5	1196	4	US-09-149-476-225	Sequence 25, App	c 211	16	0.5	2980	4	US-08-456-200B-12	Sequence 12, Appl
c 139	16	0.5	1220	4	US-09-149-476-57	Sequence 57, Appl	c 212	16	0.5	2996	4	US-09-404-879A-311	Sequence 311, App
c 140	16	0.5	1244	2	US-08-204-288-3	Sequence 3, Appli	c 213	16	0.5	3014	2	US-08-808-982-1	Sequence 1, Appli
c 141	16	0.5	1284	1	US-07-882-790-3	Sequence 3, Appli	c 214	16	0.5	3014	4	US-09-306-902A-1	Sequence 1, Appli
c 142	16	0.5	1311	4	US-09-134-001C-386	Sequence 386, App	c 215	16	0.5	3018	3	US-08-942-572-1	Sequence 1, Appli
c 143	16	0.5	1330	2	US-08-868-288A-4	Sequence 4, Appli	c 216	16	0.5	3147	4	US-08-887-534A-84	Sequence 84, Appl
c 144	16	0.5	1330	3	US-09-235-373-4	Sequence 4, Appli	c 217	16	0.5	3209	4	US-08-837-199A-5	Sequence 5, Appli
c 145	16	0.5	1330	3	US-09-388-993-4	Sequence 4, Appli	c 218	16	0.5	3209	4	US-08-837-199A-37	Sequence 37, Appl
c 146	16	0.5	1343	4	US-09-455-921A-1	Sequence 1, Appli	c 219	16	0.5	3218	2	US-08-677-862-1	Sequence 1, Appli
c 147	16	0.5	1370	1	US-08-592-126-79	Sequence 79, Appl	c 220	16	0.5	3218	2	US-09-252-571-1	Sequence 1, Appli
c 148	16	0.5	1404	3	US-08-961-083-9	Sequence 9, Appli	c 221	16	0.5	3218	3	US-09-434-065-1	Sequence 1, Appli
c 149	16	0.5	1431	4	US-09-465-558-67	Sequence 67, Appl	c 222	16	0.5	3403	4	US-08-448-489-2	Sequence 2, Appli
c 150	16	0.5	1455	1	US-08-423-399B-32	Sequence 32, Appl	c 223	16	0.5	3437	3	US-08-704-711A-9	Sequence 9, Appli
c 151	16	0.5	1477	3	US-08-096-181A-7	Sequence 7, Appli	c 224	16	0.5	3437	4	US-09-521-220-9	Sequence 9, Appli
c 152	16	0.5	1477	5	PCT-US94-08326-7	Sequence 7, Appli	c 225	16	0.5	3456	3	US-08-704-711A-8	Sequence 8, Appli
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c 154	16	0.5	1502	4	US-08-868-373-11	Sequence 11, Appl	c 227	16	0.5	3636	4	US-09-090-535-5	Sequence 5, Appli
c 155	16	0.5	1509	1	US-08-113-052-1	Sequence 1, Appli	c 228	16	0.5	3636	4	US-09-090-535-6	Sequence 6, Appli
c 156	16	0.5	1514	4	US-08-946-165A-219	Sequence 219, App	c 229	16	0.5	3636	4	US-09-090-535-7	Sequence 7, Appli
c 157	16	0.5	1636	4	US-09-117-853-7	Sequence 7, Appli	c 230	16	0.5	3636	4	US-09-058-535-8	Sequence 8, Appli
c 158	16	0.5	1642	4	US-09-117-853-5	Sequence 5, Appli	c 231	16	0.5	3722	4	US-09-058-947A-1	Sequence 1, Appli
c 159	16	0.5	1642	4	US-09-117-853-9	Sequence 9, Appli	c 232	16	0.5	3957	1	US-07-689-008-5	Sequence 5, Appli
c 160	16	0.5	1643	4	US-09-117-853-3	Sequence 3, Appli	c 233	16	0.5	4059	4	US-09-500-123-11	Sequence 11, Appl
c 161	16	0.5	1669	4	US-08-984-709A-51	Sequence 51, Appl	c 234	16	0.5	4130	4	US-09-657-452A-10	Sequence 10, Appl
c 162	16	0.5	1755	1	US-07-912-900-29	Sequence 29, App	c 235	16	0.5	4157	2	US-08-162-146-2	Sequence 2, Appli
c 163	16	0.5	1755	1	US-08-285-309-29	Sequence 29, Appl	c 236	16	0.5	4157	4	US-09-314-127-2	Sequence 2, Appli
c 164	16	0.5	1755	2	US-08-502-046-29	Sequence 29, App	c 237	16	0.5	4161	3	US-08-790-517-1	Sequence 1, Appli
c 165	16	0.5	1761	4	US-09-404-879A-387	Sequence 387, App	c 238	16	0.5	4161	3	US-08-790-517-19	Sequence 19, Appl
c 166	16	0.5	1796	4	US-09-276-531-113	Sequence 113, App	c 239	16	0.5	4181	1	US-07-670-611-1	Sequence 1, Appli
c 167	16	0.5	1807	4	US-09-058-947A-2	Sequence 2, Appli	c 240	16	0.5	4181	1	US-08-220-674-1	Sequence 1, Appli
c 168	16	0.5	1812	1	US-07-912-900-28	Sequence 28, Appl	c 241	16	0.5	4181	1	US-08-445-186-1	Sequence 1, Appli
c 169	16	0.5	1812	1	US-08-285-309-28	Sequence 28, Appl	c 242	16	0.5	4181	1	US-08-446-549-1	Sequence 1, Appli
c 170	16	0.5	1812	1	US-08-313-075A-37	Sequence 37, Appl	c 243	16	0.5	4181	2	US-08-446-550-1	Sequence 1, Appli
c 171	16	0.5	1812	2	US-08-502-046-28	Sequence 28, Appl	c 244	16	0.5	4258	3	US-07-765-830A-5	Sequence 5, Appli
c 172	16	0.5	1821	4	US-09-537-682-2	Sequence 2, Appli	c 245	16	0.5	4335	4	US-08-974-549A-6	Sequence 6, Appli
c 173	16	0.5	1824	3	US-08-606-505B-1	Sequence 1, Appli	c 246	16	0.5	4337	3	US-09-187-049-1	Sequence 1, Appli



247	16	0.5	4550	4	US-09-338-907-182	Sequence 182, App	C 320	15	0.5	33	4	US-09-424-620B-22	Sequence 22, Appl
248	16	0.5	4550	4	US-09-218-207-182	Sequence 182, App	C 321	15	0.5	132	3	US-08-866-340-8	Sequence 8, Appl
249	16	0.5	4566	1	US-08-484-101B-37	Sequence 37, Appl	C 322	15	0.5	173	4	US-09-020-956-147	Sequence 147, App
250	16	0.5	4567	4	US-08-714-524B-37	Sequence 37, Appl	C 323	15	0.5	173	4	US-09-030-607-147	Sequence 147, App
251	16	0.5	4581	4	US-08-961-527-125	Sequence 125, App	C 324	15	0.5	173	4	US-09-605-785-147	Sequence 147, App
252	16	0.5	4940	1	US-08-484-105-1	Sequence 1, Appl	C 325	15	0.5	173	4	US-09-439-313-147	Sequence 147, App
253	16	0.5	4940	1	US-08-484-106-1	Sequence 1, Appl	C 326	15	0.5	173	4	US-09-352-616A-147	Sequence 147, App
254	16	0.5	5089	6	517797-31	Patent No. 517797	C 327	15	0.5	173	4	US-09-232-149A-147	Sequence 147, App
255	16	0.5	5111	4	US-09-004-838-118	Sequence 118, App	C 328	15	0.5	203	1	US-08-222-177A-7	Sequence 7, Appl
256	16	0.5	5247	1	US-08-920-812-15	Sequence 15, App	C 329	15	0.5	203	1	US-08-466-033-19	Sequence 19, Appl
257	16	0.5	5247	1	US-08-920-827-15	Sequence 15, App	C 330	15	0.5	203	1	US-08-444-733-19	Sequence 19, Appl
258	16	0.5	5247	1	US-08-921-177-15	Sequence 15, App	C 331	15	0.5	203	2	US-08-461-134-19	Sequence 19, Appl
259	16	0.5	5247	1	US-08-362-577C-15	Sequence 15, App	C 332	15	0.5	203	2	US-08-461-361-19	Sequence 19, Appl
260	16	0.5	5247	2	US-08-920-828-15	Sequence 15, App	C 333	15	0.5	203	2	US-08-485-910-19	Sequence 19, Appl
261	16	0.5	5402	4	US-09-221-017B-194	Sequence 194, App	C 334	15	0.5	203	5	PCT-US95-06266-19	Sequence 19, Appl
262	16	0.5	6463	2	US-08-962-284-3	Sequence 3, Appl	C 335	15	0.5	207	3	US-09-012-515A-25	Sequence 25, Appl
263	16	0.5	6755	3	US-08-931-999-4	Sequence 4, Appl	C 336	15	0.5	207	3	US-08-360-144A-25	Sequence 25, Appl
264	16	0.5	6822	4	US-09-426-998-3	Sequence 3, Appl	C 337	15	0.5	207	4	US-09-012-504A-25	Sequence 25, Appl
265	16	0.5	7082	4	US-09-362-831-1	Sequence 1, Appl	C 338	15	0.5	207	5	PCT-US95-06722-25	Sequence 25, Appl
266	16	0.5	7125	1	US-07-745-206A-1	Sequence 1, Appl	C 339	15	0.5	210	4	US-09-134-001C-1661	Sequence 1661, Ap
267	16	0.5	7125	2	US-08-311-363-1	Sequence 1, Appl	C 340	15	0.5	227	4	US-08-991-789A-183	Sequence 183, App
268	16	0.5	7635	1	US-08-455-543A-1	Sequence 1, Appl	C 341	15	0.5	227	4	US-09-062-451-183	Sequence 183, App
269	16	0.5	7635	1	US-08-455-543A-23	Sequence 23, Appl	C 342	15	0.5	227	4	US-09-598-326-183	Sequence 183, App
270	16	0.5	7635	2	US-08-193-078B-1	Sequence 1, Appl	C 343	15	0.5	237	1	US-08-466-033-3	Sequence 3, Appl
271	16	0.5	7635	2	US-08-193-078B-29	Sequence 29, Appl	C 344	15	0.5	237	1	US-08-444-733-3	Sequence 3, Appl
272	16	0.5	7635	2	US-08-223-305C-1	Sequence 1, Appl	C 345	15	0.5	237	2	US-08-464-134-3	Sequence 3, Appl
273	16	0.5	7635	2	US-08-223-305C-23	Sequence 23, Appl	C 346	15	0.5	237	2	US-08-461-361-3	Sequence 3, Appl
274	16	0.5	7635	3	US-08-149-097D-1	Sequence 1, Appl	C 347	15	0.5	237	2	US-08-611-757-106	Sequence 106, App
275	16	0.5	7635	3	US-08-949-386-1	Sequence 1, Appl	C 348	15	0.5	237	2	US-08-485-910-3	Sequence 3, Appl
276	16	0.5	7635	3	US-08-450-562-1	Sequence 1, Appl	C 349	15	0.5	237	5	PCT-US95-05980-106	Sequence 106, App
277	16	0.5	7635	4	US-08-984-709A-1	Sequence 1, Appl	C 350	15	0.5	237	5	PCT-US95-06266-3	Sequence 3, Appl
278	16	0.5	7635	4	US-08-450-272-1	Sequence 1, Appl	C 351	15	0.5	240	1	US-08-222-177A-32	Sequence 32, Appl
279	16	0.5	7741	4	US-09-426-998-4	Sequence 4, Appl	C 352	15	0.5	249	1	US-09-103-675-13	Sequence 13, Appl
280	16	0.5	7832	4	US-09-004-838-94	Sequence 94, Appl	C 353	15	0.5	255	1	US-08-618-164-6	Sequence 6, Appl
281	16	0.5	7898	4	US-08-984-709A-49	Sequence 49, Appl	C 354	15	0.5	284	4	US-09-030-607-211	Sequence 211, App
282	16	0.5	8651	4	US-08-961-527-181	Sequence 181, App	C 355	15	0.5	264	4	US-09-605-785-211	Sequence 211, App
283	16	0.5	9540	1	US-07-689-008-1	Sequence 1, Appl	C 356	15	0.5	264	4	US-09-439-313-211	Sequence 211, App
284	16	0.5	10380	4	US-09-077-354B-3	Sequence 3, Appl	C 357	15	0.5	264	4	US-09-352-616A-211	Sequence 211, App
285	16	0.5	11459	4	US-09-454-721A-3	Sequence 3, Appl	C 358	15	0.5	264	4	US-09-232-149A-211	Sequence 211, App
286	16	0.5	12597	4	US-09-705-299-12	Sequence 12, Appl	C 359	15	0.5	267	3	US-09-188-930-72	Sequence 72, Appl
287	16	0.5	12847	1	US-08-550-715-1	Sequence 1, Appl	C 360	15	0.5	268	1	US-08-466-033-33	Sequence 33, Appl
288	16	0.5	14602	1	US-08-597-236-1	Sequence 1, Appl	C 361	15	0.5	268	1	US-08-444-733-33	Sequence 33, Appl
289	16	0.5	14602	1	US-08-746-682A-1	Sequence 1, Appl	C 362	15	0.5	268	2	US-08-464-134-33	Sequence 33, Appl
290	16	0.5	16836	4	US-09-147-236-1	Sequence 1, Appl	C 363	15	0.5	268	2	US-08-461-361-33	Sequence 33, Appl
291	16	0.5	16836	4	US-09-147-236-10	Sequence 10, Appl	C 364	15	0.5	268	2	US-08-485-910-33	Sequence 33, Appl
292	16	0.5	17606	4	US-08-943-731-4	Sequence 4, Appl	C 365	15	0.5	279	1	US-08-466-033-68	Sequence 68, Appl
293	16	0.5	18073	4	US-09-078-294-12	Sequence 12, Appl	C 366	15	0.5	279	1	US-08-444-733-68	Sequence 68, Appl
294	16	0.5	19011	1	US-08-310-356-36	Sequence 36, Appl	C 367	15	0.5	279	2	US-08-461-361-68	Sequence 68, Appl
295	16	0.5	19557	5	PCT-US92-06300-1	Sequence 1, Appl	C 368	15	0.5	279	2	US-08-485-910-68	Sequence 68, Appl
296	16	0.5	20598	4	US-09-593-995-10	Sequence 10, Appl	C 369	15	0.5	279	4	US-09-506-729-30	Sequence 30, Appl
297	16	0.5	22846	2	US-08-469-461-3	Sequence 3, Appl	C 370	15	0.5	279	5	PCT-US95-06266-52	Sequence 52, Appl
298	16	0.5	22846	3	US-07-890-609-3	Sequence 3, Appl	C 371	15	0.5	279	5	PCT-US95-06266-52	Sequence 52, Appl
299	16	0.5	24183	4	US-08-943-731-3	Sequence 3, Appl	C 372	15	0.5	282	1	US-08-466-033-66	Sequence 66, Appl
300	16	0.5	29604	3	US-08-781-891-207	Sequence 207, App	C 373	15	0.5	282	1	US-08-444-733-66	Sequence 66, Appl
301	16	0.5	32768	4	US-08-961-527-71	Sequence 71, App	C 374	15	0.5	282	2	US-08-464-134-66	Sequence 66, Appl
302	16	0.5	62804	4	US-09-800-960-3	Sequence 3, Appl	C 375	15	0.5	282	2	US-08-461-361-66	Sequence 66, Appl
303	16	0.5	72928	3	US-09-009-913-1	Sequence 1, Appl	C 376	15	0.5	282	2	US-08-485-910-66	Sequence 66, Appl
304	16	0.5	84495	4	US-09-797-906-3	Sequence 3, Appl	C 377	15	0.5	282	5	PCT-US95-06266-50	Sequence 50, Appl
305	16	0.5	98844	4	US-09-791-211-10	Sequence 10, Appl	C 378	15	0.5	291	1	US-08-171-385-24	Sequence 24, Appl
306	16	0.5	111282	4	US-09-754-250-3	Sequence 3, Appl	C 379	15	0.5	291	3	US-08-361-441B-24	Sequence 24, Appl
307	16	0.5	162450	4	US-09-345-882-1	Sequence 1, Appl	C 380	15	0.5	293	1	US-07-781-254A-23	Sequence 23, Appl
308	15	0.5	17	3	US-08-945-654-4	Sequence 4, Appl	C 381	15	0.5	297	4	US-09-134-001C-1862	Sequence 1862, Ap
309	15	0.5	20	4	US-09-487-445-67	Sequence 67, Appl	C 382	15	0.5	302	4	US-08-638-931-63	Sequence 63, Appl
310	15	0.5	20	4	US-09-657-481A-65	Sequence 65, Appl	C 383	15	0.5	310	4	US-09-404-879A-81	Sequence 81, Appl
311	15	0.5	24	4	US-09-103-875-87	Sequence 87, Appl	C 384	15	0.5	310	4	US-09-404-879A-308	Sequence 308, App
312	15	0.5	24	4	US-09-103-875-88	Sequence 88, Appl	C 385	15	0.5	317	4	US-08-991-789A-75	Sequence 75, Appl
313	15	0.5	29	3	US-09-029-819-13	Sequence 13, Appl	C 386	15	0.5	317	4	US-09-062-451-75	Sequence 75, Appl
314	15	0.5	30	4	US-09-264-693-7	Sequence 7, Appl	C 387	15	0.5	317	4	US-09-598-326-75	Sequence 75, Appl
315	15	0.5	32	1	US-08-453-862-5	Sequence 5, Appl	C 388	15	0.5	323	4	US-08-638-931-64	Sequence 64, Appl
316	15	0.5	32	2	US-08-452-734A-5	Sequence 5, Appl	C 389	15	0.5	325	4	US-08-638-931-53	Sequence 53, Appl
317	15	0.5	32	4	US-08-176-401B-5	Sequence 5, Appl	C 390	15	0.5	327	1	US-07-745-382-21	Sequence 21, Appl
318	15	0.5	33	4	US-09-424-620B-10	Sequence 10, Appl	C 391	15	0.5	327	1	US-07-921-848-21	Sequence 21, Appl
319	15	0.5	33	4	US-09-424-620B-16	Sequence 16, Appl	C 392	15	0.5	327	1	US-08-165-301A-21	Sequence 21, Appl

c 393	15	0.5	327	3	US-08-810-436-21	Sequence 21, Appl	c 466	15	0.5	450	3	US-09-032-894-16	Sequence 16, Appl
c 394	15	0.5	327	4	US-09-166-966E-6	Sequence 6, Appl	c 467	15	0.5	450	4	US-09-031-626-16	Sequence 16, Appl
c 395	15	0.5	327	5	PCT-US94-14179-21	Sequence 21, Appl	c 468	15	0.5	452	1	US-08-466-033-115	Sequence 115, Appl
c 396	15	0.5	328	1	US-08-455-550-5	Sequence 5, Appl	c 469	15	0.5	452	2	US-08-444-733-115	Sequence 115, Appl
c 397	15	0.5	330	1	US-08-466-033-90	Sequence 90, Appl	c 470	15	0.5	452	2	US-08-464-134-115	Sequence 115, Appl
c 398	15	0.5	330	1	US-08-444-733-90	Sequence 90, Appl	c 471	15	0.5	452	2	US-08-461-361-115	Sequence 115, Appl
c 399	15	0.5	330	2	US-08-464-134-90	Sequence 90, Appl	c 472	15	0.5	452	2	US-08-485-910-115	Sequence 115, Appl
c 400	15	0.5	330	2	US-08-461-361-90	Sequence 90, Appl	c 473	15	0.5	452	2	US-09-625-040-2	Sequence 2, Appl
c 401	15	0.5	330	2	US-08-485-910-90	Sequence 90, Appl	c 474	15	0.5	452	5	PCT-US95-06266-96	Sequence 96, Appl
c 402	15	0.5	330	4	US-09-134-001C-1138	Sequence 1138, Ap	c 475	15	0.5	455	1	US-08-843-521-3	Sequence 3, Appl
c 403	15	0.5	330	5	PCT-US95-06266-74	Sequence 74, Appl	c 476	15	0.5	455	4	US-09-012-871-3	Sequence 3, Appl
c 404	15	0.5	334	1	US-08-594-931-170	Sequence 170, App	c 477	15	0.5	458	2	US-08-486-663A-15	Sequence 15, Appl
c 405	15	0.5	336	4	US-08-638-931-1	Sequence 1, Appl	c 478	15	0.5	458	2	US-08-247-904B-15	Sequence 15, Appl
c 406	15	0.5	336	4	US-08-638-931-26	Sequence 26, Appl	c 479	15	0.5	458	3	US-08-767-942A-16	Sequence 16, Appl
c 407	15	0.5	336	4	US-08-638-931-27	Sequence 27, Appl	c 480	15	0.5	459	3	US-09-358-580-11	Sequence 11, Appl
c 408	15	0.5	336	4	US-08-638-931-28	Sequence 28, Appl	c 481	15	0.5	468	4	US-09-370-838-133	Sequence 133, Appl
c 409	15	0.5	336	4	US-08-638-931-29	Sequence 29, Appl	c 482	15	0.5	470	3	US-08-763-332-195	Sequence 195, Appl
c 410	15	0.5	336	4	US-08-638-931-32	Sequence 32, Appl	c 483	15	0.5	470	4	US-09-448-894-195	Sequence 195, Appl
c 411	15	0.5	336	4	US-08-638-931-33	Sequence 33, Appl	c 484	15	0.5	479	4	US-09-221-017B-652	Sequence 652, Appl
c 412	15	0.5	336	4	US-08-638-931-36	Sequence 36, Appl	c 485	15	0.5	483	4	US-09-171-461-37	Sequence 37, Appl
c 413	15	0.5	336	4	US-08-638-931-37	Sequence 37, Appl	c 486	15	0.5	484	4	US-09-370-838-276	Sequence 276, Appl
c 414	15	0.5	336	4	US-08-638-931-38	Sequence 38, Appl	c 487	15	0.5	494	4	US-09-221-017B-529	Sequence 529, Appl
c 415	15	0.5	336	4	US-08-638-931-40	Sequence 40, Appl	c 488	15	0.5	497	4	US-09-484-970B-76	Sequence 76, Appl
c 416	15	0.5	336	4	US-08-638-931-41	Sequence 41, Appl	c 489	15	0.5	500	1	US-07-753-462-1	Sequence 1, Appl
c 417	15	0.5	336	4	US-08-638-931-44	Sequence 44, Appl	c 490	15	0.5	500	1	US-08-199-317-1	Sequence 1, Appl
c 418	15	0.5	336	4	US-08-638-931-46	Sequence 46, Appl	c 491	15	0.5	500	4	US-09-147-751-3	Sequence 3, Appl
c 419	15	0.5	336	4	US-08-638-931-47	Sequence 47, Appl	c 492	15	0.5	501	4	US-09-741-243C-3	Sequence 3, Appl
c 420	15	0.5	340	4	US-08-638-931-62	Sequence 62, Appl	c 493	15	0.5	506	4	US-08-916-576B-10	Sequence 10, Appl
c 421	15	0.5	342	4	US-08-638-931-54	Sequence 54, Appl	c 494	15	0.5	507	4	US-09-257-894-5	Sequence 5, Appl
c 422	15	0.5	347	1	US-08-171-385-13	Sequence 13, Appl	c 495	15	0.5	514	6	5405952-3	Patent No. 5405952
c 423	15	0.5	347	3	US-08-361-441B-13	Sequence 13, Appl	c 496	15	0.5	536	3	US-09-040-508-3	Sequence 3, Appl
c 424	15	0.5	348	1	US-08-618-164-5	Sequence 5, Appl	c 497	15	0.5	536	4	US-09-500-654-3	Sequence 3, Appl
c 425	15	0.5	348	4	US-08-638-931-57	Sequence 57, Appl	c 498	15	0.5	543	4	US-09-221-017B-681	Sequence 681, Appl
c 426	15	0.5	349	4	US-08-638-931-55	Sequence 55, Appl	c 499	15	0.5	546	2	US-08-477-493-2	Sequence 2, Appl
c 427	15	0.5	350	4	US-08-638-931-49	Sequence 49, Appl	c 500	15	0.5	546	4	US-09-788-070-3	Sequence 3, Appl
c 428	15	0.5	350	4	US-08-638-931-66	Sequence 66, Appl	c 501	15	0.5	565	4	US-09-643-597-137	Sequence 137, Appl
c 429	15	0.5	353	4	US-09-242-901-21	Sequence 21, Appl	c 502	15	0.5	570	1	US-08-466-033-37	Sequence 37, Appl
c 430	15	0.5	354	2	US-08-958-201-1	Sequence 1, Appl	c 503	15	0.5	570	2	US-08-444-733-37	Sequence 37, Appl
c 431	15	0.5	354	2	US-08-958-201-3	Sequence 3, Appl	c 504	15	0.5	570	2	US-08-464-134-37	Sequence 37, Appl
c 432	15	0.5	354	4	US-08-638-931-60	Sequence 60, Appl	c 505	15	0.5	570	2	US-08-461-361-37	Sequence 37, Appl
c 433	15	0.5	359	4	US-08-638-931-51	Sequence 51, Appl	c 506	15	0.5	570	2	US-08-485-910-37	Sequence 37, Appl
c 434	15	0.5	360	4	US-08-638-931-67	Sequence 67, Appl	c 507	15	0.5	570	4	US-09-328-111-91	Sequence 91, Appl
c 435	15	0.5	360	4	US-09-011-769A-87	Sequence 87, Appl	c 508	15	0.5	570	5	PCT-US95-06266-28	Sequence 28, Appl
c 436	15	0.5	362	3	US-09-026-343-11	Sequence 11, Appl	c 509	15	0.5	573	2	US-08-286-819A-20	Sequence 20, Appl
c 437	15	0.5	362	4	US-08-638-931-52	Sequence 52, Appl	c 510	15	0.5	576	3	US-08-980-357-20	Sequence 20, Appl
c 438	15	0.5	362	4	US-09-362-871-11	Sequence 11, Appl	c 511	15	0.5	576	3	US-08-465-375-3	Sequence 3, Appl
c 439	15	0.5	364	1	US-08-466-033-50	Sequence 50, Appl	c 512	15	0.5	587	4	US-09-166-966E-1	Sequence 1, Appl
c 440	15	0.5	364	1	US-08-444-733-50	Sequence 50, Appl	c 513	15	0.5	589	4	US-09-328-111-149	Sequence 149, Appl
c 441	15	0.5	364	2	US-08-464-134-50	Sequence 50, Appl	c 514	15	0.5	597	4	US-09-623-040-3	Sequence 3, Appl
c 442	15	0.5	364	2	US-08-461-361-50	Sequence 50, Appl	c 515	15	0.5	608	4	US-09-328-111-655	Sequence 655, Appl
c 443	15	0.5	364	2	US-08-485-910-50	Sequence 50, Appl	c 516	15	0.5	610	4	US-09-812-484-27	Sequence 27, Appl
c 444	15	0.5	364	5	PCT-US95-06266-34	Sequence 34, Appl	c 517	15	0.5	613	4	US-09-442-143A-6	Sequence 6, Appl
c 445	15	0.5	370	2	US-08-457-752-1	Sequence 1, Appl	c 518	15	0.5	621	4	US-09-328-111-204	Sequence 204, Appl
c 446	15	0.5	374	4	US-08-638-931-48	Sequence 48, Appl	c 519	15	0.5	635	1	US-08-644-664B-7	Sequence 7, Appl
c 447	15	0.5	374	4	US-08-638-931-61	Sequence 61, Appl	c 520	15	0.5	635	2	US-08-761-277A-7	Sequence 7, Appl
c 448	15	0.5	390	1	US-08-203-196-5	Sequence 5, Appl	c 521	15	0.5	654	4	US-09-098-789-5	Sequence 5, Appl
c 449	15	0.5	390	5	PCT-US95-01976-5	Sequence 5, Appl	c 522	15	0.5	656	4	US-09-328-111-256	Sequence 256, Appl
c 450	15	0.5	402	1	US-08-466-033-159	Sequence 159, App	c 523	15	0.5	657	4	US-09-385-982-344	Sequence 344, Appl
c 451	15	0.5	402	1	US-08-444-733-159	Sequence 159, App	c 524	15	0.5	660	4	US-09-373-750-2	Sequence 2, Appl
c 452	15	0.5	402	2	US-08-464-134-159	Sequence 159, App	c 525	15	0.5	661	4	US-08-943-731-186	Sequence 186, Appl
c 453	15	0.5	402	2	US-08-461-361-159	Sequence 159, App	c 526	15	0.5	684	4	US-09-328-111-306	Sequence 306, Appl
c 454	15	0.5	402	2	US-08-485-910-159	Sequence 159, App	c 527	15	0.5	691	3	US-08-933-750C-57	Sequence 57, Appl
c 455	15	0.5	406	4	US-09-060-756-563	Sequence 563, App	c 528	15	0.5	691	3	US-09-234-613-57	Sequence 57, Appl
c 456	15	0.5	427	4	US-08-615-192A-128	Sequence 128, App	c 529	15	0.5	696	4	US-08-998-416-1134	Sequence 1134, Ap
c 457	15	0.5	430	2	US-08-611-757-104	Sequence 104, App	c 530	15	0.5	697	4	US-09-347-001-5	Sequence 5, Appl
c 458	15	0.5	430	5	PCT-US95-05980-104	Sequence 104, App	c 531	15	0.5	702	4	US-08-858-207A-211	Sequence 211, App
c 459	15	0.5	436	4	US-09-397-787-253	Sequence 253, App	c 532	15	0.5	705	4	US-09-134-001C-358	Sequence 358, App
c 460	15	0.5	439	4	US-09-397-787-273	Sequence 273, App	c 533	15	0.5	717	4	US-09-124-238A-7	Sequence 7, Appl
c 461	15	0.5	441	1	US-07-781-254A-8	Sequence 8, Appl	c 534	15	0.5	717	4	US-09-721-975-7	Sequence 7, Appl
c 462	15	0.5	441	2	US-08-975-316-60	Sequence 60, Appl	c 535	15	0.5	722	4	US-08-998-416-1095	Sequence 1095, Ap
c 463	15	0.5	441	4	US-09-615-192A-60	Sequence 60, Appl	c 536	15	0.5	745	4	US-09-328-111-693	Sequence 683, App
c 464	15	0.5	450	2	US-08-890-980-16	Sequence 16, Appl	c 537	15	0.5				
c 465	15	0.5	450	3	US-08-890-979-16	Sequence 16, Appl	c 538	15	0.5				

539	15	0.5	755	4	US-09-198-119C-80	Sequence 80, Appl	c 612	15	0.5	1116	2	US-08-805-965-4	Sequence 4, Appl
540	15	0.5	763	4	US-09-221-017B-723	Sequence 723, Appl	c 613	15	0.5	1116	4	US-09-221-017B-125	Sequence 125, App
c 541	15	0.5	773	4	US-09-227-357-47	Sequence 47, Appl	c 614	15	0.5	1121	1	US-08-086-410-36	Sequence 36, Appl
542	15	0.5	775	3	US-09-124-476-1	Sequence 1, Appl	c 615	15	0.5	1121	1	US-08-314-586-39	Sequence 39, Appl
543	15	0.5	775	4	US-09-577-796A-1	Sequence 1, Appl	616	15	0.5	1122	1	US-08-375-962B-10	Sequence 10, Appl
544	15	0.5	793	4	US-09-198-119C-90	Sequence 90, Appl	617	15	0.5	1122	2	US-08-562-114B-10	Sequence 10, Appl
545	15	0.5	795	3	US-08-969-644-15	Sequence 15, Appl	618	15	0.5	1122	4	US-08-729-594A-10	Sequence 10, Appl
546	15	0.5	795	3	US-08-444-189-15	Sequence 15, Appl	619	15	0.5	1122	4	US-09-134-001C-1192	Sequence 1192, Ap
547	15	0.5	795	4	US-08-468-544-15	Sequence 15, Appl	620	15	0.5	1122	4	US-08-937-993-10	Sequence 10, Appl
548	15	0.5	807	1	US-08-431-080-21	Sequence 21, Appl	621	15	0.5	1123	1	US-08-700-626-2	Sequence 2, Appl
c 549	15	0.5	807	1	US-08-431-080-31	Sequence 31, Appl	622	15	0.5	1128	2	US-08-562-114B-14	Sequence 14, Appl
550	15	0.5	807	2	US-08-938-534-21	Sequence 21, Appl	623	15	0.5	1128	4	US-08-729-594A-14	Sequence 14, Appl
c 551	15	0.5	807	2	US-08-938-534-31	Sequence 31, Appl	624	15	0.5	1128	4	US-09-880-427-5	Sequence 5, Appl
552	15	0.5	807	4	US-09-345-294-21	Sequence 21, Appl	625	15	0.5	1128	4	US-09-306-538B-5	Sequence 5, Appl
c 553	15	0.5	807	4	US-09-345-294-31	Sequence 31, Appl	626	15	0.5	1128	4	US-09-134-001C-2242	Sequence 2242, Ap
554	15	0.5	832	4	US-09-198-119C-82	Sequence 82, Appl	627	15	0.5	1128	4	US-08-937-993-14	Sequence 14, Appl
555	15	0.5	833	2	US-08-837-029-1	Sequence 1, Appl	c 628	15	0.5	1137	1	US-08-706-214-2	Sequence 2, Appl
556	15	0.5	846	2	US-08-179-557-32	Sequence 32, Appl	c 629	15	0.5	1140	2	US-08-698-805-5	Sequence 5, Appl
c 557	15	0.5	863	1	US-08-592-126-71	Sequence 71, Appl	c 630	15	0.5	1168	4	US-09-484-970B-89	Sequence 89, Appl
c 558	15	0.5	870	4	US-09-360-017-2	Sequence 2, Appl	c 631	15	0.5	1176	4	US-09-134-001C-853	Sequence 853, App
c 559	15	0.5	898	1	US-08-419-078-3	Sequence 3, Appl	c 632	15	0.5	1183	1	US-08-188-582-25	Sequence 25, Appl
c 560	15	0.5	898	1	US-08-726-883-3	Sequence 3, Appl	c 633	15	0.5	1183	1	US-08-646-715-25	Sequence 25, Appl
c 561	15	0.5	900	1	US-08-459-264-1	Sequence 1, Appl	c 634	15	0.5	1197	4	US-09-134-001C-1516	Sequence 1516, Ap
c 562	15	0.5	900	1	US-08-459-263-1	Sequence 1, Appl	c 635	15	0.5	1206	2	US-08-318-947A-1	Sequence 1, Appl
c 563	15	0.5	906	1	US-07-920-519-3	Sequence 3, Appl	c 636	15	0.5	1206	2	US-08-795-303-1	Sequence 1, Appl
c 564	15	0.5	906	1	US-07-920-519-4	Sequence 4, Appl	637	15	0.5	1221	2	US-08-934-846-3	Sequence 3, Appl
c 565	15	0.5	906	1	US-07-920-519-6	Sequence 6, Appl	638	15	0.5	1221	2	US-09-238-557-3	Sequence 3, Appl
c 566	15	0.5	906	1	US-08-314-586-3	Sequence 3, Appl	c 639	15	0.5	1227	2	US-08-683-007A-1	Sequence 1, Appl
c 567	15	0.5	906	1	US-08-314-586-4	Sequence 4, Appl	640	15	0.5	1230	4	US-08-940-424-1	Sequence 1, Appl
c 568	15	0.5	906	1	US-08-314-586-6	Sequence 6, Appl	c 641	15	0.5	1235	4	US-08-642-274D-36	Sequence 36, Appl
c 569	15	0.5	906	3	US-08-115-753-31	Sequence 31, Appl	c 642	15	0.5	1235	4	US-08-952-014C-36	Sequence 36, Appl
c 570	15	0.5	906	4	US-09-347-878-57	Sequence 57, Appl	c 643	15	0.5	1240	5	US-08-103-998-1	Sequence 1, Appl
c 571	15	0.5	913	2	US-08-975-316-61	Sequence 61, Appl	644	15	0.5	1242	5	PCT-US91-00909-3	Sequence 3, Appl
c 572	15	0.5	913	2	US-09-615-192B-61	Sequence 61, Appl	645	15	0.5	1254	2	US-08-934-846-1	Sequence 1, Appl
c 573	15	0.5	920	1	US-07-920-519-36	Sequence 36, Appl	646	15	0.5	1254	4	US-09-238-557-1	Sequence 1, Appl
c 574	15	0.5	920	1	US-08-314-586-36	Sequence 36, Appl	647	15	0.5	1254	5	PCT-US91-00909-1	Sequence 1, Appl
575	15	0.5	930	4	US-09-134-001C-202	Sequence 202, App	648	15	0.5	1261	3	US-08-961-083-25	Sequence 25, Appl
576	15	0.5	973	3	US-09-013-881-16	Sequence 16, Appl	c 649	15	0.5	1262	4	US-07-715-751B-3	Sequence 3, Appl
c 577	15	0.5	973	3	US-09-013-881-16	Sequence 16, Appl	650	15	0.5	1262	4	US-09-359-161-1	Sequence 1, Appl
578	15	0.5	980	1	US-08-452-267-1	Sequence 1, Appl	651	15	0.5	1277	1	US-08-176-427B-1	Sequence 1, Appl
579	15	0.5	980	3	US-09-123-044-1	Sequence 1, Appl	652	15	0.5	1277	2	US-08-356-060A-1	Sequence 1, Appl
580	15	0.5	993	1	US-08-466-033-165	Sequence 165, App	653	15	0.5	1277	4	US-08-460-900C-1	Sequence 1, Appl
581	15	0.5	993	3	US-08-444-733-165	Sequence 165, App	654	15	0.5	1277	4	US-08-674-509B-1	Sequence 1, Appl
582	15	0.5	993	2	US-08-464-134-165	Sequence 165, App	655	15	0.5	1277	4	US-08-954-698-1	Sequence 1, Appl
583	15	0.5	993	2	US-08-461-361-165	Sequence 165, App	656	15	0.5	1277	4	US-08-957-874-1	Sequence 1, Appl
584	15	0.5	993	2	US-08-485-910-165	Sequence 165, App	657	15	0.5	1277	4	US-09-325-256-5	Sequence 5, Appl
585	15	0.5	1001	4	US-09-641-638-82	Sequence 82, Appl	c 658	15	0.5	1278	4	US-09-134-001C-58	Sequence 58, Appl
c 586	15	0.5	1001	4	US-09-641-638-209	Sequence 209, App	c 659	15	0.5	1286	2	US-08-807-200-3	Sequence 3, Appl
587	15	0.5	1002	4	US-09-625-040-4	Sequence 4, Appl	c 660	15	0.5	1286	4	US-09-001-777-3	Sequence 3, Appl
c 588	15	0.5	1002	4	US-09-641-638-583	Sequence 583, App	661	15	0.5	1287	4	US-08-845-258-11	Sequence 11, Appl
c 589	15	0.5	1002	4	US-09-641-638-594	Sequence 594, App	662	15	0.5	1287	4	US-08-990-571-11	Sequence 11, Appl
590	15	0.5	1005	2	US-08-844-312-3	Sequence 3, Appl	663	15	0.5	1287	4	US-08-723-142A-11	Sequence 11, Appl
c 591	15	0.5	1007	4	US-09-247-155-81	Sequence 81, Appl	664	15	0.5	1287	4	US-09-528-784A-11	Sequence 11, Appl
592	15	0.5	1008	4	US-09-095-117-1	Sequence 1, Appl	665	15	0.5	1290	1	US-08-638-911A-55	Sequence 55, Appl
593	15	0.5	1008	4	US-09-095-117-3	Sequence 3, Appl	666	15	0.5	1290	2	US-08-844-312-1	Sequence 1, Appl
c 594	15	0.5	1009	4	US-09-291-922-15	Sequence 15, Appl	c 667	15	0.5	1301	5	US-08-983-502-19	Sequence 19, Appl
595	15	0.5	1011	1	US-08-466-033-161	Sequence 161, App	c 668	15	0.5	1301	5	PCT-US96-10521-19	Sequence 19, Appl
596	15	0.5	1011	2	US-08-444-733-161	Sequence 161, App	669	15	0.5	1302	4	US-09-255-368-5	Sequence 5, Appl
597	15	0.5	1011	2	US-08-464-134-161	Sequence 161, App	670	15	0.5	1320	4	US-09-370-838-22	Sequence 22, Appl
598	15	0.5	1011	2	US-08-461-361-161	Sequence 161, App	c 671	15	0.5	1322	1	US-08-419-078-1	Sequence 1, Appl
599	15	0.5	1011	2	US-08-485-910-161	Sequence 161, App	c 672	15	0.5	1322	1	US-08-726-883-1	Sequence 1, Appl
c 600	15	0.5	1013	1	US-07-920-519-30	Sequence 30, Appl	c 673	15	0.5	1322	4	US-09-579-236-3	Sequence 3, Appl
c 601	15	0.5	1013	1	US-08-086-410-23	Sequence 23, Appl	c 674	15	0.5	1323	4	US-08-983-502-15	Sequence 15, Appl
c 602	15	0.5	1013	1	US-08-314-586-30	Sequence 30, Appl	c 675	15	0.5	1323	5	PCT-US96-10521-15	Sequence 15, Appl
c 603	15	0.5	1037	2	US-08-824-405-1	Sequence 1, Appl	676	15	0.5	1328	4	US-09-370-838-24	Sequence 24, Appl
c 604	15	0.5	1038	1	US-07-661-610C-13	Sequence 13, Appl	c 677	15	0.5	1330	2	US-08-807-200-1	Sequence 1, Appl
605	15	0.5	1046	1	US-08-361-467B-4	Sequence 4, Appl	c 678	15	0.5	1330	4	US-09-001-777-1	Sequence 27, Appl
606	15	0.5	1046	1	US-08-484-332C-4	Sequence 4, Appl	679	15	0.5	1331	4	US-09-370-838-27	Sequence 27, Appl
607	15	0.5	1065	2	US-08-512-955-1	Sequence 1, Appl	680	15	0.5	1333	4	US-09-370-838-28	Sequence 28, Appl
608	15	0.5	1073	3	US-08-311-423-1	Sequence 1, Appl	c 681	15	0.5	1334	4	US-08-922-957-2	Sequence 2, Appl
609	15	0.5	1079	1	US-08-270-583-1	Sequence 1, Appl	c 682	15	0.5	1335	3	US-08-714-918-94	Sequence 94, Appl
610	15	0.5	1079	1	US-08-783-889A-1	Sequence 1, Appl	c 683	15	0.5	1335	4	US-09-265-315-94	Sequence 94, Appl
611	15	0.5	1102	3	US-09-067-089-1	Sequence 1, Appl	c 684	15	0.5	1335	4	US-09-265-315-94	Sequence 94, Appl

c 685	15	0.5	1335	4	US-09-266-417-94	Sequence 94, Appl	c 758	15	0.5	1615	3	US-09-040-508-1	Sequence 1, Appl
c 686	15	0.5	1335	4	US-09-740-028A-1	Sequence 1, Appl	c 759	15	0.5	1615	4	US-09-500-654-1	Sequence 1, Appl
687	15	0.5	1339	4	US-09-556-877-64	Sequence 64, Appl	c 760	15	0.5	1617	4	US-09-444-336-4	Sequence 4, Appl
688	15	0.5	1339	4	US-09-620-412C-64	Sequence 64, Appl	761	15	0.5	1620	4	US-09-124-238A-32	Sequence 32, Appl
689	15	0.5	1344	1	US-08-844-010-1	Sequence 1, Appl	762	15	0.5	1620	4	US-09-721-975-32	Sequence 32, Appl
690	15	0.5	1344	1	US-08-341-456A-10	Sequence 10, Appl	c 763	15	0.5	1620	4	US-08-464-517-35	Sequence 35, Appl
691	15	0.5	1344	2	US-08-478-414A-10	Sequence 10, Appl	c 764	15	0.5	1624	2	US-08-246-361A-35	Sequence 35, Appl
692	15	0.5	1344	2	US-08-325-240A-10	Sequence 10, Appl	c 765	15	0.5	1624	2	US-08-463-772-35	Sequence 35, Appl
693	15	0.5	1344	3	US-09-012-873-1	Sequence 1, Appl	c 766	15	0.5	1624	5	PCT-US93-05000-35	Sequence 35, Appl
694	15	0.5	1344	3	US-08-898-983-10	Sequence 10, Appl	767	15	0.5	1626	4	US-09-158-767-14	Sequence 14, Appl
695	15	0.5	1344	4	US-09-371-261-10	Sequence 10, Appl	c 768	15	0.5	1631	1	US-08-583-318-4	Sequence 4, Appl
c 696	15	0.5	1355	2	US-08-618-408B-3	Sequence 3, Appl	769	15	0.5	1634	4	US-09-126-420A-2	Sequence 2, Appl
697	15	0.5	1355	4	US-09-370-838-31	Sequence 31, Appl	770	15	0.5	1636	4	US-09-117-853-7	Sequence 7, Appl
c 698	15	0.5	1360	4	US-08-858-207A-65	Sequence 65, Appl	771	15	0.5	1642	4	US-09-117-853-5	Sequence 5, Appl
c 699	15	0.5	1377	1	US-08-638-911A-38	Sequence 38, Appl	772	15	0.5	1642	4	US-09-117-853-9	Sequence 9, Appl
700	15	0.5	1378	1	US-08-592-126-72	Sequence 72, Appl	773	15	0.5	1643	3	US-09-117-853-3	Sequence 3, Appl
c 701	15	0.5	1382	1	US-08-350-325A-6	Sequence 6, Appl	c 774	15	0.5	1644	3	US-08-852-782-1	Sequence 1, Appl
702	15	0.5	1382	5	PCT-US94-03856-6	Sequence 6, Appl	775	15	0.5	1644	4	US-09-124-238A-9	Sequence 9, Appl
703	15	0.5	1383	1	US-08-484-044-1	Sequence 1, Appl	776	15	0.5	1644	4	US-09-721-975-9	Sequence 9, Appl
c 704	15	0.5	1393	4	US-09-147-751-4	Sequence 4, Appl	c 777	15	0.5	1653	4	US-09-741-243C-1	Sequence 1, Appl
705	15	0.5	1401	4	US-09-134-001C-183	Sequence 183, App	778	15	0.5	1665	4	US-09-124-238A-33	Sequence 33, Appl
706	15	0.5	1404	4	US-09-134-001C-398	Sequence 398, App	779	15	0.5	1665	4	US-09-721-975-33	Sequence 33, Appl
c 707	15	0.5	1408	1	US-08-447-554-3	Sequence 3, Appl	c 780	15	0.5	1673	4	US-09-381-849-6	Sequence 6, Appl
c 708	15	0.5	1408	1	US-08-448-160-3	Sequence 3, Appl	781	15	0.5	1689	4	US-09-124-238A-22	Sequence 22, Appl
709	15	0.5	1408	2	US-08-632-470-40	Sequence 40, Appl	782	15	0.5	1689	5	US-09-721-975-22	Sequence 22, Appl
c 710	15	0.5	1412	4	US-09-615-192A-129	Sequence 129, App	783	15	0.5	1709	4	US-08-936-165A-188	Sequence 188, App
711	15	0.5	1420	3	US-08-358-171-1	Sequence 1, Appl	c 784	15	0.5	1720	3	US-09-227-357-139	Sequence 139, App
712	15	0.5	1420	3	US-09-090-947-1	Sequence 1, Appl	c 785	15	0.5	1728	4	US-08-913-805A-1	Sequence 1, Appl
713	15	0.5	1427	2	US-08-632-470-27	Sequence 27, Appl	786	15	0.5	1728	4	US-09-442-629-1	Sequence 1, Appl
714	15	0.5	1430	2	US-08-204-288-4	Sequence 4, Appl	787	15	0.5	1730	3	US-09-222-817-11	Sequence 11, Appl
715	15	0.5	1432	2	US-08-632-470-25	Sequence 25, Appl	788	15	0.5	1730	3	US-09-222-817-13	Sequence 13, Appl
716	15	0.5	1432	2	US-08-632-470-32	Sequence 32, Appl	789	15	0.5	1730	4	US-09-222-786-11	Sequence 11, Appl
717	15	0.5	1436	2	US-08-632-470-34	Sequence 34, Appl	790	15	0.5	1730	4	US-09-222-786-13	Sequence 13, Appl
718	15	0.5	1438	2	US-08-632-470-24	Sequence 24, Appl	791	15	0.5	1737	4	US-09-126-420A-1	Sequence 1, Appl
719	15	0.5	1439	2	US-08-632-470-31	Sequence 31, Appl	792	15	0.5	1744	4	US-09-221-017B-219	Sequence 219, App
720	15	0.5	1439	2	US-08-632-470-42	Sequence 42, Appl	793	15	0.5	1758	4	US-09-370-838-25	Sequence 25, Appl
c 721	15	0.5	1440	2	US-08-807-200-11	Sequence 11, Appl	794	15	0.5	1785	2	US-08-559-507-3	Sequence 3, Appl
722	15	0.5	1440	2	US-08-632-470-23	Sequence 23, Appl	c 795	15	0.5	1785	2	US-08-749-907-3	Sequence 3, Appl
723	15	0.5	1440	2	US-08-632-470-26	Sequence 26, Appl	c 796	15	0.5	1785	4	US-09-241-581B-7	Sequence 7, Appl
724	15	0.5	1440	2	US-08-632-470-28	Sequence 28, Appl	c 797	15	0.5	1785	5	PCT-US95-07721-7	Sequence 7, Appl
725	15	0.5	1440	2	US-08-632-470-29	Sequence 29, Appl	c 798	15	0.5	1788	2	US-08-559-505-1	Sequence 1, Appl
726	15	0.5	1440	2	US-08-632-470-33	Sequence 33, Appl	c 799	15	0.5	1788	2	US-08-737-371A-3	Sequence 3, Appl
727	15	0.5	1440	2	US-08-632-470-35	Sequence 35, Appl	c 800	15	0.5	1788	2	US-08-741-907-1	Sequence 1, Appl
728	15	0.5	1440	2	US-08-632-470-36	Sequence 36, Appl	c 801	15	0.5	1788	4	US-08-265-428-3	Sequence 3, Appl
729	15	0.5	1440	2	US-08-632-470-39	Sequence 39, Appl	c 802	15	0.5	1788	5	PCT-US95-07721-3	Sequence 3, Appl
730	15	0.5	1440	2	US-08-632-470-37	Sequence 37, Appl	c 803	15	0.5	1788	4	US-08-265-428-3	Sequence 3, Appl
731	15	0.5	1440	2	US-08-632-470-41	Sequence 41, Appl	c 804	15	0.5	1812	4	US-09-008-097-3	Sequence 3, Appl
732	15	0.5	1440	2	US-08-632-470-43	Sequence 43, Appl	c 805	15	0.5	1814	2	US-08-483-151-1	Sequence 1, Appl
733	15	0.5	1440	2	US-08-632-470-46	Sequence 46, Appl	806	15	0.5	1814	5	PCT-US96-06427-1	Sequence 1, Appl
c 734	15	0.5	1440	3	US-08-852-782-2	Sequence 2, Appl	c 807	15	0.5	1825	2	US-08-890-980-3	Sequence 3, Appl
c 735	15	0.5	1440	4	US-09-001-777-11	Sequence 11, Appl	c 808	15	0.5	1825	3	US-08-890-979-3	Sequence 3, Appl
736	15	0.5	1441	2	US-08-632-470-38	Sequence 38, Appl	c 809	15	0.5	1825	3	US-09-032-894-3	Sequence 3, Appl
737	15	0.5	1442	2	US-08-632-470-30	Sequence 30, Appl	c 810	15	0.5	1825	4	US-09-031-626-3	Sequence 3, Appl
c 738	15	0.5	1443	4	US-08-983-502-33	Sequence 33, Appl	c 811	15	0.5	1827	2	US-08-737-371A-3	Sequence 3, Appl
c 739	15	0.5	1443	5	PCT-US96-10521-33	Sequence 33, Appl	812	15	0.5	1827	5	US-09-310-275-1	Sequence 1, Appl
740	15	0.5	1448	4	US-09-625-040-1	Sequence 1, Appl	c 813	15	0.5	1840	1	US-08-399-696-126	Sequence 126, App
741	15	0.5	1450	3	US-09-108-020-15	Sequence 15, Appl	c 814	15	0.5	1846	3	US-09-173-581-15	Sequence 15, Appl
742	15	0.5	1458	2	US-08-632-470-45	Sequence 45, Appl	c 815	15	0.5	1846	4	US-09-420-915-15	Sequence 15, Appl
743	15	0.5	1488	4	US-09-124-238A-8	Sequence 8, Appl	c 816	15	0.5	1849	1	US-08-399-696-3	Sequence 3, Appl
744	15	0.5	1488	4	US-09-721-975-8	Sequence 8, Appl	c 817	15	0.5	1853	4	US-08-952-061-1	Sequence 1, Appl
c 745	15	0.5	1493	4	US-09-561-756-25	Sequence 25, Appl	818	15	0.5	1855	3	US-08-961-083-71	Sequence 71, Appl
c 746	15	0.5	1493	4	US-09-227-721-25	Sequence 25, Appl	c 819	15	0.5	1855	3	US-08-706-214-1	Sequence 1, Appl
747	15	0.5	1508	2	US-08-632-470-44	Sequence 44, Appl	c 820	15	0.5	1859	4	US-09-724-864-22	Sequence 22, Appl
c 748	15	0.5	1512	4	US-09-134-001C-643	Sequence 643, App	c 821	15	0.5	1860	4	US-09-178-252-19	Sequence 19, Appl
749	15	0.5	1530	4	US-09-444-336-3	Sequence 3, Appl	c 822	15	0.5	1863	1	US-07-781-254A-4	Sequence 4, Appl
c 750	15	0.5	1533	5	PCT-US91-04274A-1	Sequence 1, Appl	c 823	15	0.5	1863	1	US-07-781-254A-4	Sequence 4, Appl
751	15	0.5	1535	4	US-09-668-680-12	Sequence 12, Appl	824	15	0.5	1880	2	US-08-845-161A-3	Sequence 3, Appl
c 752	15	0.5	1582	4	US-09-210-422-4	Sequence 4, Appl	825	15	0.5	1880	4	US-09-168-218B-2	Sequence 2, Appl
753	15	0.5	1588	4	US-08-617-785-7	Sequence 7, Appl	826	15	0.5	1881	6	5268290-1	Patent No. 5268290
754	15	0.5	1594	2	US-08-933-750C-61	Sequence 61, Appl	c 827	15	0.5	1881	4	US-09-168-218B-2	Sequence 2, Appl
755	15	0.5	1594	3	US-09-234-613-61	Sequence 61, Appl	c 828	15	0.5	1883	1	US-08-665-220-3	Sequence 3, Appl
756	15	0.5	1597	1	US-08-166-316-1	Sequence 1, Appl	c 829	15	0.5	1883	4	US-09-487-445-3	Sequence 3, Appl
c 757	15	0.5	1600	1	US-08-631-427A-6	Sequence 6, Appl	c 830	15	0.5	1883	4	US-09-487-445-3	Sequence 3, Appl

c 831	15	0.5	1883	4	US-09-291-692-3	Sequence 3, Appli	904	15	0.5	2287	4	US-09-528-784A-8	Sequence 8, Appli
c 832	15	0.5	1897	6	RE34606-5	Patent No. RE34,60	c 905	15	0.5	2309	4	US-09-091-725-9	Sequence 9, Appli
c 833	15	0.5	1910	4	US-09-071-709-8	Sequence 8, Appli	c 906	15	0.5	2322	4	US-08-618-164-1	Sequence 1, Appli
c 834	15	0.5	1910	4	US-09-221-017B-234	Sequence 234, App	c 907	15	0.5	2350	1	US-08-843-521-1	Sequence 1, Appli
c 835	15	0.5	1911	1	US-08-258-420-8	Sequence 8, Appli	c 908	15	0.5	2350	1	US-09-012-871-1	Sequence 1, Appli
c 836	15	0.5	1915	1	US-08-496-855A-5	Sequence 5, Appli	c 909	15	0.5	2360	1	US-08-039-364-1	Sequence 1, Appli
c 837	15	0.5	1915	2	US-08-466-589-11	Sequence 11, Appl	c 910	15	0.5	2360	1	US-09-158-710-1	Sequence 9, Appli
c 838	15	0.5	1915	2	US-08-700-636-11	Sequence 11, Appl	c 911	15	0.5	2375	1	US-08-468-853-9	Sequence 9, Appli
c 839	15	0.5	1915	3	US-08-467-574-11	Sequence 11, Appl	c 912	15	0.5	2375	1	US-08-468-855-9	Sequence 9, Appli
c 840	15	0.5	1915	4	US-09-217-345-11	Sequence 11, Appl	c 913	15	0.5	2375	1	US-08-310-357-9	Sequence 9, Appli
c 841	15	0.5	1915	4	US-08-487-596-17	Sequence 17, Appl	c 914	15	0.5	2375	1	US-08-468-852-9	Sequence 9, Appli
c 842	15	0.5	1920	2	US-08-855-714-1	Sequence 1, Appli	c 915	15	0.5	2375	2	US-08-468-857-9	Sequence 9, Appli
c 843	15	0.5	1934	4	US-09-579-236-1	Sequence 1, Appli	c 916	15	0.5	2381	2	US-08-736-770-4	Sequence 4, Appli
c 844	15	0.5	1953	3	US-08-826-246-1	Sequence 1, Appli	c 917	15	0.5	2388	1	US-08-638-911A-56	Sequence 56, Appl
c 845	15	0.5	1953	3	US-08-944-495-1	Sequence 1, Appli	c 918	15	0.5	2389	1	US-08-153-563-2	Sequence 2, Appli
c 846	15	0.5	1953	3	US-09-126-640-1	Sequence 1, Appli	c 919	15	0.5	2389	2	US-08-460-507-2	Sequence 2, Appli
c 847	15	0.5	1953	4	US-08-925-588-1	Sequence 1, Appli	c 920	15	0.5	2415	4	US-08-989-299-3	Sequence 3, Appli
c 848	15	0.5	1953	4	US-09-288-292A-1	Sequence 1, Appli	c 921	15	0.5	2430	2	US-08-488-199-3	Sequence 3, Appli
c 849	15	0.5	1962	1	US-08-399-696-1	Sequence 1, Appli	c 922	15	0.5	2431	3	US-08-985-526-35	Sequence 35, Appl
c 850	15	0.5	1964	4	US-09-117-853-1	Sequence 1, Appli	c 923	15	0.5	2435	4	US-09-484-970B-134	Sequence 134, App
c 851	15	0.5	1965	1	US-08-258-420-9	Sequence 9, Appli	c 924	15	0.5	2472	4	US-09-626-589-6	Sequence 6, Appli
c 852	15	0.5	2000	4	US-09-537-720B-3	Sequence 3, Appli	c 925	15	0.5	2477	1	US-08-429-742-1	Sequence 1, Appli
c 853	15	0.5	2001	3	US-08-850-961-13	Sequence 13, Appl	c 926	15	0.5	2481	2	US-08-937-931-7	Sequence 7, Appli
c 854	15	0.5	2001	4	US-09-479-776-13	Sequence 13, Appl	c 927	15	0.5	2481	4	US-09-285-502-7	Sequence 7, Appli
c 855	15	0.5	2001	4	US-09-315-127-10	Sequence 10, Appl	c 928	15	0.5	2481	4	US-09-709-126-7	Sequence 7, Appli
c 856	15	0.5	2002	4	US-09-315-127-7	Sequence 7, Appli	c 929	15	0.5	2481	4	US-09-871-385A-7	Sequence 7, Appli
c 857	15	0.5	2009	4	US-09-380-061B-17	Sequence 17, Appl	c 930	15	0.5	2492	3	US-08-695-191-3	Sequence 3, Appli
c 858	15	0.5	2010	4	US-08-487-183A-15	Sequence 15, Appl	c 931	15	0.5	2492	3	US-08-682-080-3	Sequence 3, Appli
c 859	15	0.5	2019	4	US-09-160-494-3	Sequence 3, Appli	c 932	15	0.5	2555	2	US-08-960-022-15	Sequence 15, Appl
c 860	15	0.5	2031	2	US-08-933-750C-53	Sequence 53, Appl	c 933	15	0.5	2556	3	US-08-699-103B-9	Sequence 9, Appli
c 861	15	0.5	2031	3	US-09-234-613-53	Sequence 53, Appl	c 934	15	0.5	2556	4	US-09-229-059-9	Sequence 9, Appli
c 862	15	0.5	2042	2	US-08-933-821-16	Sequence 16, Appl	c 935	15	0.5	2566	4	US-09-270-542-124	Sequence 124, App
c 863	15	0.5	2042	3	US-08-934-494-5	Sequence 5, Appli	c 936	15	0.5	2575	1	US-08-135-511-33	Sequence 33, Appl
c 864	15	0.5	2042	3	US-08-960-507-16	Sequence 16, Appl	c 937	15	0.5	2575	1	US-08-483-852-10	Sequence 10, Appl
c 865	15	0.5	2042	3	US-09-143-068-5	Sequence 5, Appli	c 938	15	0.5	2575	1	US-08-361-458-5	Sequence 5, Appli
c 866	15	0.5	2042	4	US-09-143-707-5	Sequence 5, Appli	c 939	15	0.5	2575	1	US-08-477-953-10	Sequence 10, Appl
c 867	15	0.5	2042	4	US-09-202-089-5	Sequence 5, Appli	c 940	15	0.5	2575	2	US-08-187-453-33	Sequence 33, Appl
c 868	15	0.5	2042	4	US-09-136-828-16	Sequence 16, Appl	c 941	15	0.5	2575	2	US-08-477-952-10	Sequence 10, Appl
c 869	15	0.5	2042	4	US-09-332-928A-16	Sequence 16, Appl	c 942	15	0.5	2581	4	US-09-363-708-1	Sequence 1, Appli
c 870	15	0.5	2042	4	US-09-511-133-5	Sequence 5, Appli	c 943	15	0.5	2599	2	US-08-239-276-7	Sequence 7, Appli
c 871	15	0.5	2042	4	US-09-136-801-16	Sequence 16, Appl	c 944	15	0.5	2599	2	US-08-468-579B-7	Sequence 7, Appli
c 872	15	0.5	2042	4	US-09-332-929-16	Sequence 16, Appl	c 945	15	0.5	2599	3	US-08-468-577B-7	Sequence 7, Appli
c 873	15	0.5	2042	4	US-09-690-169-5	Sequence 5, Appli	c 946	15	0.5	2617	1	US-08-430-024-1	Sequence 1, Appli
c 874	15	0.5	2042	4	US-09-511-631-5	Sequence 5, Appli	c 947	15	0.5	2617	1	US-08-782-009-1	Sequence 1, Appli
c 875	15	0.5	2087	4	US-09-257-894-9	Sequence 9, Appli	c 948	15	0.5	2619	3	US-09-017-302-1	Sequence 1, Appli
c 876	15	0.5	2111	1	US-08-528-255A-2	Sequence 2, Appli	c 949	15	0.5	2619	5	US-08-983-502-17	Sequence 17, Appl
c 877	15	0.5	2111	4	US-08-717-365-2	Sequence 2, Appli	c 950	15	0.5	2619	2	PCT-US96-10521-17	Sequence 17, Appl
c 878	15	0.5	2138	2	US-09-276-531-22	Sequence 22, Appl	c 951	15	0.5	2630	2	US-08-890-980-1	Sequence 1, Appli
c 879	15	0.5	2156	2	US-08-899-514-1	Sequence 1, Appli	c 952	15	0.5	2630	3	US-08-890-979-1	Sequence 1, Appli
c 880	15	0.5	2165	4	US-09-257-894-8	Sequence 8, Appli	c 953	15	0.5	2630	3	US-09-032-894-1	Sequence 1, Appli
c 881	15	0.5	2180	2	US-09-003-217-1	Sequence 1, Appli	c 954	15	0.5	2630	4	US-09-031-626-1	Sequence 1, Appli
c 882	15	0.5	2180	4	US-09-218-942-1	Sequence 1, Appli	c 955	15	0.5	2643	4	US-08-961-527-277	Sequence 277, App
c 883	15	0.5	2181	4	US-09-158-767-10	Sequence 10, Appl	c 956	15	0.5	2649	2	US-08-718-964-1	Sequence 1, Appli
c 884	15	0.5	2239	4	US-09-196-390-1	Sequence 1, Appli	c 957	15	0.5	2649	2	US-09-059-964A-1	Sequence 1, Appli
c 885	15	0.5	2243	3	US-08-084-079-4	Sequence 4, Appli	c 958	15	0.5	2649	2	US-08-842-341-1	Sequence 1, Appli
c 886	15	0.5	2268	3	US-08-890-853-1	Sequence 1, Appli	c 959	15	0.5	2665	4	US-09-257-894-1	Sequence 5, Appli
c 887	15	0.5	2268	2	US-09-099-125A-1	Sequence 1, Appli	c 960	15	0.5	2675	2	US-08-070-165F-5	Sequence 5, Appli
c 888	15	0.5	2268	2	US-09-099-124A-1	Sequence 1, Appli	c 961	15	0.5	2675	2	US-08-885-418-5	Sequence 5, Appli
c 889	15	0.5	2268	2	US-09-197-008-1	Sequence 1, Appli	c 962	15	0.5	2681	1	US-08-070-165F-9	Sequence 9, Appli
c 890	15	0.5	2268	4	US-09-032-476-1	Sequence 1, Appli	c 963	15	0.5	2681	2	US-08-885-418-9	Sequence 9, Appli
c 891	15	0.5	2268	4	US-08-890-854-1	Sequence 1, Appli	c 964	15	0.5	2725	3	US-08-941-445A-14	Sequence 14, Appl
c 892	15	0.5	2268	4	US-09-023-324-1	Sequence 1, Appli	c 965	15	0.5	2731	3	US-08-699-103B-11	Sequence 11, Appl
c 893	15	0.5	2271	4	US-08-910-820-8	Sequence 8, Appli	c 966	15	0.5	2731	4	US-09-229-059-11	Sequence 11, Appl
c 894	15	0.5	2277	4	US-09-232-191-10	Sequence 10, Appl	c 967	15	0.5	2736	4	US-08-617-785-1	Sequence 1, Appli
c 895	15	0.5	2277	4	US-09-232-200-10	Sequence 10, Appl	c 968	15	0.5	2745	4	US-08-617-785-11	Sequence 11, Appl
c 896	15	0.5	2277	4	US-09-232-200-72	Sequence 72, Appl	c 969	15	0.5	2766	4	US-08-617-785-13	Sequence 13, Appl
c 897	15	0.5	2277	4	US-09-232-197-10	Sequence 10, Appl	c 970	15	0.5	2802	2	US-08-215-805A-79	Sequence 79, Appl
c 898	15	0.5	2277	4	US-09-232-197-72	Sequence 72, Appl	c 971	15	0.5	2848	2	US-08-805-918-1	Sequence 1, Appli
c 899	15	0.5	2277	4	US-09-232-201-10	Sequence 10, Appl	c 972	15	0.5	2853	4	US-09-221-017B-843	Sequence 843, App
c 900	15	0.5	2277	4	US-09-232-201-72	Sequence 72, Appl	c 973	15	0.5	2882	1	US-08-424-567-1	Sequence 1, Appli
c 901	15	0.5	2287	4	US-08-845-258-8	Sequence 8, Appli	c 974	15	0.5	2882	2	US-08-711-928-1	Sequence 1, Appli
c 902	15	0.5	2287	4	US-08-990-571-8	Sequence 8, Appli	c 975	15	0.5	2882	2	US-08-724-394A-12	Sequence 12, Appl
c 903	15	0.5	2287	4	US-08-723-142A-8	Sequence 8, Appli	c 976	15	0.5	2882	4	US-09-184-937-1	Sequence 1, Appli



STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/747,221B  
APPLICATION NUMBER: 6063610ember 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1515 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1515  
NAME/KEY: Asx - Asn or Asp  
LOCATION: 298  
US-08-747-221B-16

Query Match 0.6%; Score 18; DB 3; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCGAATTCAGAAATCC 984  
|||||  
Db 363 CTCGAATTCAGAAATCC 346

RESULT 4  
US-08-747-221B-17  
Sequence 17, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/747,221B  
APPLICATION NUMBER: 6063610ember 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1515 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-747-221B-17

Query Match 0.6%; Score 18; DB 3; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCGAATTCAGAAATCC 984  
|||||  
Db 1153 CTCGAATTCAGAAATCC 1170

RESULT 5  
US-09-005-051-16/c  
Sequence 16, Application US/09005051  
Patent No. 6291222  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/747,221  
FILING DATE: No. 6291222ember 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1515 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1515  
NAME/KEY: Asx - Asn or Asp  
LOCATION: 298

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; LOCATION: 298
; US-09-005-051-16

Query Match          0.6%; Score 18; DB 4; Length 1515;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
   |||||
Db 363 CTCCAAAATTCAGAAATCC 346

RESULT 6
US-09-005-051-17
; Sequence 17, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1515 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-005-051-17

Query Match          0.6%; Score 18; DB 4; Length 1515;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
   |||||
Db 1153 CTCCAAAATTCAGAAATCC 1170

RESULT 7
5213972-6/c
; Patent No. 5213972
; APPLICANT: MCCANDLISS, RUSSELL J.; ANDERSON, DAVID M.
; TITLE OF INVENTION: FERMENTATION PROCESS FOR THE PRODUCTION
; OF PYRIMIDINE DEOXYRIBONUCLEOSIDES

; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/448,158
; FILING DATE: 08-DEC-1989
; SEQ ID NO: 6:
; LENGTH: 1611
; 5213972-6

Query Match          0.6%; Score 18; DB 6; Length 1611;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 AGGATTTAAAGGACTTGT 325
   |||||
Db 979 AGGATTTAAAGGACTTGT 962

RESULT 8
US-08-747-221B-60/c
; Sequence 60, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1650
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 433
US-08-747-221B-60

Query Match          0.6%; Score 18; DB 3; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
   |||||
Db 498 CTCCAAAATTCAGAAATCC 481
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RESULT 9
US-08-747-221B-61
; Sequence 61, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-747-221B-61

Query Match 0.6%; Score 18; DB 3; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
Db 1153 CTCCAAAATTCAGAAATCC 1170
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RESULT 10
US-09-005-051-60/c
; Sequence 60, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-005-051-60
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1650
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 433
US-09-005-051-60

Query Match 0.6%; Score 18; DB 4; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
Db 498 CTCCAAAATTCAGAAATCC 481
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RESULT 11
US-09-005-051-61
; Sequence 61, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
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; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: FC-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1650 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-005-051-61

Query Match 0.6%; Score 18; DB 4; Length 1650;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCGAATTCAGAAATCC 984  
|||||  
DB 1153 CTCGAATTCAGAAATCC 1170

RESULT 12  
US-08-857-213-2/C  
; Sequence 2, Application US/08857213  
; Patent No. 6034290  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: HUMAN VESICLE BINDING PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/857,213  
; FILING DATE: Herewith  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0297 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1721 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: FIBRGT01  
; CLONE: 148415

US-08-857-213-2  
Query Match 0.6%; Score 18; DB 3; Length 1721;

Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATTTTCATAAAGGAC 18  
|||||  
DB 1538 ATGAATTTTCATAAAGGAC 1521

RESULT 13  
US-08-139-937-11  
; Sequence 11, Application US/08139937  
; Patent No. 5821070  
; GENERAL INFORMATION:  
; APPLICANT: LEE, WEN-HWA  
; APPLICANT: SHAN, BEI  
; TITLE OF INVENTION: CELLULAR GENES ENCODING  
; TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 92122

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/139,937  
; FILING DATE: 20-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/979,156  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, CATHRYN  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CJ 9370  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-535-9001  
; TELEFAX: 619-535-8949  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1800 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-139-937-11

Query Match 0.6%; Score 18; DB 1; Length 1800;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2796 AAAGAACCCCTCTGAAAAA 2813  
|||||  
DB 307 AAAGAACCCCTCTGAAAAA 324

RESULT 14  
PCT-US93-11310-11  
; Sequence 11, Application PC/TUS9311310  
; GENERAL INFORMATION:  
; APPLICANT: BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM  
; TITLE OF INVENTION: CELLULAR GENES ENCODING  
; TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE

```

; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11310
; FILING DATE: 19-NOV-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: FP-CJ 9790
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
;
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US93-11310-11
;
; Query Match 0.6%; Score 18; DB 5; Length 1800;
; Best Local Similarity 100.0%; Pred. No. 60;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2796 AAGAACCCTCTGAAAAA 2813
Db 307 AAGAACCCTCTGAAAAA 324
;
RESULT 15
US-09-079-955-10
; Sequence 10, Application US/09079955A
; Patent No. 6465209
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Kimberly Brown
; APPLICANT: Elizabeth Golightly
; APPLICANT: Tony Byun
; APPLICANT: Thomas Mathiasen
; APPLICANT: Lene V. Kofoed
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Shizuoka
; TITLE OF INVENTION: Methods For Producing Protein
; FILE REFERENCE: 5253.500-US
; CURRENT APPLICATION NUMBER: US/09/079,955A
; CURRENT FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Sphingomonas capsulata
US-09-079-955-10
;
; Query Match 0.6%; Score 18; DB 4; Length 1926;
; Best Local Similarity 100.0%; Pred. No. 61;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2092 GCTGGTGTGCTGGAAC 2109
Db 1242 GCTGGTGTGCTGGAAC 1259

```

```

RESULT 16
US-08-747-221B-13/c
; Sequence 13, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1517
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 300
;
US-08-747-221B-13
;
; Query Match 0.6%; Score 18; DB 3; Length 1982;
; Best Local Similarity 100.0%; Pred. No. 61;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 967 CTCCAAATTCAGAAATCC 984
Db 365 CTCCAAATTCAGAAATCC 348
;
RESULT 17
US-08-747-221B-15
; Sequence 15, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins

```

```
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-747-221B-15

Query Match 0.6%; Score 18; DB 3; Length 1982;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 1618 CTCCAAAATTCAGAAATCC 1635

RESULT 18
US-09-005-051-13/c
; Sequence 13, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-005-051-13
```

```
Query Match 0.6%; Score 18; DB 4; Length 1982;
Best Local Similarity 100.0%; Pred. No. 61;
```

```
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1517
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 300
US-09-005-051-13

Query Match 0.6%; Score 18; DB 4; Length 1982;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 365 CTCCAAAATTCAGAAATCC 348

RESULT 19
US-09-005-051-15
; Sequence 15, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-005-051-15
```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 CTCGAAATTCAGAAATCC 984  
|||||  
Db 1618 CTCGAAATTCAGAAATCC 1635

## RESULT 20

US-08-747-221B-57/c  
; Sequence 57, Application US/08747221B  
; Patent No. 6063610  
; GENERAL INFORMATION:  
; APPLICANT: Silver, Gary W.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid  
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Hesk Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,221B  
; FILING DATE: No. 6063610ember 12, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: FC-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2144 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

US-08-747-221B-57  
; NAME/KEY: CDS  
; LOCATION: 30..1682  
; FEATURE:  
; NAME/KEY: Asx = Asn or Asp  
; LOCATION: 462  
; US-08-747-221B-57  
Query Match 0.6%; Score 18; DB 3; Length 2144;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 CTCGAAATTCAGAAATCC 984  
|||||  
Db 527 CTCGAAATTCAGAAATCC 510

## RESULT 21

US-08-747-221B-59  
; Sequence 59, Application US/08747221B  
; Patent No. 6063610  
; GENERAL INFORMATION:  
; APPLICANT: Silver, Gary W.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Hesk Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,221B  
; FILING DATE: No. 6063610ember 12, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: FC-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2144 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-747-221B-59

Query Match 0.6%; Score 18; DB 3; Length 2144;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 CTCGAAATTCAGAAATCC 984  
|||||  
Db 1618 CTCGAAATTCAGAAATCC 1635

## RESULT 22

US-09-005-051-57/c  
; Sequence 57, Application US/09005051  
; Patent No. 6291222  
; GENERAL INFORMATION:  
; APPLICANT: Silver, Gary W.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid  
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Hesk Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,051  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/747,221

```
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2144 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1682
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 462
; US-09-005-051-57

Query Match 0.6%; Score 18; DB 4; Length 2144;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
Db 527 CTCCAAAATTCAGAAATCC 510

RESULT 23
US-09-005-051-59
; Sequence 59, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/005,051
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2144 nucleotides
; TYPE: nucleic acid
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```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-005-051-59

Query Match 0.6%; Score 18; DB 4; Length 2144;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
Db 1618 CTCCAAAATTCAGAAATCC 1635

RESULT 24
US-09-192-104-1
; Sequence 1, Application US/09192104B
; Patent No. 6184020
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Aminopeptidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.200-US
; CURRENT APPLICATION NUMBER: US/09/192,104B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/069719
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: 1465/97
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: PA 1998 00670
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Sphingomonas
; US-09-192-104-1

Query Match 0.6%; Score 18; DB 4; Length 3000;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2092 GCTGGTGTGGCTGGAAGC 2109
Db 1911 GCTGGTGTGGCTGGAAGC 1928

RESULT 25
US-09-543-446-1
; Sequence 1, Application US/09543446
; Patent No. 6303360
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Aminopeptidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.210-US
; CURRENT APPLICATION NUMBER: US/09/543,446
; CURRENT FILING DATE: 2000-04-05
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; EARLIER APPLICATION NUMBER: 60/069719  
; EARLIER FILING DATE: 1997-12-16  
; EARLIER APPLICATION NUMBER: 1465/97  
; EARLIER FILING DATE: 1997-12-16  
; EARLIER APPLICATION NUMBER: PA 1998 00670  
; EARLIER FILING DATE: 1998-03-15  
; EARLIER APPLICATION NUMBER: 09/192,104  
; EARLIER FILING DATE: 1998-11-13  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3000  
; TYPE: DNA  
; ORGANISM: Spingomonas  
US-09-543-446-1

Query Match 0.6%; Score 18; DB 4; Length 3000;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2092 GCTGCTGTGGCTGGAAGC 2109  
|||||  
Db 1911 GCTGCTGTGGCTGGAAGC 1928

RESULT 26  
US-09-518-386B-4/c  
; Sequence 4, Application US/09518386B  
; Patent No. 6365386  
; GENERAL INFORMATION:  
; APPLICANT: HOSHINO, Tatsuo  
; APPLICANT: OJIMA, Kazuyuki  
; APPLICANT: SETOGUCHI, Yutaka  
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE  
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE  
; CURRENT APPLICATION NUMBER: US/09/518,386B  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: EP 99104668.1  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EP 00101666.6  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 3969  
; TYPE: DNA  
; ORGANISM: Phaffia rhodozyma  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (517)..(518)  
; NAME/KEY: intron  
; LOCATION: (784)..(898)  
; NAME/KEY: intron  
; LOCATION: (1016)..(1087)  
; NAME/KEY: intron  
; LOCATION: (1180)..(1302)  
; NAME/KEY: intron  
; LOCATION: (1518)..(1600)  
; NAME/KEY: intron  
; LOCATION: (1635)..(1723)  
; NAME/KEY: intron  
; LOCATION: (1867)..(1939)  
; NAME/KEY: intron  
; LOCATION: (2000)..(2081)  
; NAME/KEY: intron  
; LOCATION: (2182)..(2257)  
; NAME/KEY: intron  
; LOCATION: (2355)..(2431)  
; NAME/KEY: intron  
; LOCATION: (2543)..(2618)  
; NAME/KEY: intron  
; LOCATION: (2653)..(2742)  
; NAME/KEY: intron

; LOCATION: (2815)..(2962)  
; NAME/KEY: intron  
; LOCATION: (3051)..(3113)  
; NAME/KEY: intron  
; LOCATION: (3172)..(3247)  
; NAME/KEY: intron  
; LOCATION: (3322)..(3398)  
; NAME/KEY: intron  
; LOCATION: (3424)..(3513)  
; NAME/KEY: polyA\_site  
; LOCATION: (3865)..(3866)  
; NAME/KEY: intron  
; LOCATION: (653)..(734)  
US-09-518-386B-4

Query Match 0.6%; Score 18; DB 4; Length 3969;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 AACTTGAAGCACCTTC 402  
|||||  
Db 1193 AACTTGAAGCACCTTC 1176

RESULT 27  
US-08-699-103B-1/c  
; Sequence 1, Application US/08699103B  
; Patent No. 6107462  
; GENERAL INFORMATION:  
; APPLICANT: Rine, Jasper D.  
; APPLICANT: Hampton, Randolph  
; TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING  
; TITLE OF INVENTION: CHOLESTEROL SYNTHESIS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/699,103B  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/002,581  
; FILING DATE: 17-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Green, Grant D.  
; REGISTRATION NUMBER: 31,259  
; REFERENCE/DOCKET NUMBER: 09272/005001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/322-5070  
; TELEFAX: 650/854-0875  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4982 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
US-08-699-103B-1

Query Match 0.6%; Score 18; DB 3; Length 4982;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 CCCTTGGTGAAGATATTG 373

Db 1743 CCCTGGTGAAGATATTG 1726  
|||||

## RESULT 28

US-09-229-059-1/C  
; Sequence 1, Application US/09229059  
; Patent No. 633172  
; GENERAL INFORMATION:  
; APPLICANT: Rine, Jasper D.  
; APPLICANT: Hampton, Randolph  
; TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING  
; TITLE OF INVENTION: CHOLESTEROL SYNTHESIS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/229,059  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/699,103  
; FILING DATE: 16-AUG-1996  
; APPLICATION NUMBER: 60/002,581  
; FILING DATE: 17-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Green, Grant D.  
; REGISTRATION NUMBER: 31,259  
; REFERENCE/DOCKET NUMBER: 09272/005001  
; TELEPHONE: 650/322-5070  
; TELEFAX: 650/854-0875  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4982 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA

US-09-229-059-1  
Query Match 0.6%; Score 18; DB 4; Length 4982;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 CCCTGGTGAAGATATTG 373  
Db 1743 CCCTGGTGAAGATATTG 1726  
|||||

## RESULT 29

US-08-801-308-2  
; Sequence 2, Application US/08801308  
; Patent No. 6368790  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Robert E.  
; TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF  
; TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS IN  
; TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,  
; TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weiser & Associates, P.C.  
; STREET: 230 S. Fifteenth Street, Suite 500

; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/801,308  
; FILING DATE: 18-FEB-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 372.6435P  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5173 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-801-308-2

Query Match 0.6%; Score 18; DB 4; Length 5173;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2796 AAAGAACCCCTCGAAAAA 2813  
Db 3187 AAAGAACCCCTCGAAAAA 3204  
|||||

## RESULT 30

US-09-037-990B-27  
; Sequence 27, Application US/09037990B  
; Patent No. 6248519  
; GENERAL INFORMATION:  
; APPLICANT: ENGEL, Stacia R.  
; DESCENZO, Richard A.  
; MORENZONI, Richard A.  
; IRELAN, Nancy A.  
; TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED  
; MICROORGANISMS  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/037,990B  
; FILING DATE: 11-Mar-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharp, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 29520/30001



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-037-990B-27

Query Match 0.6%; Score 17; DB 4; Length 290;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1117 AAAAACAACACAACA 1133  
|||||  
Db 209 AAAAACAACACAACA 225

RESULT 31  
US-08-991-789A-171/c  
Sequence 171, Application US/08991789A  
Patent No. 6225054  
GENERAL INFORMATION:  
APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 292

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed IP Law Group  
STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991.789A  
FILING DATE: 11-Dec-1997  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 210121.419C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 171:  
SEQUENCE CHARACTERISTICS:

LENGTH: 383 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 171:  
US-08-991-789A-171

Query Match 0.6%; Score 17; DB 4; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 ACATTATTTTAACTTG 390  
|||||  
Db 35 ACATTATTTTAACTTG 19

RESULT 32  
US-09-062-451-171/c  
Sequence 171, Application US/09062451  
Patent No. 6344550  
GENERAL INFORMATION:  
APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 297  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/062,451  
FILING DATE: 04-APR-1997

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.419C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 171:  
SEQUENCE CHARACTERISTICS:

LENGTH: 383 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-062-451-171

Query Match 0.6%; Score 17; DB 4; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 ACATTATTTTAACTTG 390  
|||||  
Db 35 ACATTATTTTAACTTG 19

RESULT 33

US-09-598-326-171/c

Sequence 171, Application US/09598326  
Patent No. 6423496  
GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 247  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed Intellectual Property Law Group PLLC

STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle  
STATE: Washington

COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/598,326  
FILING DATE: 20-Jun-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 210121.419D1  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 171:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 383 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 171:  
US-09-598-326-171

Query Match 0.6%; Score 17; DB 4; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 ACATTATTTTAACTTG 390  
|||||

Db 35 ACATTATTTTAACTTG 19

RESULT 34  
US-09-037-990B-8  
Sequence 8, Application US/09037990B  
Patent No. 6248519  
GENERAL INFORMATION:  
APPLICANT: ENGEL, Stacia R.  
DESCENZO, Richard A.  
MORENZONI, Richard A.  
IRELAN, Nancy A.

TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED  
MICROORGANISMS  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,990B  
FILING DATE: 11-Mar-1999

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 29520/30001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:

LENGTH: 661 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-037-990B-8

Query Match 0.6%; Score 17; DB 4; Length 661;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 AAAACAAACACAAACA 1133  
|||||

Db 209 AAAACAAACACAAACA 225

RESULT 35  
US-08-998-416-818  
Sequence 818, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Rebischung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII  
AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 818:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 685 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1520UP  
US-08-998-416-818

Query Match 0.6%; Score 17; DB 4; Length 685;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 CTGAATGGCCTCTGTGCA 476  
|||||  
Db 111 CTGAATGGCCTCTGTGCA 127

## RESULT 36

US-09-134-001C-621  
; Sequence 621, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 621  
; LENGTH: 939  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-621

Query Match 0.6%; Score 17; DB 4; Length 939;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3040 GTTATTACAGGTGCTTT 3056

|||||

Db 799 GTTATTACAGGTGCTTT 815

## RESULT 37

US-09-221-017B-138  
; Sequence 138, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998  
; ATTORNEY/AGENT INFORMATION:

; NAME: Monroy, Gladys H  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 138:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 963 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORYPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1...963  
US-09-221-017B-138

Query Match 0.6%; Score 17; DB 4; Length 963;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2310 GGATACATAAAGATGCA 2326

|||||

Db 943 GGATACATAAAGATGCA 959

## RESULT 38

US-09-134-001C-828  
; Sequence 828, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 828  
; LENGTH: 1302  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-828

Query Match

Best Local Similarity 100.0%; Score 17; DB 4; Length 1302;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1728 AGCTTTCTTTCAAGGTA 1744

|||||

Db 975 AGCTTTCTTTCAAGGTA 991

## RESULT 39

US-09-318-443-5/c  
; Sequence 5, Application US/09318443  
; Patent No. 6197947  
; GENERAL INFORMATION:  
; APPLICANT: Hemmati-Brivanlou, Ali  
; APPLICANT: Weinstein, Daniel C.  
; TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE  
; FILE REFERENCE: 600-1-211 N

;; CURRENT APPLICATION NUMBER: US/09/318,443  
;; CURRENT FILING DATE: 1999-05-25  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 1536  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-318-443-5

Query Match 0.6%; Score 17; DB 4; Length 1536;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1339 CAGGAGTACACAGCAGG 1355  
|||||

DB 1360 CAGGAGTACACAGCAGG 1344  
|||||

## RESULT 40

US-08-743-637B-183/c  
; Sequence 183, Application US/08743637B  
; Patent No. 5994066  
; GENERAL INFORMATION:

; APPLICANT: BERGERON, Michel G.  
; APPLICANT: PICARD, Francois J.  
; APPLICANT: OUELLETTE, Marc  
; APPLICANT: ROY, Paul H.

; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA

; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND

; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED

; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

; NUMBER OF SEQUENCES: 273

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: QUARLES & BRADY

; STREET: 411 EAST WISCONSIN AVENUE

; CITY: MILWAUKEE

; STATE: WISCONSIN

; COUNTRY: USA

; ZIP: 53202-4497

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743,637B

; FILING DATE: 04-NOV-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/526,840

; FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BAKER, Jean C.

; REGISTRATION NUMBER: 35,433

; REFERENCE/DOCKET NUMBER: 850586.90012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (414) 277-5000

; TELEFAX: (414) 277-5591

; INFORMATION FOR SEQ ID NO: 183:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1563 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORGANISM: Klebsiella pneumoniae

US-08-743-637B-183

Query Match 0.6%; Score 17; DB 2; Length 1563;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 TCCTGCAGGCTCTTCAG 486  
|||||

DB 74 TCCTGCAGGCTCTTCAG 58  
|||||

## RESULT 41

US-09-318-443-7/c  
; Sequence 7, Application US/09318443  
; Patent No. 6197947  
; GENERAL INFORMATION:

; APPLICANT: Hemmati-Brivanlou, Ali

; APPLICANT: Weinstein, Daniel C.

; TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIIIL, AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 600-1-211 N

; CURRENT APPLICATION NUMBER: US/09/318,443

; CURRENT FILING DATE: 1999-05-25

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1682

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-318-443-7

Query Match 0.6%; Score 17; DB 4; Length 1682;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1339 CAGGAGTACACAGCAGG 1355  
|||||

DB 1501 CAGGAGTACACAGCAGG 1485  
|||||

## RESULT 42

US-09-178-252-26  
; Sequence 26, Application US/09178252  
; Patent No. 6218188  
; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.

; APPLICANT: Stelman, Steven J.

; APPLICANT: Narva, Kenneth E.

; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

; FILE REFERENCE: MA-714XC2

; CURRENT APPLICATION NUMBER: US/09/178,252

; CURRENT FILING DATE: 1998-10-23

; EARLIER APPLICATION NUMBER: 60/065,215

; EARLIER FILING DATE: 1997-11-12

; EARLIER APPLICATION NUMBER: 60/076,445

; EARLIER FILING DATE: 1998-03-02

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26

; LENGTH: 1965

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic B.t. toxin gene

US-09-178-252-26

Query Match 0.6%; Score 17; DB 4; Length 1965;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ACCAACACCATCACCGC 444  
|||||

DB 1519 ACCAACACCATCACCGC 1535  
|||||

## RESULT 43

US-08-960-780-10  
; Sequence 10, Application US/08960780

Patent No. 6204435  
GENERAL INFORMATION:  
APPLICANT: Feitelson, Jerald S.  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide  
SEQUENCES Which Encode These Toxins  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/960,780  
FILING DATE: 30-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA-708  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 158C2-pt1  
US-08-960-780-10

Query Match 0.68; Score 17; DB 4; Length 2035;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2585 AAGATGGAATGAAGCT 2601  
|||||  
Db 1973 AAGATGGAATGAAGCT 1989

RESULT 44  
US-09-073-898-10  
Sequence 10, Application US/09073898  
Patent No. 6242669  
GENERAL INFORMATION:  
APPLICANT: Feitelson, Jerald S.  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy

APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Einstad-Lee, Stacey  
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide  
SEQUENCES Which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/073,898  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 158C2-pt1  
US-09-073-898-10

Query Match 0.68; Score 17; DB 4; Length 2035;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2585 AAGATGGAATGAAGCT 2601  
|||||  
Db 1973 AAGATGGAATGAAGCT 1989

RESULT 45  
US-09-227-357-31/C  
Sequence 31, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (14)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-31
```

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Query Match          0.6%; Score 17; DB 4; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1117 AAAAAACAAACAAACA 1133
|||||
Db 483 AAAAAACAAACAAACA 467
|||||

RESULT 46
US-09-115-446-1/c
; Sequence 1, Application US/09115446
; Patent No. 6165719
; GENERAL INFORMATION:
; APPLICANT: Chandy, George K.
; APPLICANT: Gargus, Jay J.
; APPLICANT: Gutman, George
; APPLICANT: Fantino, Emmanuelle
; APPLICANT: Kalman, Katarin
; TITLE OF INVENTION: hKCA3/KCNN3 SMALL CONDUCTANCE CALCIUM
; TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
; FILE REFERENCE: 07306/014001
; CURRENT APPLICATION NUMBER: US/09/115,446
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 60/052,556
; EARLIER FILING DATE: 1997-07-15
; EARLIER APPLICATION NUMBER: 60/070,741
; EARLIER FILING DATE: 1998-01-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (287)...(2479)
US-09-115-446-1
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Query Match          0.6%; Score 17; DB 4; Length 2521;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 704 TGCTGCTGAAGCTGCGG 720
|||||
Db 492 TGCTGCTGAAGCTGCGG 476
|||||
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```
RESULT 47
US-09-115-446-5/c
; Sequence 5, Application US/09115446
; Patent No. 6165719
; GENERAL INFORMATION:
; APPLICANT: Chandy, George K.
; APPLICANT: Gargus, Jay J.
; APPLICANT: Gutman, George
; APPLICANT: Fantino, Emmanuelle
; APPLICANT: Kalman, Katarin
; TITLE OF INVENTION: hKCA3/KCNN3 SMALL CONDUCTANCE CALCIUM
; TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
; TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
; FILE REFERENCE: 07306/014001
; CURRENT APPLICATION NUMBER: US/09/115,446
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 60/052,556
; EARLIER FILING DATE: 1997-07-15
; EARLIER APPLICATION NUMBER: 60/070,741
; EARLIER FILING DATE: 1998-01-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2526
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-115-446-5
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Query Match          0.6%; Score 17; DB 4; Length 2526;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 704 TGCTGCTGAAGTGGG 720
    |||||
Db 497 TGCTGCTGAAGTGGG 481

RESULT 48
US-08-095-737-1/c
; Sequence 1, Application US/08095737
; Patent No. 5487979
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,737
; FILING DATE: 19930722
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 21..2709
US-08-095-737-1

Query Match          0.6%; Score 17; DB 1; Length 4165;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2776 ATTTAGGTGCATTTT 2792
    |||||
Db 4070 ATTTAGGTGCATTTT 4054

RESULT 49
US-08-480-145-1/c
; Sequence 1, Application US/08480145
; Patent No. 5717067
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
```

```
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,145
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095,737
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 21..2709
US-08-480-145-1

Query Match          0.6%; Score 17; DB 1; Length 4165;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2776 ATTTAGGTGCATTTT 2792
    |||||
Db 4070 ATTTAGGTGCATTTT 4054

RESULT 50
US-08-477-389-1/c
; Sequence 1, Application US/08477389
; Patent No. 5872219
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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Search completed: January 31, 2003, 04:09:34  
Job time : 269 secs



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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 00:11:05 ; Search time 170 Seconds  
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Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaatttcataaaggacaa.....cttttaaacagtagtaactgct 3072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 396772 seqs, 224632407 residues

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Total number of hits satisfying chosen parameters: 84721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

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Database : Published\_Applications\_NA.\*  
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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3072	100.0	3072	10 US-09-841-739-3	Sequence 3, Appli
2	3072	100.0	3133	10 US-09-841-739-1	Sequence 1, Appli
3	2868	93.4	3396	9 US-09-864-921-96	Sequence 96, Appli
4	2634	85.7	3612	10 US-09-841-739-6	Sequence 6, Appli
5	2634	85.7	3615	10 US-09-841-739-4	Sequence 4, Appli
6	2634	85.7	3615	10 US-09-841-739-12	Sequence 12, Appli
7	840	27.3	891	9 US-09-864-921-179	Sequence 179, App
8	815	26.5	1395	9 US-09-864-921-98	Sequence 98, Appli
9	618	20.1	618	9 US-09-864-921-181	Sequence 181, App
10	461	15.0	768	9 US-09-864-921-102	Sequence 102, App
11	420	13.7	608	10 US-09-764-864-339	Sequence 339, App
12	304	9.9	522	10 US-09-764-864-754	Sequence 754, App
13	269	8.8	578	9 US-09-864-921-100	Sequence 100, App
14	261	8.5	261	9 US-09-864-921-177	Sequence 177, App
15	242	7.9	421	10 US-09-864-761-4236	Sequence 4236, App
16	220	7.2	220	10 US-09-864-761-20988	Sequence 20988, A
17	114	3.7	165	9 US-09-864-921-183	Sequence 183, App
18	29	0.9	29	9 US-09-864-921-160	Sequence 160, App
19	25	0.8	25	9 US-09-864-921-161	Sequence 161, App

c	20	25	0.8	25	9	US-09-864-921-162	Sequence 162, App
	21	25	0.8	25	9	US-09-864-921-165	Sequence 165, App
	22	24	0.8	24	9	US-09-864-921-159	Sequence 159, App
	23	24	0.8	33	9	US-09-864-921-157	Sequence 157, App
c	24	23	0.7	23	9	US-09-864-921-153	Sequence 153, App
	25	23	0.7	23	9	US-09-864-921-163	Sequence 163, App
	26	21	0.7	21	9	US-09-864-921-156	Sequence 156, App
c	27	21	0.7	30	9	US-09-864-921-158	Sequence 158, App
	28	21	0.7	483	10	US-09-728-445-337	Sequence 337, App
	29	20	0.7	475	10	US-09-974-300-6263	Sequence 6263, Ap
c	30	20	0.7	768	9	US-09-864-921-102	Sequence 102, App
	31	19	0.6	30310	10	US-09-800-631-96	Sequence 96, Appli
c	32	18	0.6	21	9	US-09-864-921-155	Sequence 155, App
	33	18	0.6	216	10	US-09-867-701-9442	Sequence 9442, Ap
	34	18	0.6	273	10	US-09-878-574-9387	Sequence 9387, Ap
c	35	18	0.6	454	10	US-09-864-761-4716	Sequence 4716, Ap
	36	18	0.6	469	10	US-09-998-598-1369	Sequence 1369, Ap
	37	18	0.6	472	10	US-09-864-761-1714	Sequence 1714, Ap
c	38	18	0.6	501	10	US-09-728-446-43	Sequence 43, Appli
	39	18	0.6	960	9	US-09-738-626-2121	Sequence 2121, Ap
	40	18	0.6	1163	10	US-09-764-877-3957	Sequence 3957, Ap
c	41	18	0.6	1721	9	US-09-360-540-2	Sequence 2, Appli
	42	18	0.6	2619	10	US-09-764-864-1654	Sequence 1654, Ap
	43	18	0.6	3000	9	US-09-957-189-1	Sequence 1, Appli
	44	18	0.6	3460	10	US-09-764-864-1656	Sequence 1656, Ap
c	45	18	0.6	4951	10	US-09-070-937A-261	Sequence 261, App
	46	18	0.6	5173	10	US-09-811-045A-2	Sequence 2, Appli
	47	18	0.6	7386	10	US-09-764-855-208	Sequence 208, App
	48	18	0.6	17252	10	US-09-764-860-1102	Sequence 1102, Ap
	49	18	0.6	17509	10	US-09-880-107-2097	Sequence 2097, Ap
	50	18	0.6	202001	10	US-09-734-674-3	Sequence 3, Appli
c	51	18	0.6	684973	10	US-09-263-959-1	Sequence 1, Appli
	52	17	0.6	51	9	US-09-801-371A-10	Sequence 10, Appli
c	53	17	0.6	136	10	US-09-878-574-10039	Sequence 10039, A
	54	17	0.6	149	10	US-09-770-696-500	Sequence 500, App
c	55	17	0.6	160	10	US-09-878-574-14853	Sequence 14853, A
	56	17	0.6	169	10	US-09-878-574-7678	Sequence 7678, Ap
	57	17	0.6	175	10	US-09-983-965-1317	Sequence 1317, A
c	58	17	0.6	214	10	US-09-960-352-12982	Sequence 12982, A
	59	17	0.6	247	10	US-09-878-574-15571	Sequence 15571, A
c	60	17	0.6	257	10	US-09-878-574-6585	Sequence 6585, Ap
	61	17	0.6	260	10	US-09-878-574-10137	Sequence 10137, A
c	62	17	0.6	264	10	US-09-923-876-4513	Sequence 4513, Ap
	63	17	0.6	272	10	US-09-878-574-8191	Sequence 8191, Ap
c	64	17	0.6	272	9	US-09-878-574-12627	Sequence 12627, A
	65	17	0.6	276	9	US-10-040-739-1415	Sequence 1415, Ap
c	66	17	0.6	276	10	US-09-878-574-14107	Sequence 14107, A
	67	17	0.6	312	9	US-09-738-626-1862	Sequence 1862, Ap
c	68	17	0.6	316	9	US-09-796-692-5152	Sequence 5152, Ap
	69	17	0.6	341	10	US-09-878-574-1163	Sequence 1163, Ap
c	70	17	0.6	355	10	US-09-867-701-8170	Sequence 8170, Ap
	71	17	0.6	356	10	US-09-867-550-2095	Sequence 2095, Ap
c	72	17	0.6	356	10	US-09-867-550-2125	Sequence 2125, Ap
	73	17	0.6	357	10	US-09-878-574-2059	Sequence 2059, Ap
c	74	17	0.6	367	10	US-09-878-574-3303	Sequence 3303, Ap
	75	17	0.6	371	10	US-09-878-574-2835	Sequence 2835, Ap
c	76	17	0.6	383	9	US-09-924-400-171	Sequence 171, App
	77	17	0.6	383	10	US-09-810-936-171	Sequence 171, App
c	78	17	0.6	383	10	US-09-429-755-171	Sequence 171, App
	79	17	0.6	386	10	US-09-878-574-3140	Sequence 3140, Ap
c	80	17	0.6	399	10	US-09-983-965-1564	Sequence 1564, Ap
	81	17	0.6	415	10	US-09-878-574-3289	Sequence 3289, Ap
c	82	17	0.6	417	10	US-09-960-352-10604	Sequence 10604, A
	83	17	0.6	418	10	US-09-764-847-232	Sequence 232, App
c	84	17	0.6	422	10	US-09-960-352-12761	Sequence 12761, A
	85	17	0.6	432	10	US-09-925-300-772	Sequence 772, App
c	86	17	0.6	435	10	US-09-864-761-4687	Sequence 4687, Ap
	87	17	0.6	500	10	US-09-827-998-57	Sequence 57, Appli
c	88	17	0.6	522	10	US-09-880-107-1314	Sequence 1314, Ap
	89	17	0.6	541	10	US-09-864-761-21427	Sequence 21427, A
c	90	17	0.6	551	10	US-09-917-800A-722	Sequence 722, App
	91	17	0.6	575	10	US-09-864-761-9538	Sequence 9538, Ap
c	92	17	0.6	588	9	US-09-764-868-342	Sequence 342, App

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c 94	17	0.6	590	10	US-09-917-800A-975	Sequence 975, App	c 167	16	0.5	145	10	US-09-864-761-28942	Sequence 28942, A
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c 96	17	0.6	818	10	US-09-770-445-739	Sequence 739, App	c 169	16	0.5	165	9	US-10-025-380-601	Sequence 601, App
c 97	17	0.6	843	9	US-09-984-245-43	Sequence 43, Appl	c 170	16	0.5	165	10	US-09-922-217-601	Sequence 601, App
c 98	17	0.6	950	10	US-09-867-550-1541	Sequence 1541, Ap	c 171	16	0.5	165	10	US-09-833-263-601	Sequence 601, App
c 99	17	0.6	1001	10	US-09-798-029-3	Sequence 3, Appli	c 172	16	0.5	170	10	US-09-783-590-11272	Sequence 11272, A
c 100	17	0.6	1128	9	US-09-938-842A-1107	Sequence 1107, Ap	c 173	16	0.5	175	10	US-09-864-761-25901	Sequence 25901, A
c 101	17	0.6	1332	9	US-10-023-437-8	Sequence 8, Appli	c 174	16	0.5	182	10	US-09-878-574-15700	Sequence 15700, A
c 102	17	0.6	1339	10	US-09-778-844-73	Sequence 73, Appl	c 175	16	0.5	189	10	US-09-864-761-28808	Sequence 28808, A
c 103	17	0.6	1341	9	US-09-938-842A-2465	Sequence 2465, Ap	c 176	16	0.5	193	10	US-09-960-352-3980	Sequence 3980, Ap
c 104	17	0.6	1359	9	US-09-738-626-526	Sequence 58, App	c 177	16	0.5	206	10	US-09-925-299-726	Sequence 726, App
c 105	17	0.6	1369	10	US-09-778-844-58	Sequence 58, Appl	c 178	16	0.5	218	10	US-09-728-446-257	Sequence 257, App
c 106	17	0.6	1409	9	US-09-895-593-1	Sequence 1, Appli	c 179	16	0.5	220	10	US-09-864-761-19964	Sequence 19964, A
c 107	17	0.6	1409	10	US-09-895-943-1	Sequence 1, Appli	c 180	16	0.5	249	10	US-09-923-876-936	Sequence 936, App
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c 109	17	0.6	1536	10	US-09-755-325-5	Sequence 5, Appli	c 182	16	0.5	253	10	US-09-728-446-896	Sequence 896, App
c 110	17	0.6	1682	10	US-09-755-325-7	Sequence 7, Appli	c 183	16	0.5	254	10	US-09-878-574-15520	Sequence 15520, A
c 111	17	0.6	1700	10	US-09-728-952-26	Sequence 26, Appl	c 184	16	0.5	264	10	US-09-878-574-14820	Sequence 14820, A
c 112	17	0.6	1857	10	US-09-822-830A-338	Sequence 338, App	c 185	16	0.5	270	10	US-09-867-701-8694	Sequence 8694, Ap
c 113	17	0.6	1949	10	US-09-778-844-57	Sequence 57, Appl	c 186	16	0.5	281	10	US-09-864-761-18446	Sequence 18446, A
c 114	17	0.6	1965	10	US-09-826-660-26	Sequence 26, Appl	c 187	16	0.5	284	10	US-09-878-574-7963	Sequence 7963, Ap
c 115	17	0.6	1974	9	US-09-938-842A-248	Sequence 248, App	c 188	16	0.5	289	10	US-09-878-574-5087	Sequence 5087, Ap
c 116	17	0.6	2000	10	US-09-887-576-110	Sequence 110, App	c 189	16	0.5	293	10	US-09-294-093B-1793	Sequence 1793, Ap
c 117	17	0.6	2035	10	US-09-850-351A-10	Sequence 10, Appl	c 190	16	0.5	298	10	US-09-294-093B-3207	Sequence 3207, Ap
c 118	17	0.6	2073	10	US-09-880-107-1601	Sequence 1601, Ap	c 191	16	0.5	311	10	US-09-864-864-32	Sequence 32, Appl
c 119	17	0.6	2136	9	US-09-938-842A-2144	Sequence 2144, Ap	c 192	16	0.5	322	10	US-09-783-590-7028	Sequence 7028, Ap
c 120	17	0.6	2224	9	US-09-922-364A-44	Sequence 44, Appl	c 193	16	0.5	328	10	US-09-960-352-5993	Sequence 5993, Ap
c 121	17	0.6	2224	9	US-09-254-590-44	Sequence 44, Appl	c 194	16	0.5	330	9	US-09-954-531-713	Sequence 713, App
c 122	17	0.6	2224	9	US-10-115-695-44	Sequence 44, Appl	c 195	16	0.5	341	10	US-09-764-860-157	Sequence 157, App
c 123	17	0.6	2451	9	US-09-764-868-19	Sequence 19, Appl	c 196	16	0.5	341	10	US-09-728-445-565	Sequence 565, App
c 124	17	0.6	2462	9	US-09-922-364A-48	Sequence 48, Appl	c 197	16	0.5	345	10	US-09-864-761-29498	Sequence 29498, A
c 125	17	0.6	2462	9	US-09-254-590-48	Sequence 48, Appl	c 198	16	0.5	351	9	US-09-938-842A-614	Sequence 614, App
c 126	17	0.6	2462	9	US-10-115-695-48	Sequence 48, Appl	c 199	16	0.5	355	9	US-09-924-400-78	Sequence 78, Appl
c 127	17	0.6	2521	10	US-09-925-300-521	Sequence 521, App	c 200	16	0.5	355	9	US-09-924-400-248	Sequence 248, App
c 128	17	0.6	2626	12	US-10-002-600-45	Sequence 45, Appl	c 201	16	0.5	355	10	US-09-810-936-78	Sequence 78, Appl
c 129	17	0.6	2670	12	US-10-002-600-44	Sequence 44, Appl	c 202	16	0.5	355	10	US-09-810-936-248	Sequence 248, App
c 130	17	0.6	2805	9	US-09-938-842A-991	Sequence 991, App	c 203	16	0.5	355	10	US-09-429-755-78	Sequence 78, Appl
c 131	17	0.6	2805	10	US-09-887-576-679	Sequence 679, App	c 204	16	0.5	355	10	US-09-429-755-248	Sequence 248, App
c 132	17	0.6	2911	10	US-09-764-864-104	Sequence 104, App	c 205	16	0.5	360	10	US-09-867-701-385	Sequence 385, App
c 133	17	0.6	3183	10	US-09-801-368-409	Sequence 409, App	c 206	16	0.5	362	10	US-09-920-300A-903	Sequence 903, App
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c 135	17	0.6	3378	9	US-09-964-899-48	Sequence 48, Appl	c 208	16	0.5	364	10	US-09-728-445-73	Sequence 73, Appl
c 136	17	0.6	3406	10	US-09-954-456-1789	Sequence 1789, Ap	c 209	16	0.5	370	10	US-09-960-352-7378	Sequence 7378, Ap
c 137	17	0.6	3406	10	US-09-880-107-1628	Sequence 1628, Ap	c 210	16	0.5	375	10	US-09-563-817-869	Sequence 869, App
c 138	17	0.6	3531	9	US-09-918-508-1	Sequence 1, Appli	c 211	16	0.5	387	10	US-09-878-574-487	Sequence 487, App
c 139	17	0.6	3572	10	US-09-925-302-280	Sequence 280, App	c 212	16	0.5	387	10	US-09-983-965-5819	Sequence 5819, Ap
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c 143	17	0.6	4407	10	US-10-052-586-351	Sequence 351, App	c 216	16	0.5	395	10	US-09-960-352-8799	Sequence 8799, Ap
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c 148	17	0.6	7465	10	US-09-880-107-3357	Sequence 3357, Ap	c 221	16	0.5	401	10	US-09-795-668-756	Sequence 756, App
c 149	17	0.6	10195	10	US-09-764-864-1600	Sequence 1600, Ap	c 222	16	0.5	401	10	US-09-795-668-757	Sequence 757, App
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c 153	17	0.6	24023	9	US-10-094-679-1	Sequence 1, Appli	c 226	16	0.5	403	10	US-09-960-352-8222	Sequence 8222, Ap
c 154	17	0.6	32190	10	US-09-764-877-2844	Sequence 2844, Ap	c 227	16	0.5	404	10	US-09-960-352-11963	Sequence 11963, A
c 155	17	0.6	38374	10	US-09-880-107-3463	Sequence 3463, Ap	c 228	16	0.5	406	9	US-09-933-797-763	Sequence 763, App
c 156	17	0.6	46718	10	US-09-816-093-3	Sequence 3, Appli	c 229	16	0.5	413	10	US-09-962-832-82	Sequence 82, Appl
c 157	17	0.6	106323	10	US-09-803-661-3	Sequence 3, Appli	c 230	16	0.5	413	10	US-09-967-768A-105	Sequence 105, App
c 158	17	0.6	155074	9	US-10-026-188-6	Sequence 6, Appli	c 231	16	0.5	415	10	US-09-864-761-3185	Sequence 3185, Ap
c 159	17	0.6	249487	9	US-10-026-188-3	Sequence 3, Appli	c 232	16	0.5	418	10	US-09-925-299-503	Sequence 503, App
c 160	17	0.6	640681	10	US-09-790-988-1	Sequence 1, Appli	c 233	16	0.5	420	10	US-09-764-860-909	Sequence 909, App
c 161	17	0.5	3309400	9	US-09-738-626-1	Sequence 1, Appli	c 234	16	0.5	420	10	US-09-960-352-3554	Sequence 3554, Ap
c 162	16	0.5	109	10	US-09-864-761-28485	Sequence 28485, A	c 235	16	0.5	422	10	US-09-960-352-2763	Sequence 2763, Ap
c 163	16	0.5	109	10	US-09-783-590-5809	Sequence 5809, Ap	c 236	16	0.5	423	10	US-09-960-352-8117	Sequence 8117, Ap
c 164	16	0.5	112	10	US-09-864-761-30612	Sequence 30612, Ap	c 237	16	0.5	423	10	US-09-983-965-3069	Sequence 3069, Ap
c 165	16	0.5	113	10	US-09-294-093B-3496	Sequence 3496, Ap	c 238	16	0.5	423	10	US-09-983-965-5648	Sequence 5648, Ap

c 239	16	0.5	426	10	US-09-764-860-161	Sequence 161, App	312	16	0.5	545	10	US-09-864-761-32206	Sequence 32206, A
c 240	16	0.5	427	10	US-09-867-701-3928	Sequence 3928, App	313	16	0.5	549	10	US-09-974-300-2944	Sequence 2944, App
c 241	16	0.5	430	10	US-09-960-352-5031	Sequence 5031, App	314	16	0.5	551	10	US-09-864-761-12228	Sequence 12228, A
c 242	16	0.5	432	9	US-09-933-797-440	Sequence 440, App	c 315	16	0.5	555	10	US-09-864-761-9512	Sequence 9512, App
c 243	16	0.5	432	10	US-09-867-701-1792	Sequence 1792, App	c 316	16	0.5	558	9	US-09-796-692-8615	Sequence 8615, App
c 244	16	0.5	434	10	US-09-822-849A-587	Sequence 587, App	c 317	16	0.5	561	10	US-09-560-863-616	Sequence 616, App
c 245	16	0.5	434	10	US-09-954-531-13569	Sequence 13569, A	c 318	16	0.5	563	9	US-09-996-140-64	Sequence 64, Appl
c 246	16	0.5	435	9	US-09-954-531-463	Sequence 463, App	c 319	16	0.5	563	10	US-09-864-761-9542	Sequence 9542, App
c 247	16	0.5	435	10	US-09-867-550-65	Sequence 65, Appl	c 320	16	0.5	563	10	US-09-864-761-12387	Sequence 12387, A
c 248	16	0.5	435	10	US-09-867-701-4813	Sequence 4813, App	c 321	16	0.5	567	10	US-09-864-761-7531	Sequence 7531, App
c 249	16	0.5	437	10	US-09-917-800A-431	Sequence 431, App	c 322	16	0.5	569	10	US-09-864-761-8268	Sequence 8268, App
c 250	16	0.5	438	10	US-09-920-300A-283	Sequence 283, App	c 323	16	0.5	569	10	US-09-864-761-9387	Sequence 9387, App
c 251	16	0.5	438	12	US-10-033-528-288	Sequence 283, App	c 324	16	0.5	576	10	US-09-920-300A-1018	Sequence 1018, App
c 252	16	0.5	440	10	US-09-864-761-10165	Sequence 10165, A	c 325	16	0.5	576	12	US-10-033-528-1018	Sequence 1018, App
c 253	16	0.5	444	10	US-09-925-301-696	Sequence 696, App	c 326	16	0.5	576	12	US-10-033-528-1839	Sequence 1839, App
c 254	16	0.5	445	10	US-09-864-761-2177	Sequence 2177, App	c 327	16	0.5	577	9	US-09-996-140-38	Sequence 38, Appl
c 255	16	0.5	446	10	US-09-770-444-781	Sequence 781, App	c 328	16	0.5	578	10	US-09-998-598-1023	Sequence 1023, App
c 256	16	0.5	449	10	US-09-864-761-11513	Sequence 11513, A	c 329	16	0.5	581	10	US-09-864-761-11910	Sequence 11910, A
c 257	16	0.5	451	10	US-09-833-790-330	Sequence 330, App	c 330	16	0.5	587	10	US-09-864-761-9026	Sequence 9026, App
c 258	16	0.5	454	10	US-09-864-761-5563	Sequence 5563, App	c 331	16	0.5	587	10	US-09-828-302-5	Sequence 5, Appl
c 259	16	0.5	455	10	US-09-880-107-2497	Sequence 2497, App	c 332	16	0.5	588	10	US-09-917-800A-999	Sequence 999, App
c 260	16	0.5	457	10	US-09-867-701-10703	Sequence 10703, A	c 333	16	0.5	593	10	US-09-864-761-13697	Sequence 13697, A
c 261	16	0.5	459	10	US-09-960-352-5700	Sequence 5700, App	c 334	16	0.5	595	10	US-09-833-381-706	Sequence 706, App
c 262	16	0.5	460	10	US-09-864-761-14052	Sequence 14052, A	c 335	16	0.5	595	10	US-09-867-701-1526	Sequence 1526, App
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c 264	16	0.5	462	10	US-09-922-217-272	Sequence 272, App	c 337	16	0.5	599	10	US-09-864-761-9356	Sequence 9356, App
c 265	16	0.5	462	10	US-09-833-263-272	Sequence 272, App	c 338	16	0.5	599	10	US-09-864-761-8623	Sequence 8623, App
c 266	16	0.5	463	10	US-09-770-444-378	Sequence 378, App	c 339	16	0.5	600	10	US-09-864-761-8623	Sequence 8623, App
c 267	16	0.5	463	10	US-09-864-761-5550	Sequence 5550, App	c 340	16	0.5	600	10	US-09-864-761-13553	Sequence 13553, A
c 268	16	0.5	463	10	US-09-983-965-3664	Sequence 3664, App	c 341	16	0.5	604	10	US-09-864-761-17057	Sequence 17057, A
c 269	16	0.5	465	10	US-09-864-761-649	Sequence 649, App	c 342	16	0.5	607	10	US-09-879-536-205	Sequence 205, App
c 270	16	0.5	465	10	US-09-864-761-10244	Sequence 10244, A	c 343	16	0.5	610	9	US-10-040-739-475	Sequence 475, App
c 271	16	0.5	466	10	US-09-917-800A-263	Sequence 263, App	c 344	16	0.5	634	10	US-09-815-343-215	Sequence 215, App
c 272	16	0.5	467	10	US-09-864-761-3483	Sequence 3483, App	c 345	16	0.5	640	9	US-10-025-380-630	Sequence 630, App
c 273	16	0.5	469	10	US-09-864-761-13881	Sequence 13881, A	c 346	16	0.5	640	10	US-09-922-217-630	Sequence 630, App
c 274	16	0.5	471	10	US-09-864-761-2416	Sequence 2416, App	c 347	16	0.5	640	10	US-09-833-263-630	Sequence 630, App
c 275	16	0.5	471	10	US-09-864-761-11002	Sequence 11002, A	c 348	16	0.5	640	10	US-09-833-381-974	Sequence 974, App
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c 279	16	0.5	475	10	US-09-864-761-2609	Sequence 2609, App	c 352	16	0.5	700	10	US-09-910-943-261	Sequence 261, App
c 280	16	0.5	477	9	US-09-981-286A-12	Sequence 12, Appl	c 353	16	0.5	728	9	US-10-066-500-53	Sequence 53, Appl
c 281	16	0.5	477	10	US-09-864-761-146	Sequence 146, App	c 354	16	0.5	730	10	US-09-867-550-677	Sequence 677, App
c 282	16	0.5	479	10	US-09-867-701-2300	Sequence 2300, App	c 355	16	0.5	811	9	US-09-938-842A-4121	Sequence 4121, App
c 283	16	0.5	482	10	US-09-864-761-27002	Sequence 27002, A	c 356	16	0.5	819	12	US-10-044-090-427	Sequence 427, App
c 284	16	0.5	482	10	US-09-920-300A-1363	Sequence 1363, App	c 357	16	0.5	823	9	US-09-842-777-2	Sequence 2, Appl
c 285	16	0.5	482	12	US-10-033-528-1363	Sequence 1363, App	c 358	16	0.5	830	9	US-09-842-777-16	Sequence 16, Appl
c 286	16	0.5	483	9	US-09-796-692-4807	Sequence 4807, App	c 359	16	0.5	843	10	US-09-974-300-5379	Sequence 5379, App
c 287	16	0.5	483	10	US-09-919-580-455	Sequence 455, App	c 360	16	0.5	844	9	US-09-842-777-3	Sequence 3, Appl
c 288	16	0.5	483	10	US-09-974-300-5149	Sequence 5149, App	c 361	16	0.5	846	9	US-09-842-777-4	Sequence 4, Appl
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c 290	16	0.5	486	10	US-09-920-300A-981	Sequence 981, App	c 363	16	0.5	851	9	US-09-842-777-17	Sequence 17, Appl
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385	16	0.5	1151	10	US-09-778-844-164	Sequence 164, App	458	16	0.5	2005	10	US-09-887-576-304	Sequence 304, App
386	16	0.5	1157	10	US-09-778-844-166	Sequence 166, App	c 459	16	0.5	2047	10	US-09-864-761-32004	Sequence 32004, A
387	16	0.5	1158	9	US-09-938-842A-739	Sequence 739, App	c 460	16	0.5	2092	10	US-09-764-869-1930	Sequence 1930, App
388	16	0.5	1159	9	US-09-842-777-1	Sequence 1, Appli	c 461	16	0.5	2093	10	US-09-880-107-3941	Sequence 3941, App
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390	16	0.5	1172	10	US-09-778-844-163	Sequence 163, App	c 463	16	0.5	2139	9	US-10-095-139-3	Sequence 3, Appli
391	16	0.5	1173	9	US-09-842-777-15	Sequence 15, Appli	c 464	16	0.5	2139	9	US-10-095-139-24	Sequence 24, Appli
392	16	0.5	1178	10	US-09-840-787-88	Sequence 88, Appli	c 465	16	0.5	2160	9	US-09-938-842A-628	Sequence 628, App
393	16	0.5	1200	10	US-09-925-300-488	Sequence 488, App	c 466	16	0.5	2184	10	US-09-880-192-31	Sequence 31, Appli
394	16	0.5	1261	10	US-09-964-824A-579	Sequence 579, App	c 467	16	0.5	2209	10	US-09-925-301-494	Sequence 494, App
395	16	0.5	1263	9	US-09-864-761-19678	Sequence 19678, A	c 468	16	0.5	2224	10	US-09-873-637-1	Sequence 1, Appli
396	16	0.5	1317	9	US-10-011-588-16	Sequence 16, Appli	c 469	16	0.5	2232	9	US-09-774-639-26	Sequence 26, Appli
397	16	0.5	1320	12	US-10-044-090-82	Sequence 82, Appli	c 470	16	0.5	2295	10	US-09-815-242-7459	Sequence 7459, App
398	16	0.5	1362	9	US-09-938-842A-1584	Sequence 1584, App	c 471	16	0.5	2388	10	US-09-925-302-112	Sequence 112, App
399	16	0.5	1378	10	US-09-809-545A-44	Sequence 44, Appli	c 472	16	0.5	2413	10	US-09-931-087A-2	Sequence 2, Appli
400	16	0.5	1386	9	US-09-910-664-38	Sequence 38, Appli	c 473	16	0.5	2418	9	US-09-989-919-19	Sequence 19, Appli
401	16	0.5	1404	10	US-09-765-272-9	Sequence 9, Appli	c 474	16	0.5	2429	9	US-10-041-007-27	Sequence 27, Appli
402	16	0.5	1464	9	US-09-738-626-216	Sequence 216, App	c 475	16	0.5	2438	9	US-09-895-913A-327	Sequence 327, App
403	16	0.5	1468	10	US-09-967-768A-185	Sequence 185, App	c 476	16	0.5	2488	10	US-09-822-849A-358	Sequence 358, App
404	16	0.5	1470	10	US-09-974-300-6209	Sequence 6209, App	c 477	16	0.5	2526	10	US-09-864-761-21763	Sequence 21763, A
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406	16	0.5	1494	9	US-09-938-842A-569	Sequence 569, App	c 479	16	0.5	2540	9	US-09-966-955A-5	Sequence 5, Appli
407	16	0.5	1495	12	US-10-044-090-798	Sequence 798, App	c 480	16	0.5	2554	9	US-10-108-605-338	Sequence 338, App
408	16	0.5	1502	10	US-09-883-997-11	Sequence 11, Appli	c 481	16	0.5	2577	10	US-09-822-849A-335	Sequence 335, App
409	16	0.5	1514	10	US-09-939-780-219	Sequence 897, App	c 482	16	0.5	2608	10	US-09-884-441-386	Sequence 386, App
410	16	0.5	1529	10	US-09-764-860-897	Sequence 897, App	c 483	16	0.5	2617	9	US-10-016-157A-121	Sequence 121, App
411	16	0.5	1529	10	US-09-764-860-898	Sequence 898, App	c 484	16	0.5	2656	9	US-09-798-889-33	Sequence 33, Appli
412	16	0.5	1529	10	US-09-764-860-899	Sequence 899, App	c 485	16	0.5	2681	10	US-09-917-800A-1619	Sequence 1619, App
413	16	0.5	1529	10	US-09-764-860-900	Sequence 900, App	c 486	16	0.5	2798	10	US-09-954-456-1145	Sequence 1145, App
414	16	0.5	1533	9	US-09-938-842A-2430	Sequence 2430, App	c 487	16	0.5	2808	10	US-09-954-456-2205	Sequence 2205, App
c 415	16	0.5	1542	9	US-09-938-842A-2222	Sequence 2222, App	c 488	16	0.5	2916	10	US-09-956-004-22	Sequence 22, Appli
416	16	0.5	1542	10	US-09-962-832-4	Sequence 4, Appli	c 489	16	0.5	2943	10	US-09-884-441-385	Sequence 385, App
417	16	0.5	1554	9	US-09-938-842A-1059	Sequence 1059, App	c 490	16	0.5	2960	9	US-10-098-841-16	Sequence 16, Appli
418	16	0.5	1557	10	US-09-815-242-8181	Sequence 8181, App	c 491	16	0.5	2996	10	US-09-778-320-205	Sequence 205, App
419	16	0.5	1569	10	US-09-822-830A-467	Sequence 467, App	c 492	16	0.5	2996	10	US-09-910-689-205	Sequence 205, App
c 420	16	0.5	1582	10	US-09-764-877-2303	Sequence 2303, App	c 493	16	0.5	2996	10	US-09-884-441-311	Sequence 311, App
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423	16	0.5	1584	10	US-09-815-242-4211	Sequence 4211, App	c 496	16	0.5	3024	10	US-09-833-381-889	Sequence 889, App
424	16	0.5	1587	10	US-09-867-550-1879	Sequence 1879, App	c 497	16	0.5	3030	10	US-09-833-381-889	Sequence 1, Appli
425	16	0.5	1597	10	US-09-954-456-734	Sequence 734, App	c 498	16	0.5	3091	10	US-09-768-436-1	Sequence 1, Appli
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c 429	16	0.5	1636	10	US-09-884-441-467	Sequence 467, App	c 501	16	0.5	3112	8	US-08-927-939-34	Sequence 34, Appli
c 430	16	0.5	1642	10	US-09-911-513-5	Sequence 5, Appli	c 502	16	0.5	3147	10	US-09-741-669-216	Sequence 216, App
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c 435	16	0.5	1724	10	US-09-974-300-2184	Sequence 2184, App	c 507	16	0.5	3437	10	US-09-954-456-1170	Sequence 1170, App
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c 439	16	0.5	1807	10	US-09-892-325-2	Sequence 1537, App	c 511	16	0.5	3567	9	US-10-028-072-77	Sequence 77, Appli
c 440	16	0.5	1824	10	US-09-814-786-1	Sequence 2, Appli	c 512	16	0.5	3609	10	US-09-799-875-6	Sequence 6, Appli
441	16	0.5	1840	10	US-09-954-456-723	Sequence 1, Appli	c 513	16	0.5	3649	10	US-09-801-574-15	Sequence 15, Appli
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c 443	16	0.5	1931	9	US-10-098-841-102	Sequence 27095, A	c 515	16	0.5	3705	12	US-10-044-090-307	Sequence 307, App
c 444	16	0.5	1960	10	US-09-731-872-179	Sequence 102, App	c 516	16	0.5	3722	10	US-09-892-325-1	Sequence 1, Appli
c 445	16	0.5	1963	10	US-09-864-761-2897	Sequence 179, App	c 517	16	0.5	3740	9	US-09-925-300-345	Sequence 345, App
c 446	16	0.5	1964	10	US-09-911-513-1	Sequence 2897, App	c 518	16	0.5	3795	10	US-10-002-344A-25	Sequence 25, Appli
c 447	16	0.5	1969	10	US-09-814-786-1	Sequence 1, Appli	c 519	16	0.5	3795	9	US-10-002-344A-25	Sequence 25, Appli
c 448	16	0.5	1971	9	US-09-864-761-15490	Sequence 15490, A	c 520	16	0.5	3833	9	US-09-954-531-1390	Sequence 1390, App
c 449	16	0.5	1972	10	US-09-864-761-15194	Sequence 3410, App	c 521	16	0.5	3833	10	US-09-969-708-391	Sequence 391, App
450	16	0.5	1989	10	US-09-974-300-2023	Sequence 15194, A	c 522	16	0.5	3912	10	US-09-917-800A-1560	Sequence 1560, App
451	16	0.5	1991	10	US-09-864-761-5037	Sequence 2023, App	c 523	16	0.5	4006	10	US-09-768-436-3	Sequence 3, Appli
452	16	0.5	2000	9	US-09-938-842A-2949	Sequence 5037, App	c 524	16	0.5	4313	9	US-09-978-295A-424	Sequence 424, App
453	16	0.5	2000	9	US-09-938-842A-3916	Sequence 2949, App	c 525	16	0.5	4313	9	US-09-978-697-424	Sequence 424, App
454	16	0.5	2000	9	US-09-938-842A-4550	Sequence 3916, App	c 526	16	0.5	4313	9	US-09-978-192A-424	Sequence 424, App
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c 536	16	0.5	4754	10	US-09-982-091A-1	Sequence 1, Appl1	c 609	16	0.5	75270	9	US-09-790-852-1	Sequence 1, Appl1
c 537	16	0.5	4758	9	US-09-842-777-9	Sequence 9, Appl1	c 610	16	0.5	75899	10	US-09-854-883-243	Sequence 243, App
c 538	16	0.5	4764	9	US-09-900-425A-1	Sequence 1, Appl1	c 611	16	0.5	80959	9	US-09-858-546-3	Sequence 3, Appl1
c 539	16	0.5	4766	9	US-09-764-868-1443	Sequence 1443, Ap	c 612	16	0.5	111282	12	US-10-094-989-3	Sequence 3, Appl1
c 540	16	0.5	4870	12	US-10-044-090-121	Sequence 121, App	c 613	16	0.5	126512	10	US-09-804-474A-3	Sequence 3, Appl1
c 541	16	0.5	5076	10	US-09-991-258-8	Sequence 8, Appl1	c 614	16	0.5	147309	10	US-09-742-312-3	Sequence 3, Appl1
c 542	16	0.5	5439	10	US-09-764-877-3625	Sequence 3625, Ap	c 615	16	0.5	148567	10	US-09-801-876B-3	Sequence 3, Appl1
c 543	16	0.5	5530	10	US-09-070-927A-206	Sequence 206, App	c 616	16	0.5	172637	10	US-09-805-458A-3	Sequence 3, Appl1
c 544	16	0.5	5591	10	US-09-764-846-309	Sequence 309, App	c 617	16	0.5	202001	10	US-09-734-674-3	Sequence 3, Appl1
c 545	16	0.5	5983	10	US-09-799-875-4	Sequence 4, Appl1	c 618	16	0.5	203654	10	US-09-820-905-3	Sequence 3, Appl1
c 546	16	0.5	6147	9	US-09-938-842A-2441	Sequence 2441, Ap	c 619	16	0.5	326014	10	US-09-731-231A-3	Sequence 3, Appl1
c 547	16	0.5	6319	10	US-09-995-454-581	Sequence 58, Appl	c 620	16	0.5	397658	10	US-09-813-320-3	Sequence 3, Appl1
c 548	16	0.5	6381	10	US-09-969-347-216	Sequence 216, App	c 621	16	0.5	465237	10	US-09-933-267A-1	Sequence 1, Appl1
c 549	16	0.5	6457	10	US-09-880-107-3389	Sequence 3389, Ap	c 622	16	0.5	640681	10	US-09-790-988-1	Sequence 1, Appl1
c 550	16	0.5	6501	9	US-10-029-413A-3	Sequence 3, Appl1	c 623	16	0.5	659158	9	US-09-771-208-20	Sequence 20, Appl
c 551	16	0.5	6915	10	US-09-983-531A-1	Sequence 1, Appl1	c 624	16	0.5	1503841	9	US-09-946-807-1	Sequence 1, Appl1
c 552	16	0.5	7193	9	US-10-029-413A-17	Sequence 17, Appl	c 625	16	0.5	1503841	10	US-09-795-668-1	Sequence 1, Appl1
c 553	16	0.5	7193	9	US-10-029-413A-19	Sequence 19, Appl	c 626	16	0.5	1503841	10	US-09-795-686-1	Sequence 1, Appl1
c 554	16	0.5	7237	10	US-09-070-927A-239	Sequence 239, App	c 627	15	0.5	20	9	US-09-946-807-103	Sequence 103, App
c 555	16	0.5	7362	9	US-10-029-413A-15	Sequence 15, Appl	c 628	15	0.5	20	10	US-09-795-668-103	Sequence 103, App
c 556	16	0.5	7414	10	US-09-764-853-876	Sequence 876, App	c 629	15	0.5	20	10	US-09-795-686-103	Sequence 103, App
c 557	16	0.5	7509	10	US-09-772-316-4	Sequence 4, Appl1	c 630	15	0.5	22	9	US-09-978-295A-312	Sequence 312, App
c 558	16	0.5	7537	10	US-09-764-869-1735	Sequence 1735, Ap	c 631	15	0.5	22	9	US-09-978-697-312	Sequence 312, App
c 559	16	0.5	7736	10	US-09-764-846-333	Sequence 333, App	c 632	15	0.5	22	9	US-09-978-192A-312	Sequence 312, App
c 560	16	0.5	8001	10	US-09-070-927A-622	Sequence 622, App	c 633	15	0.5	22	9	US-09-999-832A-312	Sequence 312, App
c 561	16	0.5	8253	9	US-09-790-852-9	Sequence 9, Appl1	c 634	15	0.5	22	9	US-09-978-189-312	Sequence 312, App
c 562	16	0.5	8761	9	US-10-098-841-11	Sequence 11, Appl	c 635	15	0.5	30	9	US-10-004-551-63	Sequence 63, Appl
c 563	16	0.5	9664	10	US-09-764-869-2126	Sequence 2126, Ap	c 636	15	0.5	50	10	US-09-738-847-32	Sequence 32, Appl
c 564	16	0.5	10758	12	US-10-044-090-61	Sequence 61, Appl	c 637	15	0.5	57	10	US-09-756-250B-4	Sequence 4, Appl1
c 565	16	0.5	11071	10	US-09-764-877-2793	Sequence 2793, Ap	c 638	15	0.5	60	10	US-09-756-250B-8	Sequence 8, Appl1
c 566	16	0.5	11176	10	US-09-738-968-43	Sequence 43, Appl	c 639	15	0.5	86	10	US-09-864-761-29742	Sequence 29742, A
c 567	16	0.5	11469	10	US-09-764-877-2791	Sequence 2791, Ap	c 640	15	0.5	89	10	US-09-878-574-6486	Sequence 6486, Ap
c 568	16	0.5	11764	10	US-09-070-927A-48	Sequence 48, Appl	c 641	15	0.5	93	10	US-09-864-761-20218	Sequence 20218, A
c 569	16	0.5	12001	10	US-09-955-807-13	Sequence 13, Appl	c 642	15	0.5	108	10	US-09-969-373-121	Sequence 121, App
c 570	16	0.5	12104	10	US-09-764-877-2761	Sequence 2761, Ap	c 643	15	0.5	113	10	US-09-864-761-23072	Sequence 23072, A
c 571	16	0.5	12327	10	US-09-764-869-2424	Sequence 2424, Ap	c 644	15	0.5	114	10	US-09-864-761-23381	Sequence 23381, A
c 572	16	0.5	14175	9	US-09-764-868-1474	Sequence 1474, Ap	c 645	15	0.5	116	10	US-09-878-574-12211	Sequence 7211, Ap
c 573	16	0.5	15418	10	US-09-783-203-1	Sequence 1, Appl1	c 646	15	0.5	118	9	US-09-796-692-6756	Sequence 6756, Ap
c 574	16	0.5	15418	10	US-09-994-427A-1	Sequence 1, Appl1	c 647	15	0.5	121	9	US-09-728-444-883	Sequence 883, App
c 575	16	0.5	15819	10	US-09-764-877-2765	Sequence 2765, Ap	c 648	15	0.5	121	10	US-09-815-242-2575	Sequence 2575, Ap
c 576	16	0.5	16150	10	US-09-764-869-2316	Sequence 2316, Ap	c 649	15	0.5	123	10	US-09-864-761-19617	Sequence 19617, A
c 577	16	0.5	16489	9	US-09-764-869-1483	Sequence 1483, Ap	c 650	15	0.5	129	10	US-09-864-761-25002	Sequence 25002, A
c 578	16	0.5	16511	10	US-09-764-869-2064	Sequence 2064, Ap	c 651	15	0.5	134	10	US-09-969-373-415	Sequence 415, App
c 579	16	0.5	17946	10	US-09-764-867-504	Sequence 504, App	c 652	15	0.5	136	10	US-09-864-761-28718	Sequence 28718, A
c 580	16	0.5	18501	10	US-09-764-869-2312	Sequence 2312, Ap	c 653	15	0.5	136	10	US-09-920-300A-511	Sequence 511, App
c 581	16	0.5	20268	10	US-09-764-847-1916	Sequence 1916, Ap	c 654	15	0.5	136	12	US-10-033-528-511	Sequence 511, App
c 582	16	0.5	20268	10	US-09-764-855-173	Sequence 173, App	c 655	15	0.5	140	10	US-09-864-761-17413	Sequence 17413, A
c 583	16	0.5	20860	10	US-09-070-927A-355	Sequence 355, App	c 656	15	0.5	141	10	US-09-783-590-12243	Sequence 12243, A
c 584	16	0.5	21536	10	US-09-416-384A-3	Sequence 3, Appl1	c 657	15	0.5	142	10	US-09-833-381-1409	Sequence 1409, Ap
c 585	16	0.5	22452	9	US-09-764-868-1487	Sequence 1487, Ap	c 658	15	0.5	142	10	US-09-960-352-13462	Sequence 13462, A
c 586	16	0.5	22452	9	US-09-764-868-1489	Sequence 1489, Ap	c 659	15	0.5	148	10	US-09-864-761-20604	Sequence 20604, A
c 587	16	0.5	22494	10	US-09-768-436-5	Sequence 5, Appl1	c 660	15	0.5	151	10	US-09-864-761-26359	Sequence 26359, A
c 588	16	0.5	26006	10	US-09-764-869-1963	Sequence 1963, Ap	c 661	15	0.5	151	10	US-09-960-352-123	Sequence 123, App
c 589	16	0.5	26006	10	US-09-764-864-1638	Sequence 1638, Ap	c 662	15	0.5	151	10	US-09-770-696-408	Sequence 408, App
c 590	16	0.5	26013	10	US-09-764-869-1961	Sequence 1961, Ap	c 663	15	0.5	160	10	US-09-864-761-31886	Sequence 31886, A
c 591	16	0.5	26013	10	US-09-764-864-1636	Sequence 1636, Ap	c 664	15	0.5	160	10	US-09-864-761-32962	Sequence 32962, A
c 592	16	0.5	26018	10	US-09-764-869-1962	Sequence 1962, Ap	c 665	15	0.5	163	9	US-09-796-692-7707	Sequence 7707, Ap
c 593	16	0.5	26018	10	US-09-764-864-1637	Sequence 1637, Ap	c 666	15	0.5	165	10	US-09-864-761-17210	Sequence 17210, A
c 594	16	0.5	27377	10	US-09-816-248-18	Sequence 18, Appl	c 667	15	0.5	171	9	US-09-864-761-18068	Sequence 18068, A
c 595	16	0.5	31132	10	US-09-764-864-1690	Sequence 1690, Ap	c 668	15	0.5	173	9	US-09-232-880-147	Sequence 147, App
c 596	16	0.5	31132	10	US-09-764-877-3062	Sequence 3062, Ap	c 669	15	0.5	173	9	US-10-012-896-147	Sequence 147, App
c 597	16	0.5	31885	10	US-09-764-860-775	Sequence 775, App	c 670	15	0.5	173	9	US-09-895-793-147	Sequence 147, App
c 598	16	0.5	31885	10	US-09-764-877-2530	Sequence 2530, Ap	c 671	15	0.5	173	9	US-09-895-814-147	Sequence 147, App
c 599	16	0.5	31885	10	US-09-764-877-2541	Sequence 2541, Ap	c 672	15	0.5	173	10	US-09-759-143-147	Sequence 147, App
c 600	16	0.5	32132	10	US-09-764-877-2308	Sequence 2308, Ap	c 673	15	0.5	173	10	US-09-864-761-31312	Sequence 31312, A
c 601	16	0.5	41907	10	US-09-967-013-5	Sequence 5, Appl1	c 674	15	0.5	173	10	US-09-780-669-147	Sequence 147, App
c 602	16	0.5	43058	10	US-09-934-456-292	Sequence 292, App	c 675	15	0.5	173	10	US-09-030-606-147	Sequence 147, App
c 603	16	0.5	43058	10	US-09-954-456-529	Sequence 529, App	c 676	15	0.5	173	10	US-09-822-827-147	Sequence 147, App

c 677	15	0.5	173	10	US-09-115-453-147	Sequence 147, App	c 750	15	0.5	263	10	US-09-783-590-8506	Sequence 8506, Ap
c 678	15	0.5	179	10	US-09-864-761-18380	Sequence 18380, A	c 751	15	0.5	263	10	US-09-960-352-5188	Sequence 5188, Ap
c 679	15	0.5	181	10	US-09-770-696-280	Sequence 280, App	c 752	15	0.5	264	9	US-09-232-880-211	Sequence 211, App
c 680	15	0.5	184	10	US-09-864-761-22332	Sequence 22332, A	c 753	15	0.5	264	9	US-10-012-896-211	Sequence 211, App
c 681	15	0.5	185	10	US-09-815-242-2036	Sequence 2036, Ap	c 754	15	0.5	264	9	US-09-895-793-211	Sequence 211, App
c 682	15	0.5	186	10	US-09-864-761-17986	Sequence 17986, A	c 755	15	0.5	264	9	US-09-895-814-211	Sequence 211, App
c 683	15	0.5	186	10	US-09-864-761-19162	Sequence 19162, A	c 756	15	0.5	264	10	US-09-294-093B-4047	Sequence 4047, Ap
c 684	15	0.5	187	9	US-09-796-692-2912	Sequence 2912, Ap	c 757	15	0.5	264	10	US-09-759-143-211	Sequence 211, App
c 685	15	0.5	187	10	US-09-860-352-5772	Sequence 5772, Ap	c 758	15	0.5	264	10	US-09-780-669-211	Sequence 211, App
c 686	15	0.5	191	10	US-09-878-574-8273	Sequence 8273, Ap	c 759	15	0.5	264	10	US-09-030-606-211	Sequence 211, App
c 687	15	0.5	191	10	US-09-783-590-7728	Sequence 7728, Ap	c 760	15	0.5	264	10	US-09-822-827-211	Sequence 211, App
c 688	15	0.5	192	9	US-09-736-457-243	Sequence 243, App	c 761	15	0.5	264	10	US-09-115-453-211	Sequence 211, App
c 689	15	0.5	192	9	US-09-902-941-243	Sequence 243, App	c 762	15	0.5	264	10	US-09-115-453-211	Sequence 211, App
c 690	15	0.5	192	9	US-09-849-626-243	Sequence 243, App	c 763	15	0.5	265	10	US-09-878-574-15020	Sequence 15020, A
c 691	15	0.5	193	10	US-09-998-598-2473	Sequence 2473, Ap	c 764	15	0.5	265	10	US-09-864-761-30086	Sequence 30086, A
c 692	15	0.5	194	9	US-09-736-457-1241	Sequence 1241, Ap	c 765	15	0.5	265	10	US-09-878-574-6402	Sequence 6402, Ap
c 693	15	0.5	194	9	US-09-902-941-1241	Sequence 1241, Ap	c 766	15	0.5	265	10	US-09-878-574-9323	Sequence 9323, Ap
c 694	15	0.5	194	9	US-09-849-626-1241	Sequence 1241, Ap	c 767	15	0.5	266	9	US-09-796-692-8945	Sequence 8945, Ap
c 695	15	0.5	196	10	US-09-864-761-20007	Sequence 20007, A	c 768	15	0.5	266	10	US-09-878-574-12431	Sequence 12431, A
c 696	15	0.5	197	10	US-09-864-761-32734	Sequence 32734, A	c 769	15	0.5	267	10	US-09-867-701-8481	Sequence 8481, Ap
c 697	15	0.5	197	10	US-09-960-352-10024	Sequence 10024, A	c 770	15	0.5	267	10	US-09-563-817-582	Sequence 582, App
c 698	15	0.5	199	10	US-09-783-590-8362	Sequence 8362, Ap	c 771	15	0.5	267	10	US-09-983-965-1984	Sequence 1984, Ap
c 699	15	0.5	200	10	US-09-770-696-167	Sequence 167, App	c 772	15	0.5	268	9	US-09-796-692-3102	Sequence 3102, Ap
c 700	15	0.5	200	10	US-09-903-377-3	Sequence 3, App1	c 773	15	0.5	270	9	US-09-796-692-8985	Sequence 8985, Ap
c 701	15	0.5	205	10	US-09-864-761-21903	Sequence 21903, A	c 774	15	0.5	271	9	US-09-796-692-9532	Sequence 9532, Ap
c 702	15	0.5	205	10	US-09-960-352-192	Sequence 192, App	c 775	15	0.5	271	10	US-09-923-876-164	Sequence 164, App
c 703	15	0.5	207	10	US-09-864-761-17446	Sequence 17446, A	c 776	15	0.5	271	10	US-09-867-701-7578	Sequence 7578, Ap
c 704	15	0.5	208	10	US-09-770-696-106	Sequence 106, App	c 777	15	0.5	272	9	US-10-046-935-1523	Sequence 1523, Ap
c 705	15	0.5	212	10	US-09-598-598-2047	Sequence 2047, App	c 778	15	0.5	272	9	US-09-878-178-1523	Sequence 1523, Ap
c 706	15	0.5	215	10	US-09-770-696-69	Sequence 69, App1	c 779	15	0.5	272	10	US-09-815-242-3335	Sequence 3335, Ap
c 707	15	0.5	215	10	US-09-815-242-3593	Sequence 3593, Ap	c 780	15	0.5	272	10	US-09-878-574-6734	Sequence 6734, Ap
c 708	15	0.5	215	10	US-09-815-242-3601	Sequence 3601, Ap	c 781	15	0.5	272	10	US-09-878-574-15648	Sequence 15648, A
c 709	15	0.5	215	10	US-09-833-381-459	Sequence 459, App	c 782	15	0.5	273	10	US-09-878-574-12834	Sequence 12834, A
c 710	15	0.5	215	10	US-09-864-761-23766	Sequence 23766, A	c 783	15	0.5	273	10	US-09-878-574-11827	Sequence 11827, A
c 711	15	0.5	218	10	US-09-864-761-23412	Sequence 23412, A	c 784	15	0.5	276	10	US-09-923-876-4134	Sequence 4134, Ap
c 712	15	0.5	221	9	US-09-736-968A-94	Sequence 94, Appl	c 785	15	0.5	276	10	US-09-815-242-4859	Sequence 4859, Ap
c 713	15	0.5	221	9	US-09-796-692-7336	Sequence 7336, Ap	c 786	15	0.5	276	10	US-09-815-242-8566	Sequence 8566, Ap
c 714	15	0.5	224	10	US-09-783-590-3206	Sequence 3206, Ap	c 787	15	0.5	276	10	US-09-815-242-8866	Sequence 8866, Ap
c 715	15	0.5	224	10	US-09-983-965-4934	Sequence 4934, Ap	c 788	15	0.5	276	10	US-09-815-242-9062	Sequence 9062, Ap
c 716	15	0.5	227	9	US-09-924-400-183	Sequence 183, App	c 789	15	0.5	277	10	US-09-878-574-11254	Sequence 11254, A
c 717	15	0.5	227	10	US-09-810-936-183	Sequence 183, App	c 790	15	0.5	278	9	US-09-796-692-3869	Sequence 3869, Ap
c 718	15	0.5	227	10	US-09-429-755-183	Sequence 183, App	c 791	15	0.5	279	10	US-09-864-761-19127	Sequence 19127, A
c 719	15	0.5	228	10	US-09-833-381-301	Sequence 301, App	c 792	15	0.5	280	10	US-09-004-068-5	Sequence 5, Appl1
c 720	15	0.5	229	10	US-09-294-093B-759	Sequence 759, App	c 793	15	0.5	280	10	US-09-004-068-8	Sequence 8, Appl1
c 721	15	0.5	229	10	US-09-864-761-27663	Sequence 27663, A	c 794	15	0.5	281	10	US-09-294-093B-880	Sequence 880, App
c 722	15	0.5	230	9	US-09-796-692-9407	Sequence 9407, Ap	c 795	15	0.5	282	9	US-09-954-531-392	Sequence 392, App
c 723	15	0.5	230	10	US-09-783-590-3884	Sequence 3884, Ap	c 796	15	0.5	282	9	US-09-796-692-4907	Sequence 4907, App
c 724	15	0.5	230	10	US-09-960-352-3875	Sequence 3875, Ap	c 797	15	0.5	282	10	US-09-004-068-11	Sequence 11, Appl
c 725	15	0.5	234	10	US-09-923-876-3260	Sequence 3260, Ap	c 798	15	0.5	282	10	US-09-969-708-21	Sequence 21, Appl
c 726	15	0.5	240	10	US-09-878-574-10335	Sequence 10335, A	c 799	15	0.5	283	10	US-09-294-093B-557	Sequence 557, App
c 727	15	0.5	241	10	US-09-878-574-5190	Sequence 5190, Ap	c 800	15	0.5	284	9	US-09-954-531-83	Sequence 83, Appl
c 728	15	0.5	241	10	US-09-867-701-4336	Sequence 4336, Ap	c 801	15	0.5	284	10	US-09-923-876-5170	Sequence 5170, Ap
c 729	15	0.5	242	10	US-09-923-876-1173	Sequence 1173, Ap	c 802	15	0.5	284	10	US-09-864-761-20944	Sequence 20944, A
c 730	15	0.5	244	10	US-09-923-876-3255	Sequence 3255, Ap	c 803	15	0.5	286	10	US-09-834-975-682	Sequence 682, App
c 731	15	0.5	244	10	US-09-894-882-276	Sequence 276, App	c 804	15	0.5	290	9	US-10-079-623-94	Sequence 94, Appl
c 732	15	0.5	244	10	US-09-894-882-279	Sequence 279, App	c 805	15	0.5	292	10	US-09-878-574-8225	Sequence 8225, Ap
c 733	15	0.5	244	10	US-09-894-882-282	Sequence 282, App	c 806	15	0.5	293	10	US-09-563-817-897	Sequence 897, App
c 734	15	0.5	244	10	US-09-878-574-6193	Sequence 6193, Ap	c 807	15	0.5	296	10	US-09-867-701-6616	Sequence 6616, Ap
c 735	15	0.5	245	10	US-09-878-574-8820	Sequence 8820, Ap	c 808	15	0.5	297	9	US-09-796-692-3405	Sequence 3405, Ap
c 736	15	0.5	249	10	US-09-878-574-8820	Sequence 8820, Ap	c 809	15	0.5	299	10	US-09-969-347-75	Sequence 75, Appl
c 737	15	0.5	252	9	US-09-796-692-7617	Sequence 7617, Ap	c 810	15	0.5	299	10	US-09-880-107-3086	Sequence 3086, Ap
c 738	15	0.5	252	10	US-09-878-574-10645	Sequence 10645, A	c 811	15	0.5	300	10	US-09-294-093B-3190	Sequence 3190, Ap
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ALIGNMENTS

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; Patent No. US200200347841
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
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; LENGTH: 3072
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US-09-841-739-3
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Query Match 100.0%; Score 3072; DB 10; Length 3072;  
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Db	1361	CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAAGCCAAAGTATATAA	1320
Qy	1321	TTCTTTTACAAAGTCATTCACGAGGTACACAGCAGACGACAAAGCTACAGCAGTTATTTCAGC	1380
Db	1321	TTCTTTTACAAAGTCATTCACGAGGTACACAGCAGACGACAAAGCTACAGCAGTTATTTCAGC	1380
Qy	1381	TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTTGCAGAAAAATGGTTTCCATT	1440
Db	1381	TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTTGCAGAAAAATGGTTTCCATT	1440
Qy	1441	TCGGACATTTACATCCACTTTATAGCAGCTGCTCCGGTACACCTGTGGGTCAATCTGTGGAA	1500
Db	1441	TCGGACATTTACATCCACTTTATAGCAGCTGCTCCGGTACACCTGTGGGTCAATCTGTGGAA	1500
Qy	1501	GCCACCAAGGCTCTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA	1560
Db	1501	GCCACCAAGGCTCTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA	1560
Qy	1561	CTTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1620
Db	1561	CTTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1620
Qy	1621	ACTGAGCAAGAAATTCGAAGGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Db	1621	ACTGAGCAAGAAATTCGAAGGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Qy	1681	TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAA	1740
Db	1681	TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAA	1740
Qy	1741	GGTAAAGCTTTATATCAACTCAGGGAACATCCCCGATTACTTATTGTACTTCTTTTCAA	1800
Db	1741	GGTAAAGCTTTATATCAACTCAGGGAACATCCCCGATTACTTATTGTACTTCTTTTCAA	1800
Qy	1801	CATTTCGCCAAATTTGCAAGTCTCTGAGCTTCATTAACCTGGACTTTTATGGGGAGCT	1860
Db	1801	CATTTCGCCAAATTTGCAAGTCTCTGAGCTTCATTAACCTGGACTTTTATGGGGAGCT	1860
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Db	1921	GAACCTTACATTCACAGAGGCTGTACTTTGTTCCTCAACTGGAAGCAGGAATTCAGG	1980
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Db	2041	GGGAAAAATTTACGCTCTGCCAAGCCCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG	2100
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Db	2101	GCTGGAAGCCTCAGTTTGGTCTCAGACCTCTGAAGAACATTTATCTCTCATGGTGGAA	2160
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Db	2161	GCCAGTCCCTCACCATAGAAGATGAGGGCACATCACATCTGTAAACAAACCTGAAAACC	2220
Qy	2221	TTGAGTATTTCATGACCTACAGAAATCAACGGCTGCGCGGTGCTCTGACTTGAGCTTGGT	2280
Db	2221	TTGAGTATTTCATGACCTACAGAAATCAACGGCTGCGCGGTGCTCTGACTTGAGCTTGGT	2280
Qy	2281	AACTTGGAAGAACCTTCAAAAGCTCATATATGGATATACATAAAGATGAATGAAGAAGATGCT	2340
Db	2281	AACTTGGAAGAACCTTCAAAAGCTCATATATGGATATACATAAAGATGAATGAAGAAGATGCT	2340

## RESULT 2

US-09-841-739-1

03 03 041 733 1  
; Sequence 1, Application US/09841739

; Patent No. US20020034784A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MO

FILE REFERENCE: 07334-329001

; CURRENT APPLICATION NUMBER: US/09/841,739

; CURRENT FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: US 09/697,089

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: US 60/161,822

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 1

; LENGTH: 3133

TYPE: DNA

; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
us-09-841-739-1

Query Match      100.0%; Score 3072; DB 10; Length 3133;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATTA 60
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QY 61 AAGCAATACACAGATGACCTATTGTTGGAATGTTCTGAATCGCGAAGAAGTAACATC 120
Db 96 AAGCAATACACAGATGACCTATTGTTGGAATGTTCTGAATCGCGAAGAAGTAACATC 155
QY 121 ATTGCTGCGAGAAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 180
Db 156 ATTGCTGCGAGAAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 215
QY 181 AAGGGTTACAGATGCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTA 240
Db 216 AAGGGTTACAGATGCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTA 275
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Db 276 TTTCAGAGCTTGAATGACAAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGAGAT 335
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT 360
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Db 396 GGTGAAGATATTGACATATTATTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG 455
QY 421 AGGAAGACCAACACCATCACCGTGGAGCAGCTGACCCCTGATGGCCCTCTGAGGCT 480
Db 456 AGGAAGACCAACACCATCACCGTGGAGCAGCTGACCCCTGATGGCCCTCTGAGGCT 515
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QY 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGCAGGCTCTGACCAAGTTCAAAATTCGTC 600
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QY 601 TTCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660
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Db 936 ACAGAAGACAGGCCCGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGC 995
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Db 1056 GTGGTCAATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCACACTCTCTACACACAACA 1115
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Db 1176 GTGGCTGCAAGTGAATTCATTCGGAGCTGACCACTGTGAGACCTTAGCTCTGGAGGT 1235
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Db 1236 GTGTTCTCCCAAGTTTGNATTCGAACTGTCAGAGTGTGTCAGCGTGAATGAGGATGTC 1295
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Db 1296 CTGCTGACAACTGGGCTCCTCTGTAATAATACAGCTCAAAGGTTCAGGCCAAAAGTATAA 1355
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Db 1896 ATGGCTTCATGGGAAAGGCTGCGAAGACAGAGTGAATCCACATGGAAGAGGCCCA 1955
QY 1921 GAAACTACATTTCCAGCAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 1980
Db 1956 GAAACTACATTTCCAGCAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 2015
QY 1981 ACTCTGGAGGTCACACTCCGGGATTTACAGAAAGTGAATAAGCAAGATATCACATATCTG 2040
Db 2016 ACTCTGGAGGTCACACTCCGGGATTTACAGAAAGTGAATAAGCAAGATATCACATATCTG 2075
QY 2041 GGGAAAATATTTCAGCTCTGCGCACAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTG 2100
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Qy 601 TTTCTTCCCTCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGATCAACTC 660  
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RESULT 4  
US-09-841-739-6  
; Sequence 6, Application US/09841739  
; Patent No. US20020034784A1  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 3612  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-6  
Query Match 85.7%; Score 2634; DB 10; Length 3612;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322  
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QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTTAT 382  
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QY 923 TCATCCGAGAAAGTGTGATCAAGGAGCTTGCCTGAAGGCTTGTGCTCCAAATTCAGAAAT 982  
Db 1394 TCATCCGAGAAAGTGTGATCAAGGAGCTTGCCTGAAGGCTTGTGCTCCAAATTCAGAAAT 1453  
QY 983 CCAGGTGCTTGGAGAAATCTCATGAAGACCCCTCTCTTGTGTGCTCATCTTGTGCAATCC 1042  
Db 1454 CCAGGTGCTTGGAGAAATCTCATGAAGACCCCTCTCTTGTGTGCTCATCTTGTGCAATCC 1513  
QY 1043 AGATGGGTGAAAGTGTGCTCCTCATCACAACAACAGCGCTGTGCTCATACCTTCTATG 1102  
Db 1514 AGATGGGTGAAAGTGTGCTCCTCATCACAACAACAGCGCTGTGCTCATACCTTCTATG 1573  
QY 1103 ATCTGTTGATACAGAAACAAACAAACATTAAGGTGGCTGCAAGTGACTTCAATC 1162  
Db 1574 ATCTGTTGATACAGAAACAAACAAACATTAAGGTGGCTGCAAGTGACTTCAATC 1633  
QY 1163 GGAGCTTGGACCACTGTGGAGACCTAGCTCTGTGAGGCTGTGCTCTCCCAAGTTGAT 1222  
Db 1634 GGAGCTTGGACCACTGTGGAGACCTAGCTCTGTGAGGCTGTGCTCTCCCAAGTTGAT 1693  
QY 1223 TCGAAGTGCAGGATGTGTCAGCGTGAATGAGGATCTCTGCTGCAAGCTGGGCTCTCT 1282  
Db 1694 TCGAAGTGCAGGATGTGTCAGCGTGAATGAGGATCTCTGCTGCAAGCTGGGCTCTCT 1753  
QY 1283 GTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTTCTTCAAGTCAATTCAGG 1342  
Db 1754 GTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTTCTTCAAGTCAATTCAGG 1813  
QY 1343 AGTACACAGCAGGACCAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGGAGGTGA 1402  
Db 1814 AGTACACAGCAGGACCAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGGAGGTGA 1873  
QY 1403 CCAAGGGGAATGGTTACTTTCGAGAAATTTGTTTCCATTTTCGGACATTACATCCACTATA 1462  
Db 1874 CCAAGGGGAATGGTTACTTTCGAGAAATTTGTTTCCATTTTCGGACATTACATCCACTATA 1933  
QY 1463 GCAGCTGTCTCCGTTACAGCTGTGGGTCTATCTGTGGAAGCCACAGGCTGTTATGAAG 1522  
Db 1934 GCAGCTGTCTCCGTTACAGCTGTGGGTCTATCTGTGGAAGCCACAGGCTGTTATGAAG 1993  
QY 1523 ACCTCGCAGCAGTGTATCAACAGGCTGCTTCTCGGACTTTTCCATTCGCCAAGAGCCCTC 1582  
Db 1994 ACCTCGCAGCAGTGTATCAACAGGCTGCTTCTCGGACTTTTCCATTCGCCAAGAGCCCTC 2053  
QY 1583 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACCCTAGCAGCAAGAAATTTCTGAAG 1642  
Db 2054 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACCCTAGCAGCAAGAAATTTCTGAAG 2113

QY 1643 CCATAAACATCAATCCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 1702  
Db 2114 CCATAAACATCAATCCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 2173  
QY 1703 AATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTCAAGGTAAAGCTTATATCAACT 1762  
Db 2174 AATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTCAAGGTAAAGCTTATATCAACT 2233  
QY 1763 CAGGAAACATCCCGATCTACTTATTGACTTCTTGAACATTTGCCAATTTGTGCAAGTG 1822  
Db 2234 CAGGAAACATCCCGATCTACTTATTGACTTCTTGAACATTTGCCAATTTGTGCAAGTG 2293  
QY 1823 CTCTGACTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTTCATGGGAAAAGGTG 1882  
Db 2294 CCCTGACTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTTCATGGGAAAAGGTG 2353  
QY 1883 CAGAAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATTCGCCACAGG 1942  
Db 2354 CAGAAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATTCGCCACAGG 2413  
QY 1943 CTGTATCTTTGTTCTCAACTGGAAGCAGGAATTCAGACACTCTGAGAGTCAACTCCGGG 2002  
Db 2414 CTGTATCTTTGTTCTCAACTGGAAGCAGGAATTCAGACACTCTGAGAGTCAACTCCGGG 2473  
QY 2003 ATTTACGCAAGTTGAATGAAGCAAGATATCACATATCTCGGGAAATATTCAGCTCTGCCA 2062  
Db 2474 ATTTACGCAAGTTGAATGAAGCAAGATATCACATATCTCGGGAAATATTCAGCTCTGCCA 2533  
QY 2063 CAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGTGTGGCTGGAAGCCCTCAGTTGGTCC 2122  
Db 2534 CAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGTGTGGCTGGAAGCCCTCAGTTGGTCC 2593  
QY 2123 TCAGCACCTGTGAAGCAATTTATTTCTCATGGTGGAGGCCAGTCCCTCCACCATAGAG 2182  
Db 2594 TCAGCACCTGTGAAGCAATTTATTTCTCATGGTGGAGGCCAGTCCCTCCACCATAGAG 2653  
QY 2183 ATGAGAGGCACATCATCTGTGAACAAACCTGAAACCTTGAGTATTCATGACCTACAGA 2242  
Db 2654 ATGAGAGGCACATCATCTGTGAACAAACCTGAAACCTTGAGTATTCATGACCTACAGA 2713  
QY 2243 ATCAACGGCTGCGGGTGTGCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGC 2302  
Db 2714 ATCAACGGCTGCGGGTGTGCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGC 2773  
QY 2303 TCATAATGATACATAAAGATGAATGAAGAGATGCTTATAAACTAGCTGAAGCCCTGA 2362  
Db 2774 TCATAATGATACATAAAGATGAATGAAGAGATGCTTATAAACTAGCTGAAGCCCTGA 2833  
QY 2363 AAAACCTGAAGAGATGTGTTTATTTCACTTTGACCCACTTGTCTGACATTTGGAGAGGAA 2422  
Db 2834 AAAACCTGAAGAGATGTGTTTATTTCACTTTGACCCACTTGTCTGACATTTGGAGAGGAA 2893  
QY 2423 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCTCTGACCTTGAAGAAATTCATATTAG 2482  
Db 2894 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCTCTGACCTTGAAGAAATTCATATTAG 2953  
QY 2483 TCTCTGCTGCTGTGCTGCAAAATGCAAGTGAAGTAACTTCTAGCTCAGAAATTCACAAATTTGG 2542  
Db 2954 TCTCTGCTGCTGTGCTGCAAAATGCAAGTGAAGTAACTTCTAGCTCAGAAATTCACAAATTTGG 3013  
QY 2543 TCAAACTGAGCATCTTGATTATACAGAAATTAACCTGGAAAAAGATGGAATGAAGTCT 2602  
Db 3014 TCAAACTGAGCATCTTGATTATACAGAAATTAACCTGGAAAAAGATGGAATGAAGTCT 3073  
QY 2603 TTCATGAACCTGATCAGAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCT 2662  
Db 3074 TTCATGAACCTGATCAGAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCT 3133  
QY 2663 GGGGCTGTGACGTGCAAGGCGAGCTTGAGCAGCCTGTTGAAACATTTGGAGAGGTTCCAC 2722  
Db 3134 GGGGCTGTGACGTGCAAGGCGAGCTTGAGCAGCCTGTTGAAACATTTGGAGAGGTTCCAC 3193

QY 2723 AACTGTCAAGCTTGGTTGAAAACTGGAGACTCAGACATACAGATTAAGATTTAG 2782  
Db 3194 AACTGTCAAGCTTGGTTGAAAACTGGAGACTCAGACATACAGATTAAGATTTAG 3253  
QY 2783 GTGCTTTTGGAAAGAACCTCTGAAAACTTCCAGCAGTTGAATTTGGGGGAAATC 2842  
Db 3254 GTGCTTTTGGAAAGAACCTCTGAAAACTTCCAGCAGTTGAATTTGGGGGAAATC 3313  
QY 2843 GTGCTTTTGGAAAGAACCTTGCCTTTCATGGGTGTATTTGAGAACTCTTAAGCAATTTAG 2902  
Db 3314 GTGCTTTTGGAAAGAACCTTGCCTTTCATGGGTGTATTTGAGAACTCTTAAGCAATTTAG 3373  
QY 2903 TGTGTTTGGAAAGAACCTTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACCTTA 2962  
Db 3374 TGTGTTTGGAAAGAACCTTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACCTTA 3433  
QY 2963 GCCAAATGCTTATCCAAAGTAACTTTTCTGCAAGAGCTTAGCTTCTGTTGGTGGCAATTTG 3022  
Db 3434 GCCAAATGCTTATCCAAAGTAACTTTTCTGCAAGAGCTTAGCTTCTGTTGGTGGCAATTTG 3493  
QY 3023 ATGATATGATCTCAGTCTTATACAG 3049  
Db 3494 ATGATATGATCTCAGTCTTATACAG 3520

RESULT 5  
US-09-841-739-4  
; Sequence 4, Application US/09841739  
; Patent No. US:0020034784A1  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841.739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 3615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CD3  
; LOCATION: (1)...(3612)  
US-09-841-739-4

Query Match 85.7%; Score 2634; DB 10; Length 3615;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCTTTTTCATCAGACATCAGAAGAGACTTTGGAGACTTTGGCTCAGGATTTAAAGGACT 322  
Db 734 GTCTTTTTCATCAGACATCAGAAGAGACTTTGGAGACTTTGGCTCAGGATTTAAAGGACT 793  
QY 323 TGTACCTTACCCCTCTTTTCTGAACCTTTATCCCTTGTGGAAGATATTGACATTAATT 382  
Db 794 TGTACCTTACCCCTCTTTTCTGAACCTTTATCCCTTGTGGAAGATATTGACATTAATT 853  
QY 383 TTAACCTTGAAGAGCACTTTCACAGAACCTTCTGTGAGGAAGGAGCAACCAACCATCACC 442  
Db 854 TTAACCTTGAAGAGCACTTTCACAGAACCTTCTGTGAGGAAGGAGCAACCAACCATCACC 913  
QY 443 CGCTGGAACAGCTGACCTGAATGGCTTCTGAGGCTTTCAGAGCCCTGCATCAATTG 502  
Db 914 CGCTGGAACAGCTGACCTGAATGGCTTCTGAGGCTTTCAGAGCCCTGCATCAATTG 973  
QY 503 AAGGGGAATCTGGAAGGCAAGTCCACTCTGCTGCAAGGCAATTTGGAGGCTTGGGCT 562  
Db 974 AAGGGGAATCTGGAAGGCAAGTCCACTCTGCTGCAAGGCAATTTGGAGGCTTGGGCT 1033

Qy	563	CCGAAAGTGC	AAAGGCTG	TGACCAAGTTCAAA	TTGGTCTTCTTCTCGTCTCAGCAGGG	632
Db	1034	CCGAAAGTGC	AAAGGCTG	TGACCAAGTTCAAA	TTGGTCTTCTTCTCGTCTCAGCAGGG	1093
Qy	623	CCAGGGTGG	ACHTTTT	TGAAACCC	TCTGTGATCAACTCCTGGATATACCTGGCACAATCA	682
Db	1094	CCAGGGTGG	ACHTTTT	TGAAACCC	TCTGTGATCAACTCCTGGATATACCTGGCACAATCA	1153
Qy	683	GGAGCAGAC	ATTCA	TGGCCATGCTGCTGAAGCT	CGGCAGAGGGTCTTTTCCCTCTCTG	742
Db	1154	GGAGCAGAC	ATTCA	TGGCCATGCTGCTGAAGCT	CGGCAGAGGGTCTTTTCCCTCTCTG	1213
Qy	743	ATGGCTACA	ATGAATTC	AAAGCCCCAGAACTGCCAGAAAT	CGAAGCCCTGATAAAGGAAA	802
Db	1214	ATGGCTACA	ATGAATTC	AAAGCCCCAGAACTGCCAGAAAT	CGAAGCCCTGATAAAGGAAA	1273
Qy	803	ACCACCGCT	CAAGACATGGT	CATCGTCACCACTACCACT	TGAGTGGCTGAGGCACATAC	862
Db	1274	ACCACCGCT	CAAGACATGGT	CATCGTCACCACTACCACT	TGAGTGGCTGAGGCACATAC	1333
Qy	863	GGCAGTTTGGT	GGCCCTGACTGCTGAGGTGGGGATAT	CACAGAGACAGAGCGCCACGCGTC	922	
Db	1334	GGCAGTTTGGT	GGCCCTGACTGCTGAGGTGGGGATAT	CACAGAGACAGAGCGCCACGCGTC	1393	
Qy	923	TCATCCGAGA	AGTGCTGATCAAGGAGCTTGGCTGAAGGCTTGT	TGCTCCAATTCAGAAAT	982	
Db	1394	TCATCCGAGA	AGTGCTGATCAAGGAGCTTGGCTGAAGGCTTGT	TGCTCCAATTCAGAAAT	1453	
Qy	983	CCAGGTGCT	TGAGGAATCTCATGAAGACCCCTCTCTTTGGTGGTCA	TACATCTGGCAATTC	1042	
Db	1454	CCAGGTGCT	TGAGGAATCTCATGAAGACCCCTCTCTTTGGTGGTCA	TACATCTGGCAATTC	1513	
Qy	1043	AGATGGGTGA	AGTGAGTTCCACTCTCACACAAACAACGCTGT	TCCATACCTTCTATG	1102	
Db	1514	AGATGGGTGA	AGTGAGTTCCACTCTCACACAAACAACGCTGT	TCCATACCTTCTATG	1573	
Qy	1103	ATCTGTTGTA	PACAGAAAAACAACAATAAAGGTGTGGCTGCAAGTGACTTCATTC	1162		
Db	1574	ATCTGTTGTA	PACAGAAAAACAACAATAAAGGTGTGGCTGCAAGTGACTTCATTC	1633		
Qy	1163	GGAGCCTGG	ACCACCTGTGGAGACCTTAGCTCTGGAGGGTGTGTTCTCCCAAGTTTGATT	1222		
Db	1634	GGAGCCTGG	ACCACCTGTGGAGACCTTAGCTCTGGAGGGTGTGTTCTCCCAAGTTTGATT	1693		
Qy	1223	TCGAAC	TGCAGGATGTGTCAGCGTGAATGAGGATGCTGCTGACAACTGGGCTCCCTCT	1282		
Db	1694	TCGAAC	TGCAGGATGTGTCAGCGTGAATGAGGATGCTGCTGACAACTGGGCTCCCTCT	1753		
Qy	1283	GTAATATAC	AGCTCAAGGTTCAAGCCAAAGTATAAATCTTTCACAAGTCAATTC	1342		
Db	1754	GTAATATAC	AGCTCAAGGTTCAAGCCAAAGTATAAATCTTTCACAAGTCAATTC	1813		
Qy	1343	AGTACACAG	CAGACCAAGACCTCAGCAGTTTATTGACGTCTCATGAGCCAGAGAGTGA	1402		
Db	1814	AGTACACAG	CAGACCAAGACCTCAGCAGTTTATTGACGTCTCATGAGCCAGAGAGTGA	1873		
Qy	1403	CCAAGGGGA	TGTTACTTTCGAGAAAATGGTTTCCATTTCCGACATACATCCACTTATA	1462		
Db	1874	CCAAGGGGA	TGTTACTTTCGAGAAAATGGTTTCCATTTCCGACATACATCCACTTATA	1933		
Qy	1463	GCAGCCTGCT	CCGGTACACCTGTGGGTCACTGTGGAAAGCCACAGGGCTGTTATGAAGC	1522		
Db	1934	GCAGCCTGCT	CCGGTACACCTGTGGGTCACTGTGGAAAGCCACAGGGCTGTTATGAAGC	1993		
Qy	1523	ACCTCGCAG	CAGGTGTATCAACACGGTGCCTTCTCGACTTTTCCATCGCCAAAGAGGCTC	1582		
Db	1994	ACCTCGCAG	CAGGTGTATCAACACGGTGCCTTCTCGACTTTTCCATCGCCAAAGAGGCTC	2053		
Qy	1583	TCGTGGAC	ACAGGAATCTTTTGAAAGTGTGAAAAACACACCTTGAGCAGAGAAATTC	1642		
Db	2054	TCGTGGAC	ACAGGAATCTTTTGAAAGTGTGAAAAACACACCTTGAGCAGAGAAATTC	2113		

Qy	1643	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA	1702
Db	2114		
		CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA	2173
Qy	1703	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTCAAGGTTAAAGGCTTATATCAACT	1762
Db	2174		
		AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTCAAGGTTAAAGGCTTATATCAACT	2233
Qy	1763	CAGGGAACATCCCCGATTACTTTATTTGACTCTTTTGAACATTTGCCAAATTTGTCAAAGTG	1822
Db	2234		
		CAGGGAACATCCCCGATTACTTTATTTGACTCTTTTGAACATTTGCCCAATTTGTCAAAGTG	2293
Qy	1823	CTCTGACCTTCATTTAAACTTGGACTTTTATGCGGGAGCTATGGCTTCATGCGGAAAAGCGTG	1882
Db	2294		
		CCCTGACCTTCATTTAAACTTGGACTTTTATGCGGGAGCTATGGCTTCATGCGGAAAAGCGTG	2353
Qy	1883	CAGAAGACACAGTGGAAATCCACATGGAGAGGCCCCAGAAACCTACATTTCCAGCAGAGG	1942
Db	2354		
		CAGAAGACACAGTGGAAATCCACATGGAGAGGCCCCAGAAACCTACATTTCCAGCAGAGG	2413
Qy	1943	CTGTATCTTTGTTCTTCAACTGGAAAGCAGGAATTCAGGACTCTCTGGAGTCCACACTCCGGG	2002
Db	2414		
		CTGTATCTTTGTTCTTCAACTGGAAAGCAGGAATTCAGGACTCTCTGGAGTCCACACTCCGGG	2473
Qy	2003	ATTTGACGAAAGTTGAATAAGCAAGATATACATATCTCTGGGAAAATATTCAGCTCTGCCA	2062
Db	2474		
		ATTTGACGAAAGTTGAATAAGCAAGATATACATATCTCTGGGAAAATATTCAGCTCTGCCA	2533
Qy	2063	CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTGTGGCTGGAAGCCTCAGTTTGTGTC	2122
Db	2534		
		CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTGTGGCTGGAAGCCTCAGTTTGTGTC	2593
Qy	2123	TCAGCACCTGTGAAGAACATTTATCTCTCATGGTGGAAAGCAGTCCCTCACCACATAGAAG	2182
Db	2594		
		TCAGCACCTGTGAAGAACATTTATCTCTCATGGTGGAAAGCAGTCCCTCACCACATAGAAG	2653
Qy	2183	ATGAGAGGCACATFCACATCTGTAAACAAACCTGAAAGAGATGCTTATAAACTAGCTGAAGGCGCTCGA	2242
Db	2654		
		ATGAGAGGCACATFCACATCTGTAAACAAACCTGAAAGAGATGCTTATAAACTAGCTGAAGGCGCTCGA	2713
Qy	2243	ATCAAGGCTGCGGGTGCTGTGACTGACAGCTTGGGTAACTTGAAGAACCTTCAACAGC	2302
Db	2714		
		ATCAAGGCTGCGGGTGCTGTGACTGACAGCTTGGGTAACTTGAAGAACCTTCAACAGC	2773
Qy	2303	TCATAATGGATAACATAAAGATCAATGAAGAGATGCTTATAAACTAGCTGAAGGCGCTCGA	2362
Db	2774		
		TCATAATGGATAACATAAAGATCAATGAAGAGATGCTTATAAACTAGCTGAAGGCGCTCGA	2833
Qy	2363	AAAACCTGAAGAGATGTGTTATTTCAATTTGACCCACTTGTCTGACANTTGGAGAGGAA	2422
Db	2834		
		AAAACCTGAAGAGATGTGTTATTTCAATTTGACCCACTTGTCTGACANTTGGAGAGGAA	2893
Qy	2423	TGGATTTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACCTTCAAGAAATTCAAATTAG	2482
Db	2894		
		TGGATTTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCAAATTAG	2953
Qy	2483	TCCTCTGCTGTTGCTGCAATTCAGTGAAGAAATCCTTACCTAGCTCAGAAATTTGG	2542
Db	2954		
		TCCTCTGCTGTTGCTGCAATTCAGTGAAGAAATCCTTACCTAGCTCAGAAATTTGG	3013
Qy	2543	TCAAACCTGAGCATTTCTTGATTTATCAGAAATTTACCTGGAAAAAGATGGAAATGAAGCTC	2602
Db	3014		
		TCAAACCTGAGCATTTCTTGATTTATCAGAAATTTACCTGGAAAAAGATGGAAATGAAGCTC	3073
Qy	2603	TTTATGAACTGATCGACAGATGAACGTGCTAGAACACGCTCACCGCACTGATGCTGCCCT	2662
Db	3074		
		TTTATGAACTGATCGACAGATGAACGTGCTAGAACACGCTCACCGCACTGATGCTGCCCT	3133
Qy	2663	GGGGCTGTGACGTGCAAGCAGCCTTCAGCAGCTCTTGAAACATTTGGAGAGAGTCCAC	2722
Db	3134		
		GGGGCTGTGACGTGCAAGCAGCCTTCAGCAGCTCTTGAAACATTTGGAGAGAGTCCAC	3193
Qy	2723	AACTCGTCAAGCTTGGGTTTGA AAAA ACTGGAGACTCACAGATACAGAGATTAAGATTTTAG	2782



Db	3194	AATCGTCAAGCTTGGTTTGAANAAC	TGGAGACTC	ACAGATACAGAGATTAGAAATTTT	AG	3253
Qy	2783	GTGCATTTTGTGAANAACCTCTGA	AAACTCTC	CACGAGTTGAATTTGGCGGGAATC	TC	2842
Db	3254	GTGCATTTTGTGAANAACCTCTGA	AAACTCTC	CACGAGTTGAATTTGGCGGGAATC	TC	3313
Qy	2843	GTGTGACGAGTATGATGATGGCT	TGGCTTCAT	TGGGTGTATTTGAGNACTCTTAAGCAANTTAG	TC	2902
Db	3314	GTGTGACGAGTATGATGATGGCT	TGGCTTCAT	TGGGTGTATTTGAGNACTCTTAAGCAANTTAG	TC	3373
Qy	2903	TGTTTTTTGACTTTTACTACTAA	AGATTTCT	TACCTTGATCCAGCATTTAGTCAGAAACTTA	TC	2962
Db	3374	TGTTTTTTGACTTTTACTACTAA	AGATTTCT	TACCTTGATCCAGCATTTAGTCAGAAACTTA	TC	3433
Qy	2963	GCCAAGTGTATTCAAGTTTAAC	TTTTCTG	TCTGCAAGAAGCTAGGCTGTGTTGGGTGGCAATTTG	TC	3022
Db	3434	GCCAAGTGTATTCAAGTTTAAC	TTTTCTG	TCTGCAAGAAGCTAGGCTGTGTTGGGTGGCAATTTG	TC	3493
Qy	3023	ATGATGATGATCTCAGTGTTATT	TATACAG	3049		
Db	3494	ATGATGATGATCTCAGTGTTATT	TATACAG	3520		

## RESULT 6

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US-09-841-739-12/c
; Sequence 12, Application US/09841739
; GENBANK NO. US280220034784AL
; GENERAL INFORMATION:
;   APPLICANT INFORMATION: John
;   TITLE OF INVENTION:
;   FILE REFERENCE: 07334329001
;   CURRENT APPLICATION NUMBER: US/09/841,739
;   CURRENT FILING DATE: 2001-08-29
;   PRIOR APPLICATION NUMBER: US 05/697,089
;   PRIOR FILING DATE: 2000-10-26
;   PRIOR APPLICATION NUMBER: US 60/161,822
;   PRIOR FILING DATE: 1999-10-27
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: FastSeq for Windows'Version 4.0
; SEQ ID NO 12
;   LENGTH: 3615
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-841-739-12

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Query Match	85.7%	Score 2634;	DB 10;	Length 3615;
Best Local Similarity	99.9%	Pred. No. 0;		
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2882	GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTGGCTCAGGATTTAAAGGACT	2823		
QY 323	TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTTATT	382		
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2822	TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTTATT	2763		
QY 383	TTAACTTTGAAAGACCTTCACAGAACCTGTCTGTGTGGGAAGGACCAACACATCACC	442		
Db				
2762	TTAACTTTGAAAGACCTTCACAGAACCTGTCTGTGTGGGAAGGACCAACACATCACC	2703		
QY 443	GCGTGGAGCAGCTGACCCCTGAAATGGCCCTCTCTGCAGGCTCTTTCAGAGCCCTTCGATCATTTG	502		
Db				
2702	GCGTGGAGCAGCTGACCCCTGAAATGGCCCTCTCTGCAGGCTCTTTCAGAGCCCTTCGATCATTTG	2643		
QY 503	AAGGGGAATCTGGCAAAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGCTCTGGGGCT	562		
Db				
2642	AAGGGGAATCTGGCAAAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGCTCTGGGGCT	2583		
QY 563	CCGGAAAGTCGAAGGCTCTGACCAAGTTCAAATTCGTTCTTCTTCCCTCCGCTCAGCAGGG	622		
Db				
2582	CCGGAAAGTCGAAGGCTCTGACCAAGTTCAAATTCGTTCTTCTTCCCTCCGCTCAGCAGGG	2523		



QY 1703 AATCAGCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGSTAAAAGCTTATATATCAACT 1762  
Db 1442 AATCAGCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGSTAAAAGCTTATATATCAACT 1383  
QY 1763 CAGGGAACATCCCGAATTAATTTGACTTCTTTGAAACATTTGCCAATTTGTGCAAGTG 1822  
Db 1382 CAGGGAACATCCCGAATTAATTTGACTTCTTTGAAACATTTGCCAATTTGTGCAAGTG 1323  
QY 1823 CTCTGACATTCATTAACCTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882  
Db 1322 CCTGGACTTCATTAACCTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1263  
QY 1883 CAGAAGACAGGTGGAATCCACATCGAAGAGGCCCCAGAAACCTACATTCACAGCAGGG 1942  
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QY 1943 CTGTATCTTTGTTCTTCAACTGGAACGAGAAATTCAGGACTCTGGAGGTCACACTCCGGG 2002  
Db 1202 CTGTATCTTTGTTCTTCAACTGGAACGAGAAATTCAGGACTCTGGAGGTCACACTCCGGG 1143  
QY 2003 ATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 2062  
Db 1142 ATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 1083  
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC 2122  
Db 1082 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC 1023  
QY 2123 TCAGCACCCTGTAGAACATTTATTTCTCATGTGTGAAGCCAGTCCCTCACCATAGAG 2182  
Db 1022 TCAGCACCCTGTAGAACATTTATTTCTCATGTGTGAAGCCAGTCCCTCACCATAGAG 963  
QY 2183 ATCAGAGGCACATCACATCTGTAAACAACTTGAAACCTTGAGTATTCATGACCTACAGA 2242  
Db 962 ATCAGAGGCACATCACATCTGTAAACAACTTGAAACCTTGAGTATTCATGACCTACAGA 903  
QY 2243 ATCAAGGCTGCCGGTGTCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 2302  
Db 902 ATCAAGGCTGCCGGTGTCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 843  
QY 2303 TCATATGATACATATAAGATGAATGAAGAAGATGCTATAAACHTAGCTGAAGGCTGA 2362  
Db 842 TCATATGATACATATAAGATGAATGAAGAAGATGCTATAAACHTAGCTGAAGGCTGA 783  
QY 2363 AAAACCTGAAGAAGATGTGTTATTTTCACTTGACCCACTTGCTGACATTTGGAGAGGAA 2422  
Db 782 AAAACCTGAAGAAGATGTGTTATTTTCACTTGACCCACTTGCTGACATTTGGAGAGGAA 723  
QY 2423 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAG 2482  
Db 722 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAG 663  
QY 2483 TCTCCTGCTGCTGTCTGCAATGCAAGTGAATACTAGCTAGAAATCTTCAAAATTTGG 2542  
Db 662 TCTCCTGCTGCTGTCTGCAATGCAAGTGAATACTAGCTAGAAATCTTCAAAATTTGG 603  
QY 2543 TCAAACTGAGCATCTTGTATTTATCAGAAATTTACCTGTAAGAAAGATGAAATGAAGCTC 2602  
Db 602 TCAAACTGAGCATCTTGTATTTATCAGAAATTTACCTGTAAGAAAGATGAAATGAAGCTC 543  
QY 2603 TTTATGAACCTGATCGACAGATGAACGCTGTAGAAGAGCTCACCGCACTGATGCTGCCCT 2662  
Db 542 TTTATGAACCTGATCGACAGATGAACGCTGTAGAAGAGCTCACCGCACTGATGCTGCCCT 483  
QY 2663 GGGGCTGTGACGTCGCAAGCAGCCTGAGCAGCCTGTTGAAACATTTTGGAGGAGTCCAC 2722  
Db 482 GGGGCTGTGACGTCGCAAGCAGCCTGAGCAGCCTGTTGAAACATTTTGGAGGAGTCCAC 423  
QY 2723 AACTCTCAAGCTTGGGTTGAAAACTGGAGACTTCAGATACAGATAGATTTAG 2782  
Db 422 AACTCTCAAGCTTGGGTTGAAAACTGGAGACTTCAGATACAGATAGATTTAG 363  
QY 2783 GTGCAATTTTTTGGAAAAGAACCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGGAATC 2842

Db 362 GTGCATTTTTTGGAAAAGAACCCCTCTCAAAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 303  
QY 2843 GTGTGAGCAGTATGATGGCTTGCCTTTCATGGGTGATTTGAGAATCTTAAGCAATTAG 2902  
Db 302 GTGTGAGCAGTATGATGGCTTGCCTTTCATGGGTGATTTGAGAATCTTAAGCAATTAG 243  
QY 2903 TGTGTTTTTGGACCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTA 2962  
Db 242 TGTGTTTTTGGACCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTA 183  
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCTAGGCTTGTGGTGCAATTG 3022  
Db 182 GCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCTAGGCTTGTGGTGCAATTG 123  
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049  
Db 122 ATGATGATGATCTCAGTGTATTACAG 96

RESULT 7  
US-09-864-921-179  
; Sequence 179, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sug-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Hayashi, Hideki  
; APPLICANT: Pawlowski, Krzysztof  
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
; FILE REFERENCE: P-LJ 4752  
; CURRENT APPLICATION NUMBER: US/09/864,921  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 09/579,240  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/686,347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/275,980  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 179  
; LENGTH: 891  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(891)  
US-09-864-921-179

Query Match 27.3%; Score 840; DB 9; Length 891;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 481 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGCAAAAGGCAAGTCCCACTCTGCTGCAG 540  
Db 1 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGCAAAAGGCAAGTCCCACTCTGCTGCAG 60  
QY 541 CGCATTTGCCATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 600  
Db 61 CGCATTTGCCATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 120  
QY 601 TTCCTTCCCTCGCTCAGCAGGCCCCAGGGTGAGACTTTTGTGAACCCCTCTGTGTATCAACTC 660  
Db 121 TTCCTTCCCTCGCTCAGCAGGCCCCAGGGTGAGACTTTTGTGAACCCCTCTGTGTATCAACTC 180  
QY 661 CTGGATATACCTGGCAATTCAGAAAGCAGACATTCATGGCCCATGCTGCTGAAGCTGCGG 720



[illegible]

Db 577 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATCCCTT 636  
Qy 361 GGTGAAGATATGACATTTATTTTAACTTGAAGACCACTTCACAGAACCTGTCTCTGTGG 420  
Db 637 GGTGAAGATATGACATTTATTTTAACTTGAAGACCACTTCACAGAACCTGTCTCTGTGG 696  
Qy 421 AGGAAGGACCAACCACTATCCCGGTGGAGGAGCTGACCCCT 461  
Db 697 AGGAAGGACCAACCACTATCCCGGTGGAGGAGCTGACCCCT 737

RESULT 11  
US-09-764-864-339  
; Sequence 339, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 339  
; LENGTH: 608  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (20)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (23)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (26)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (86)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-864-339

Query Match 13.7%; Score 420; DB 10; Length 608;  
Best Local Similarity 99.6%; Pred. No. 9.3e-212;  
Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1494 TGTGAAGCCACCGGCTGTATGAAGCAGCTCGCAGCACTGTATCAACACGGCTGCCT 1553  
Db 87 TGTGAAGCCACCGGCTGTATGAAGCAGCTCGCAGCACTGTATCAACACGGCTGCCT 146  
Qy 1554 TCTGGAGCTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAA 1613  
Db 147 TCTGGAGCTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAA 206  
Qy 1614 AACACCACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGG 1673  
Db 207 AACACCACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGG 266  
Qy 1674 CATCATTTATATCAAGAGATAGATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTT 1733  
Db 267 CATCATTTATATCAAGAGATAGATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTT 326  
Qy 1734 CTTTCAAGTAAAGCTTATATATCACTCAGGGAACATCCCGATTAATTTATGACTT 1793  
Db 327 CTTTCAAGTAAAGCTTATATATCACTCAGGGAACATCCCGATTAATTTATGACTT 386  
Qy 1794 CTTTGAACATTTGCCATTTCTGCAAGTCTGAGCTTCATTAAGCTGGACTTTATGG 1853  
Db 387 CTTTGAACATTTGCCATTTCTGCAAGTCTGAGCTTCATTAAGCTGGACTTTATGG 446  
Qy 1854 GGGAGCTATGCTTCATGGGAAAAGGCTGCAGAGACACAGGTCGAATCCACATGGGAAGA 1913  
|||||

Db 447 GGGACCTATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGYGGAATCCACATCGAAGA 506  
Qy 1914 GGCC CAGAAACCTACATTTCCAGCAGAGGCTGTATCTTTTCTTCAACTGGAACAGGA 1973  
Db 507 GGCC CAGAAACCTACATTTCCAGCAGAGGCTGTATCTTTTCTTCAACTGGAACAGGA 566  
Qy 1974 ATTCAGGACTCTGGAGGTACACATCCCGGATTTTCAGCAAGTT 2015  
Db 567 ATTCAGGACTCTGGAGGTACACATCCCGGATTTTCAGCAAGTT 608

RESULT 12  
US-09-764-864-754  
; Sequence 754, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 754  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (160)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (468)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (499)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (505)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-864-754

Query Match 9.9%; Score 304; DB 10; Length 522;  
Best Local Similarity 99.7%; Pred. No. 2.2e-150;  
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 236 CTCAT TCAAGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAGGAGACTTGG 295  
Db 1 CTCAT TCAAGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAGGAGACTTGG 60  
Qy 296 ACGATT TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATC 355  
Db 61 ACGATT TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATC 120  
Qy 356 CCCTTG TGAAGATATTGACATTTATTTTAACTTGAAGGACCTTCACAGAACCTGTCC 415  
Db 121 CCCTTG TGAAGATATTGACATTTATTTTAACTTGAAGGACCTTCACAGAACCTGTCC 180  
Qy 416 TGTGGAC GAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGCGCTTCCTGC 475  
Db 181 TGTGGAC GAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGCGCTTCCTGC 240  
Qy 476 AGGCTCT CAGAGCCCTGCAATCATTTAGGGGATCTGGCAAGGCAAGTCCACTCTGC 535  
Db 241 AGGCTCT CAGAGCCCTGCAATCATTTAGGGGATCTGGCAAGGCAAGTCCACTCTGC 300  
Qy 536 TGCAGCG ATTGGCATGCTCTGGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTT 590  
Db 301 TGCAGCG ATTGGCATGCTCTGGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTT 355

RESULT 13

```
US-09-864-921-100
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100
```

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Query Match      8.8%; Score 269; DB 9; Length 578;
Best Local Similarity 100.0%; Pred. No. 7.2e-132;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 60
    |||||||
Db 277 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 336

QY 61 AAGCAAAATCACAGATGACCTATTCTGTAATGGAATGTTCTGAATCGCGAAGAACTAAACATC 120
    |||||||
Db 337 AAGCAAAATCACAGATGACCTATTCTGTAATGGAATGTTCTGAATCGCGAAGAACTAAACATC 396

QY 121 ATTTCGTCGGAAGAGTGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 180
    |||||||
Db 397 ATTTCGTCGGAAGAGTGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 456

QY 181 AAGGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTATCCTCTA 240
    |||||||
Db 457 AAGGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTATCCTCTA 516

QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTT 269
    |||||||
Db 517 TTTCAGGACTTGAATGGACAAAGTCTTTT 545
```

```
RESULT 14
US-09-864-921-177
; Sequence 177, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
```

```
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(261)
US-09-864-921-177

Query Match      8.5%; Score 261; DB 9; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1e-127;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 60
    |||||||
Db 1 ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 60

QY 61 AAGCAAAATCACAGATGACCTATTCTGTAATGGAATGTTCTGAATCGCGAAGAACTAAACATC 120
    |||||||
Db 61 AAGCAAAATCACAGATGACCTATTCTGTAATGGAATGTTCTGAATCGCGAAGAACTAAACATC 120

QY 121 ATTTCGTCGGAAGAGTGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 180
    |||||||
Db 121 ATTTCGTCGGAAGAGTGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 180

QY 181 AAGGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTATCCTCTA 240
    |||||||
Db 181 AAGGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTATCCTCTA 240

QY 241 TTTCAGGACTTGAATGGACAA 261
    |||||||
Db 241 TTTCAGGACTTGAATGGACAA 261

RESULT 15
US-09-864-761-4236
; Sequence 4236, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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QY 2830 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTGCTTCATGGGTGATTTGAGAA 2889  
|||||  
Db 1 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTGCTTCATGGGTGATTTGAGAA 60  
QY 2890 CTTAAGCAATAGTGTGTTTTGACTTTGTAGTACTAAGAATTTCTACCTGATCCAGCATTA 2949  
|||||  
Db 61 CTTAAGCAATAGTGTGTTTTGACTTTGTAGTACTAAGAATTTCTACCTGATCCAGCATTA 120  
QY 2950 GTCAGAAACTTAGCCAGTGTATCCAGTTAACTTTCTCGAAGAGCTAGGCTTGT 3009  
|||||  
Db 121 GTCAGAAACTTAGCCAGTGTATCCAGTTAACTTTCTCGAAGAGCTAGGCTTGT 180  
QY 3010 GGGTGGCAATTTGATGATGATCATCTCAGTGTATTATACAG 3049  
|||||  
Db 181 GGGTGGCAATTTGATGATGATCATCTCAGTGTATTATACAG 220

## RESULT 17

US-09-864-921-183  
; Sequence 183, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sug-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Hayashi, Hideki  
; APPLICANT: Pawlowski, Krzysztof  
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
; FILE REFERENCE: P-LJ 4752  
; CURRENT APPLICATION NUMBER: US/09/864,921  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 09/579,240  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/686,347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/275,980  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 183  
; LENGTH: 165  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(165)  
US-09-864-921-183

Query Match 3.7%; Score 114; DB 9; Length 165;

Best Local Similarity 99.4%; Pred. No. 6.4e-50;

Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1924 ACCTACATCCAGCAGGCGTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGGACT 1983  
|||||  
Db 1 ACCTACATCCAGCAGGCGTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGGACT 60  
QY 1984 CTGGAGGTCACACTCCGGGATTCAGCAAGTTGAATAAGCAGAGATACATATCTGGG 2043  
|||||  
Db 61 CTGGAGGTCACACTCCGGGATTCAGCAAGTTGAATAAGCAGAGATACATATCTGGG 120  
QY 2044 AAAATATTGAGTCTGCCCAAGCCTCAGGCTGCAAAATAAGAGA 2088  
|||||  
Db 121 AAAATATTGAGTCTGCCCAAGCCTCAGGCTGCAAAATAAGAGA 165

## RESULT 18

US-09-864-921-160/c

; Sequence 160, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sug-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Hayashi, Hideki  
; APPLICANT: Pawlowski, Krzysztof  
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
; FILE REFERENCE: P-LJ 4752  
; CURRENT APPLICATION NUMBER: US/09/864,921  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 09/579,240  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/686,347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/275,980  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 160  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-09-864-921-160

Query Match 0.9%; Score 29; DB 9; Length 29;

Best Local Similarity 100.0%; Pred. No. 5e-05;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TGACCTTCATTCGGAGCCTGGACCCTGTG 1180  
|||||  
Db 29 TGACCTTCATTCGGAGCCTGGACCCTGTG 1

## RESULT 19

US-09-864-921-161

; Sequence 161, Application US/09864921

; Patent No. US20020176853A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sug-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Hayashi, Hideki  
; APPLICANT: Pawlowski, Krzysztof

; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing

; FILE REFERENCE: P-LJ 4752

; CURRENT APPLICATION NUMBER: US/09/864,921

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 09/579,240

; PRIOR FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/686,347

; PRIOR FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: US 60/275,980

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 161

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-161

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 CATCATTTGCTGCCGAGAGTGGAG 141
      ||||| ||||| ||||| ||||| |||||
Db 1 CATCATTTGCTGCCGAGAGTGGAG 25

RESULT 20
US-09-864-921-162/c
; Sequence 162, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-162

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2959 CTTAGCCAAGTGTATCCAAAGTTAA 2983
      ||||| ||||| ||||| ||||| |||||
Db 25 CTTAGCCAAGTGTATCCAAAGTTAA 1

RESULT 21
US-09-864-921-165
; Sequence 165, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-165

Query Match      0.8%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GGTGGAACAGGATGCTCTAGAGG 158
      ||||| ||||| ||||| |||||
Db 1 GGTGGAACAGGATGCTCTAGAGG 24

RESULT 23
```

```
;
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-115

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AATTTTATAAAGGACAATAGCCGAG 28
      ||||| ||||| ||||| ||||| |||||
Db 1 AATTTTATAAAGGACAATAGCCGAG 25
```

```
RESULT 22
US-09-864-921-119
; Sequence 159, Application US/09864921
; Patent No. US:0020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-151
```

```
Query Match      0.8%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GGTGGAACAGGATGCTCTAGAGG 158
      ||||| ||||| ||||| |||||
Db 1 GGTGGAACAGGATGCTCTAGAGG 24

RESULT 23
```



```
US-09-864-921-157
; Sequence 157, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-157

Query Match      0.8%; Score 24; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTCATAAAGGCAATAGC 24
   |||||
Db 10 ATGAATTTCATAAAGGCAATAGC 33

RESULT 24
US-09-864-921-153/c
; Sequence 153, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-163
; Sequence 163, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-163

Query Match      0.7%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GTAAACATCATTTGCTGCGAGAA 134
   |||||
Db 1 GTAAACATCATTTGCTGCGAGAA 23

RESULT 26
US-09-864-921-156
; Sequence 156, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
```

```
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-156

Query Match          0.7%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GTATGGAATGTTCTGAATGCG 105
      |||||
DB 1  GTATGGAATGTTCTGAATGCG 21

RESULT 27
US-09-864-921-158/c
; Sequence 158, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-158
```

```
Query Match          0.7%; Score 21; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 232 TATCCTCTATTTCAGACTTG 252
      |||||
DB 30  TATCCTCTATTTCAGACTTG 10
```

```
RESULT 28
US-09-728-445-37
; Sequence 337, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 337
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-37
```

```
Query Match          0.7%; Score 21; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2965 CAAGTATTATCCCAAGTTAACT 2985
      |||||
DB 167 CAAGTATTATCCCAAGTTAACT 187
```

## RESULT 29

```
US-09-974-300-63
; Sequence 6263, Application US/09974300
; Patent No. US 0020146721A1
; GENERAL INFORMATION:
; APPLICANT: Be rka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6263
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6253
```

```
Query Match          0.7%; Score 20; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1881 TGCAGACACACAGGTGGAA 1900
      |||||
DB 378 TGCAGACACACAGGTGGAA 397
```

## RESULT 30

```
US-09-864-921-10;/c
; Sequence 102, Application US/09864921
; Patent No. US20020176853A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102

Query Match 0.7%; Score 20; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2331 AGAAGATGCTATAAACTAG 2350
      |||||||
Db 755 AGAAGATGCTATAAACTAG 736

RESULT 31
US-09-800-631-96/c
; Sequence 96, Application US/09800631
; Patent No. US2002008228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXP
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/09/800,631
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 96
; LENGTH: 30310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19791)...(19802)
; NAME/KEY: CDS
; LOCATION: (21160)...(21370)
; NAME/KEY: CDS
; LOCATION: (24168)...(24307)
; NAME/KEY: CDS
; LOCATION: (25696)...(25908)
; NAME/KEY: CDS
; LOCATION: (27235)...(27246)
US-09-800-631-96

Query Match 0.6%; Score 19; DB 10; Length 30310;
```

```
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 TGACAACTGGGCTCCTCTG 1283
      |||||||
Db 13062 TGACAACTGGGCTCCTCTG 13044

RESULT 32
US-09-864-921-155
; Sequence 155, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-155

Query Match 0.6%; Score 18; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATAGCCGAGCCCTTATTC 37
      |||||||
Db 4 ATAGCCGAGCCCTTATTC 21

RESULT 33
US-09-867-701-9442/c
; Sequence 9442, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9442
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-9442
```

```
Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 216;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 CTGTAACCTCTTCTTAA 212
DB 128 CTGTAACCTCTTCTTAA 111

RESULT 34
US-09-878-574-9387/c
; Sequence 9387, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-08-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 9387
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102423H1
US-09-878-574-9387

Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 273;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 CCTCTGCGAGGCTCTCA 485
DB 263 CCTCTGCGAGGCTCTCA 246

RESULT 35
US-09-864-761-4716/c
; Sequence 4716, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
```

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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4715
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109823.11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
US-09-864-761-4716

Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 454;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 GGGGAATCTGCGCAAGGC 522
DB 29 GGGGAATCTGCGCAAGGC 12

RESULT 36
US-09-998-598-1359
; Sequence 1359, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xi, Jiangchun
; APPLICANT: Cienault, Ruth A.
; APPLICANT: Magher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Cor.xa Invention Disclosure Database
; SEQ ID NO 1359
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1359

Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 469;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTCATAAAGGAC 18
```

```
|||||
Db 88 ATGAATTCATAAGGAC 105

RESULT 37
US-09-864-761-1714
; Sequence 1714, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1714
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010087.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
US-09-864-761-1714

Query Match 0.6%; Score 18; DB 10; Length 472;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 AGAAGGTGGAGCAGGATG 148
|||||
Db 143 AGAAGGTGGAGCAGGATG 160

RESULT 38
US-09-728-446-43/c
; Sequence 43, Application US/09728446
; Patent No. US20020081668A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20020081668A1 Murine Polynucleotide Sequences
; FILE REFERENCE: LEX-0101-USA and Mutant Cells and Mutant Animals Defined Thereby
; CURRENT APPLICATION NUMBER: US/09/728,446
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,270
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1461
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(501)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-446-43

Query Match 0.6%; Score 18; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1958 TCAACTGGAGCAGGAAT 1975
|||||
Db 18 TCAACTGGAGCAGGAAT 1

RESULT 39
US-09-738-626-2121
; Sequence 2121, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
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; SEQ ID NO 2121
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2121

Query Match          0.6%; Score 18; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3005 TTGTTGGTGGCAATTG 3022
|||||
Db 394 TTGTTGGTGGCAATTG 411

RESULT 40
US-09-764-877-3957
; Sequence 3957, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764.877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3957
; LENGTH: 1163
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3957

Query Match          0.6%; Score 18; DB 10; Length 1163;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2047 ATATTGAGCTGCGCAC 2064
|||||
Db 379 ATATTGAGCTGCGCAC 396

RESULT 41
US-09-360-540-2/c
; Sequence 2, Application US/09360540
; Patent No. US2002015553A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN VESICLE BINDING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,540
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,213
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: EP-0297 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: FIBRNGT01
; CLONE: 148415
US-09-360-540-2

Query Match          0.6%; Score 18; DB 9; Length 1721;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAA'TTCATAAAGGAC 18
|||||
Db 1538 ATGAA'TTCATAAAGGAC 1521

RESULT 42
US-09-764-864-1654/c
; Sequence 1654, Application US/09764864
; Patent No. US:0020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764.864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1654
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1654

Query Match          0.6%; Score 18; DB 10; Length 2619;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2980 TTAAC'TTCTGCAAGAA 2997
|||||
Db 2432 TTAAC'TTCTGCAAGAA 2415

RESULT 43
US-09-957-189-1
; Sequence 1, Application US/09957189
; Patent No. US21020177210A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Aminoamidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.200-US
; CURRENT APPLICATION NUMBER: US/09/957,189
; CURRENT FILING DATE: 2001-09-19
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/192,104
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1465/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00670
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Spingomonas
; US-09-957-189-1

Query Match      0.6%; Score 18; DB 9; Length 3000;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2092 GCTGGTGTGCTGGAAGC 2109
|||||
Db 1911 GCTGGTGTGCTGGAAGC 1928

RESULT 44
US-09-764-864-1656
; Sequence 1656, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1656
; LENGTH: 3460
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-864-1656

Query Match      0.6%; Score 18; DB 10; Length 3460;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2980 TTAACCTTTCTGCAAGAA 2997
|||||
Db 1026 TTAACCTTTCTGCAAGAA 1043

RESULT 45
US-09-070-927A-261/c
; Sequence 261, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;              Patrick J. Dillon
;              Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 261:
US-09-070-927A-261

Query Match      0.6%; Score 18; DB 10; Length 4951;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2492 GCTGTCTGCAATGCAG 2509
|||||
Db 1288 GCTGTCTGCAATGCAG 1271

RESULT 46
US-09-811-045A-2
; Sequence 2, Application US/09811045A
; Patent No. US20020035080A1
; GENERAL INFORMATION:
; APPLICANT: Scott, Robert E.
; TITLE OF INVENTION: cDNA encoding P2P proteins and use of P2P cDNA-
; TITLE OF INVENTION: derived antibodies and antisense reagents
; TITLE OF INVENTION: in determining the proliferative potential of
; TITLE OF INVENTION: normal, abnormal and cancer cells in animals
; TITLE OF INVENTION: and humans
; FILE REFERENCE: D6386D
; CURRENT APPLICATION NUMBER: US/09/811,045A
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 08/801,308
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 5173
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: cDNA
; OTHER INFORMATION: P2P cDNA
US-09-811-045A-2

Query Match      0.6%; Score 18; DB 10; Length 5173;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2796 AAAGAACCCTCTGAAAAA 2813
|||||
Db 3187 AAAGAACCCTCTGAAAAA 3204

RESULT 47
US-09-764-855-208
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; Sequence 208, Application US/09764855  
; Patent No. US20020119919A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P110  
; CURRENT APPLICATION NUMBER: US/09/764,855  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 208  
; LENGTH: 7386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-855-208

Query Match 0.6%; Score 18; DB 10; Length 7386;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 131 AGAAGGTGGAGCAGGATG 148  
|||||  
Db 3282 AGAAGGTGGAGCAGGATG 3299

RESULT 48  
US-09-764-860-1102  
; Sequence 1102, Application US/09764860  
; Patent No. US20020094953A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT APPLICATION NUMBER: US/09/764,860  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1102  
; LENGTH: 17252  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-860-1102

Query Match 0.6%; Score 18; DB 10; Length 17252;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2796 AAAGAACCCCTCTGAAAAA 2813  
|||||  
Db 14764 AAAGAACCCCTCTGAAAAA 14781

RESULT 49  
US-09-880-107-2097  
; Sequence 2097, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; Prior application data removed - consult PALM or file wrapper  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20:7  
; LENGTH: 17:09  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 J03764  
US-09-880-107-097

Query Match 0.6%; Score 18; DB 10; Length 17509;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2051 TCAGCTCTGCCACAAGCC 2068  
|||||  
Db 15793 TCAGCTCTGCCACAAGCC 15810

RESULT 50  
US-09-734-674-3  
; Sequence 3, Application US/09734674  
; Patent No. US20020081648A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001018  
; CURRENT APPLICATION NUMBER: US/09/734,674  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 20201  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (1)-(20201)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-734-674-3

Query Match 0.6%; Score 18; DB 10; Length 20201;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 339 TTTTC'GAAC'TTTTATCC 356  
|||||  
Db 39930 TTTTC'GAAC'TTTTATCC 39947

Search completed: January 31, 2003, 04:22:10  
Job time : 425 :ecs



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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:49:40 ; Search time 6434 Seconds  
(without alignments)  
12004.620 Million cell updates/sec

Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaattcataaaggacaa.....ctttaactagtaactgct 3072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 24791104 seqs, 12571243825 residues

Word size : 12  
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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/pna/US080\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq:\*

7: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq:\*

8: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq:\*

9: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq:\*

10: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq:\*

11: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq:\*

12: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq:\*

13: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3072	100.0	3133	1	PCT-US00-29643-1
5	3072	100.0	3133	27	US-09-697-089-1
6	3072	100.0	3133	32	US-09-841-739-1
7	2919	95.0	3075	41	US-10-156-733-1
8	2919	95.0	3219	41	US-10-156-733-14
9	2919	95.0	3545	18	US-09-491-404-1319
10	2919	95.0	3545	34	US-09-922-279-1319
11	2919	95.0	3545	34	US-09-922-279A-1319
12	2918	95.0	3213	1	PCT-US01-07143-23
13	2918	95.0	3213	42	US-10-221-097-23
14	2868	93.4	3396	33	US-09-864-921-96
15	2849	92.7	3396	27	US-09-686-347-96
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17	2765	90.0	3260	26	US-09-667-298-66
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23	2634	85.7	3615	27	US-09-697-089-12	Sequence 12, Appl1	96	412	13.4	480	29	US-09-737-223-15784	Sequence 15784, A
24	2634	85.7	3615	32	US-09-841-739-4	Sequence 4, Appl1	97	412	13.4	480	34	US-09-918-995-15784	Sequence 15784, A
25	2634	85.7	3615	32	US-09-841-739-12	Sequence 12, Appl1	98	412	13.4	480	34	US-09-925-564-36563	Sequence 36563, A
26	2208	71.9	6012	22	US-09-557-676-911	Sequence 911, App	99	400	13.0	401	18	US-09-489-036-30983	Sequence 30983, A
27	2208	71.9	6012	22	US-09-557-676-917	Sequence 917, App	100	400	13.0	401	35	US-09-943-143-30983	Sequence 30983, A
28	2208	71.9	6012	38	US-10-043-938-911	Sequence 911, App	101	384	12.0	407	17	US-09-359-067-46762	Sequence 46762, A
29	2208	71.9	6012	38	US-10-043-938-917	Sequence 917, App	102	384	12.0	443	19	US-09-528-409-24681	Sequence 24681, A
30	2207	71.8	2343	22	US-09-578-789-15	Sequence 15, Appl	103	369	12.0	443	35	US-09-933-524-24681	Sequence 24681, A
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93	412	13.4	480	16	US-09-235-076-15784	Sequence 15784, A	166	242	7.9	548	13	US-09-686-347-100	Sequence 100, App
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177	220	7.2	220	33	US-09-864-761-20988	Sequence 20988, A	c 250	26	0.8	312	12	US-08-803-610D-7881	Sequence 7881, Ap
178	220	7.2	220	41	US-10-182-933-17035	Sequence 17035, A	c 251	26	0.8	312	12	US-08-803-610E-7881	Sequence 7881, Ap
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181	220	7.2	220	41	US-10-182-998-9197	Sequence 9197, Ap	c 254	25	0.8	25	33	US-09-864-921-162	Sequence 162, App
182	220	7.2	220	42	US-10-203-134-17385	Sequence 17385, A	255	25	0.8	25	33	US-09-864-921-165	Sequence 165, App
183	220	7.2	220	42	US-10-203-135-16875	Sequence 16875, A	256	24	0.8	24	33	US-09-864-921-159	Sequence 159, App
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185	220	7.2	220	42	US-10-203-137-17590	Sequence 17590, A	c 258	24	0.8	508	25	US-09-652-355-6270	Sequence 6270, Ap
186	220	7.2	220	42	US-10-203-138-9429	Sequence 9429, Ap	c 259	24	0.8	1523	17	US-09-396-970-7819	Sequence 7819, Ap
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188	220	7.2	220	67	US-60-236-359-12476	Sequence 12476, A	c 261	24	0.8	1523	18	US-09-404-549A-4709	Sequence 4709, Ap
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190	206	6.7	255	22	US-09-579-240-19	Sequence 19, Appl	263	24	0.8	2583	43	US-10-268-842-13	Sequence 13, Appl
191	188	6.1	366	18	US-09-489-036-9164	Sequence 9164, Ap	c 264	23	0.7	23	33	US-09-864-921-153	Sequence 153, App
192	188	6.1	366	35	US-09-943-143-9164	Sequence 9164, Ap	265	23	0.7	23	33	US-09-864-921-163	Sequence 163, App
193	186	6.1	488	16	US-09-235-076-33935	Sequence 33935, A	c 266	23	0.7	512	6	US-08-220-691-1757	Sequence 1757, Ap
194	186	6.1	488	16	US-09-277-227-3011	Sequence 3011, Ap	c 267	23	0.7	512	6	US-08-220-691B-1757	Sequence 1757, Ap
195	186	6.1	488	17	US-09-332-782-33935	Sequence 33935, A	c 268	23	0.7	512	31	US-09-813-155-1757	Sequence 1757, Ap
196	186	6.1	488	29	US-09-337-223-33935	Sequence 33935, A	c 269	23	0.7	554	18	US-09-404-549A-486	Sequence 486, App
197	186	6.1	488	34	US-09-909-627-3011	Sequence 3011, Ap	c 270	23	0.7	554	18	US-09-404-549A-486	Sequence 486, App
198	186	6.1	488	34	US-09-918-995-33935	Sequence 33935, A	c 271	23	0.7	554	23	US-09-617-182-933	Sequence 933, App
199	183	6.0	192	12	US-08-878-669-2131	Sequence 2131, Ap	c 272	23	0.7	709	25	US-09-652-355-9992	Sequence 9992, Ap
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c 204	149	4.9	251	45	US-60-012-458-225	Sequence 225, App	c 277	23	0.7	2762	30	US-09-770-174-3223	Sequence 3223, Ap
c 205	140	4.6	205	12	US-08-823-271-2555	Sequence 2555, Ap	278	22	0.7	215	22	US-09-572-409-78440	Sequence 78440, A
c 206	140	4.6	205	21	US-08-540-764-22408	Sequence 22408, A	279	22	0.7	606	18	US-09-428-151A-3571	Sequence 3571, Ap
c 207	140	4.6	205	45	US-60-015-513-2555	Sequence 2555, Ap	280	22	0.7	606	23	US-09-614-387-3333	Sequence 3333, Ap
208	135	4.4	458	18	US-09-404-284-142	Sequence 142, App	281	21	0.7	21	33	US-09-864-921-156	Sequence 156, App
209	135	4.4	458	19	US-09-528-409-38106	Sequence 38106, A	c 282	21	0.7	30	33	US-09-864-921-158	Sequence 158, App
210	135	4.4	458	38	US-09-524-038-142	Sequence 142, App	c 283	21	0.7	121	18	US-09-404-520-17539	Sequence 17539, A
211	114	3.7	165	33	US-10-011-154-142	Sequence 142, App	c 284	21	0.7	264	14	US-09-041-894-2673	Sequence 2673, A
c 212	110	3.6	500	38	US-10-029-386-11426	Sequence 11426, A	c 285	21	0.7	264	21	US-09-540-210B-1187	Sequence 1187, Ap
c 213	109	3.5	160	7	US-08-373-361A-818	Sequence 818, App	c 286	21	0.7	264	48	US-60-040-199-2673	Sequence 2673, Ap
c 214	102	3.3	386	19	US-09-528-409-38106	Sequence 38106, A	c 287	21	0.7	300	23	US-09-605-698-16749	Sequence 16749, A
c 215	102	3.3	386	35	US-09-933-524-38106	Sequence 38106, A	c 288	21	0.7	300	23	US-09-611-520-5688	Sequence 5688, Ap
c 216	102	3.3	386	35	US-09-933-524A-38106	Sequence 38106, A	c 289	21	0.7	300	39	US-10-075-564-5688	Sequence 5688, Ap
c 217	98	3.2	2595	25	US-09-644-869-8962	Sequence 8962, Ap	290	21	0.7	337	16	US-09-289-768-31863	Sequence 31863, A
c 218	98	3.2	2595	25	US-09-652-122-4263	Sequence 4263, Ap	291	21	0.7	337	35	US-09-939-397-31863	Sequence 31863, A
c 219	98	3.2	2595	25	US-09-652-123-9442	Sequence 9442, Ap	292	21	0.7	365	22	US-09-565-240-26389	Sequence 26389, A
c 220	98	3.2	2595	25	US-09-652-913-10693	Sequence 10693, A	293	21	0.7	365	58	US-60-141-136-1316	Sequence 1316, Ap
c 221	98	3.2	2595	25	US-09-652-914-9400	Sequence 9400, Ap	c 294	21	0.7	426	16	US-09-213-604B-5419	Sequence 5419, Ap
c 222	98	3.2	2595	25	US-09-652-918-8327	Sequence 8327, Ap	c 295	21	0.7	426	23	US-09-605-698-9026	Sequence 9026, Ap
c 223	98	3.2	2595	26	US-09-667-617-1970	Sequence 1970, Ap	c 296	21	0.7	426	23	US-09-611-520-2814	Sequence 2814, Ap
c 224	98	3.2	2595	27	US-09-699-998-10530	Sequence 10530, A	c 297	21	0.7	426	39	US-10-075-564-2814	Sequence 2814, Ap
c 225	98	3.2	2595	28	US-09-700-000-5800	Sequence 5800, Ap	298	21	0.7	449	19	US-09-521-640-111312	Sequence 111312
c 226	98	3.2	2595	28	US-09-710-286-4037	Sequence 4037, Ap	299	21	0.7	450	31	US-09-804-730-2425	Sequence 2425, Ap
c 227	98	3.2	2595	28	US-09-716-953-2586	Sequence 2586, Ap	300	21	0.7	450	62	US-60-189-657-2425	Sequence 2425, Ap
c 228	98	3.2	2595	29	US-09-721-589-6951	Sequence 6951, Ap	301	21	0.7	471	19	US-09-521-640-231002	Sequence 231002
c 229	98	3.2	2595	29	US-09-726-802-2827	Sequence 2827, Ap	302	21	0.7	471	58	US-60-140-769-30093	Sequence 30093, A
230	93	3.0	507	22	US-09-557-676-909	Sequence 909, App	303	21	0.7	483	29	US-09-728-445-337	Sequence 337, App
231	93	3.0	507	22	US-09-557-676-915	Sequence 915, App	c 304	21	0.7	497	16	US-09-750-456-337	Sequence 337, App
232	93	3.0	507	38	US-10-042-938-909	Sequence 909, App	c 305	21	0.7	497	16	US-09-213-604B-1365	Sequence 1365, Ap
233	93	3.0	507	38	US-10-042-938-915	Sequence 915, App	c 306	21	0.7	497	23	US-09-603-698-9362	Sequence 9362, Ap
234	92	3.0	414	18	US-09-404-284-109	Sequence 109, App	c 307	21	0.7	497	23	US-09-611-520-2772	Sequence 2772, Ap
235	92	3.0	414	19	US-09-524-038-109	Sequence 109, App	c 308	21	0.7	497	39	US-10-075-564-2772	Sequence 2772, Ap
236	92	3.0	414	38	US-10-011-154-109	Sequence 109, App	309	21	0.7	531	57	US-60-132-861-13489	Sequence 13489, A
237	90	2.9	412	18	US-09-489-036-30982	Sequence 30982, A	310	21	0.7	531	57	US-60-138-103-13273	Sequence 13273, A
238	90	2.9	412	35	US-09-943-143-30982	Sequence 30982, A	311	21	0.7	538	62	US-60-184-771-765	Sequence 765, App
239	76	2.5	275	11	US-08-792-739-868	Sequence 868, App	312	21	0.7	580	19	US-09-505-532-41223	Sequence 41223, A
240	76	2.5	275	13	US-08-951-195-868	Sequence 868, App	313	21	0.7	580	31	US-09-819-091A-41223	Sequence 41223, A

314	21	0.7	1222	18	US-09-404-520-7149	Sequence 7149, Ap	c 387	19	0.6	221	23	US-09-605-702-13997	Sequence 13997, A
315	21	0.7	1622	38	US-10-015-127-2687	Sequence 2687, Ap	c 388	19	0.6	229	20	US-09-539-806-5282	Sequence 5282, Ap
316	21	0.7	2961	16	US-09-248-796-1255	Sequence 1255, Ap	c 389	19	0.6	230	25	US-09-654-617-49153	Sequence 49153, A
317	21	0.7	2961	53	US-60-096-409-1255	Sequence 1255, Ap	c 390	19	0.6	230	25	US-09-654-617-49153	Sequence 49153, A
318	21	0.7	5097	41	US-10-179-131-1688	Sequence 1688, Ap	c 391	19	0.6	233	17	US-09-244-000A-98929	Sequence 98929, A
319	21	0.7	80346	21	US-09-534-859-669	Sequence 669, Ap	c 392	19	0.6	233	17	US-09-244-000A-98929	Sequence 98929, A
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325	21	0.7	351576	19	US-09-528-237A-1489	Sequence 1489, Ap	c 397	19	0.6	289	20	US-09-535-896-32146	Sequence 32146, A
326	20	0.7	240	64	US-60-207-458-6596	Sequence 6596, Ap	c 398	19	0.6	305	63	US-09-535-896-32146	Sequence 32146, A
327	20	0.7	302	14	US-09-070-694-897	Sequence 897, Ap	c 399	19	0.6	309	13	US-08-993-002A-1573	Sequence 1573, App
328	20	0.7	302	14	US-09-070-694-897	Sequence 897, Ap	c 400	19	0.6	321	10	US-08-993-002A-1573	Sequence 1573, App
329	20	0.7	321	25	US-09-654-617-180545	Sequence 180545, A	c 401	19	0.6	321	10	US-08-993-002A-1573	Sequence 1573, App
330	20	0.7	321	25	US-09-654-617-180545	Sequence 180545, A	c 401	19	0.6	321	10	US-08-993-002A-1573	Sequence 1573, App
331	20	0.7	333	64	US-09-207-458-18913	Sequence 18913, A	c 402	19	0.6	329	17	US-09-534-840-695	Sequence 20870, A
332	20	0.7	333	64	US-09-207-458-18913	Sequence 18913, A	c 403	19	0.6	345	29	US-09-534-840-695	Sequence 20870, A
333	20	0.7	370	58	US-09-440-687-1492	Sequence 1492, Ap	c 404	19	0.6	345	29	US-09-534-840-695	Sequence 20870, A
334	20	0.7	370	58	US-09-440-687-1492	Sequence 1492, Ap	c 404	19	0.6	345	29	US-09-534-840-695	Sequence 20870, A
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340	20	0.7	431	30	US-09-572-409-56345	Sequence 56345, A	c 409	19	0.6	351	25	US-09-803-110-5752	Sequence 4224, Ap
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342	20	0.7	439	17	US-09-304-517A-100977	Sequence 100977, A	c 411	19	0.6	351	25	US-09-803-110-5752	Sequence 4224, Ap
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345	20	0.7	460	23	US-09-605-701-985	Sequence 985, App	c 412	19	0.6	357	13	US-08-993-002A-1573	Sequence 1573, App
346	20	0.7	475	36	US-09-974-300-6263	Sequence 6263, Ap	c 413	19	0.6	392	22	US-08-993-002A-1573	Sequence 1573, App
347	20	0.7	492	6	US-08-276-163A-6495	Sequence 6495, Ap	c 414	19	0.6	395	17	US-09-362-510-35891	Sequence 35891, A
348	20	0.7	492	6	US-08-276-163B-6495	Sequence 6495, Ap	c 415	19	0.6	395	17	US-09-362-510-35891	Sequence 35891, A
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350	20	0.7	492	32	US-09-840-145-6495	Sequence 6495, Ap	c 416	19	0.6	395	17	US-09-362-510-35891	Sequence 35891, A
351	20	0.7	496	23	US-09-605-701-798	Sequence 798, App	c 417	19	0.6	395	17	US-09-362-510-35891	Sequence 35891, A
352	20	0.7	583	24	US-09-504-576A-9938	Sequence 9938, Ap	c 418	19	0.6	406	26	US-09-666-355A-22423	Sequence 22423, A
353	20	0.7	715	19	US-09-637-890-7313	Sequence 7313, Ap	c 419	19	0.6	406	26	US-09-666-355A-22423	Sequence 22423, A
354	20	0.7	768	33	US-09-686-347-102	Sequence 102, App	c 420	19	0.6	407	27	US-09-654-617-199629	Sequence 199629, A
355	20	0.7	768	33	US-09-686-347-102	Sequence 102, App	c 420	19	0.6	407	27	US-09-654-617-199629	Sequence 199629, A
356	20	0.7	1036	71	US-60-279-526-834	Sequence 834, App	c 422	19	0.6	408	22	US-09-572-409-71409	Sequence 71409, A
357	20	0.7	3811	23	US-09-614-150-36103	Sequence 36103, A	c 423	19	0.6	408	22	US-09-572-409-71409	Sequence 71409, A
358	20	0.7	3946	63	US-60-173-464-22228	Sequence 22228, A	c 424	19	0.6	408	22	US-09-572-409-71409	Sequence 71409, A
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361	20	0.7	4737	23	US-60-167-217-3594	Sequence 3594, Ap	c 427	19	0.6	409	16	US-09-637-086B-1396	Sequence 1396, Ap
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363	20	0.7	4737	61	US-60-171-625-70	Sequence 70, Appl	c 428	19	0.6	409	16	US-09-637-086B-1396	Sequence 1396, Ap
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382	19	0.6	80	58	US-09-528-237A-1180	Sequence 1180, Ap	c 449	19	0.6	451	22	US-09-572-409-50093	Sequence 16028, A
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393	19	0.6	185	12	US-10-027-632-174763	Sequence 174763, A							

460	19	0.6	468	17	US-09-362-510A-4985	Sequence 4985, Ap	533	19	0.6	1044	18	US-09-428-944-905	Sequence 905, App
461	19	0.6	468	34	US-09-904-013-4985	Sequence 4985, Ap	534	19	0.6	1099	24	US-09-634-306B-118099	Sequence 118099,
462	19	0.6	470	32	US-09-843-620-708	Sequence 708, App	535	19	0.6	1099	38	US-10-027-632-118099	Sequence 118099,
463	19	0.6	477	23	US-09-607-200-455	Sequence 455, App	536	19	0.6	1416	18	US-09-428-944-1395	Sequence 1395, Ap
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465	19	0.6	480	24	US-09-634-306B-4089	Sequence 4089, Ap	c 538	19	0.6	1425	40	US-10-115-482-63	Sequence 63, Appl
466	19	0.6	480	34	US-09-634-306B-4090	Sequence 4090, Ap	539	19	0.6	1430	58	US-60-144-351-541	Sequence 541, App
467	19	0.6	480	38	US-10-027-632-4089	Sequence 4089, Ap	540	19	0.6	1501	31	US-09-815-264-8837	Sequence 8837, Ap
468	19	0.6	480	38	US-10-027-632-4090	Sequence 4090, Ap	541	19	0.6	1501	31	US-09-815-264-47717	Sequence 47717, A
469	19	0.6	480	69	US-60-253-654-21143	Sequence 21143, A	542	19	0.6	1574	24	US-09-620-392-54056	Sequence 54056, A
470	19	0.6	480	69	US-60-255-592-21143	Sequence 21143, A	543	19	0.6	1619	27	US-09-699-997-10297	Sequence 10297, A
471	19	0.6	483	23	US-09-605-700-609	Sequence 609, App	544	19	0.6	1780	1	PCT-US01-04942A-469	Sequence 469, App
472	19	0.6	503	17	US-09-304-517A-216097	Sequence 216097,	545	19	0.6	1780	19	US-09-519-705-5525	Sequence 5525, Ap
473	19	0.6	503	17	US-09-371-146A-216097	Sequence 216097,	546	19	0.6	1780	22	US-09-574-454-5525	Sequence 5525, Ap
474	19	0.6	503	22	US-09-552-086-13036	Sequence 13036, A	547	19	0.6	1780	42	US-10-221-278-469	Sequence 469, App
475	19	0.6	511	37	US-09-985-678-216097	Sequence 216097,	c 548	19	0.6	1863	16	US-09-248-796-6543	Sequence 6543, Ap
476	19	0.6	511	20	US-09-539-802A-2357	Sequence 2357, Ap	c 549	19	0.6	1863	41	US-10-179-131-3052	Sequence 3052, Ap
477	19	0.6	514	25	US-09-654-617-187439	Sequence 187439,	c 550	19	0.6	1863	53	US-60-096-409-6543	Sequence 6543, Ap
478	19	0.6	514	27	US-09-684-016-187439	Sequence 187439,	551	19	0.6	1908	20	US-09-533-559-5521	Sequence 5521, Ap
479	19	0.6	516	69	US-60-253-654-12310	Sequence 12310, A	552	19	0.6	2005	58	US-60-140-803-227	Sequence 227, App
480	19	0.6	516	69	US-60-255-592-2899	Sequence 2899, Ap	553	19	0.6	2132	24	US-09-620-392-9532	Sequence 9532, Ap
481	19	0.6	516	69	US-60-255-592-2899	Sequence 2899, Ap	554	19	0.6	2132	24	US-09-620-392-9532	Sequence 9532, Ap
482	19	0.6	516	69	US-60-255-592-2899	Sequence 2899, Ap	555	19	0.6	2221	71	US-60-278-258-12415	Sequence 12415, A
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484	19	0.6	556	17	US-09-397-424-2185	Sequence 2185, Ap	c 556	19	0.6	2438	25	US-09-644-868-8042	Sequence 8042, Ap
485	19	0.6	556	31	US-09-824-518-5688	Sequence 5688, Ap	c 557	19	0.6	2475	17	US-09-399-932-5172	Sequence 5172, Ap
486	19	0.6	563	69	US-60-253-654-12310	Sequence 12310, A	c 558	19	0.6	2539	23	US-09-607-200-6644	Sequence 6644, Ap
487	19	0.6	563	69	US-60-253-654-12310	Sequence 12310, A	559	19	0.6	2591	25	US-09-644-868-9637	Sequence 9637, Ap
488	19	0.6	565	23	US-09-605-700-608	Sequence 608, App	560	19	0.6	2603	22	US-09-572-411-6747	Sequence 6747, Ap
489	19	0.6	566	22	US-09-572-411-6585	Sequence 3585, Ap	c 561	19	0.6	2825	24	US-09-629-469A-15005	Sequence 15005, A
490	19	0.6	567	21	US-09-540-229-126232	Sequence 126232,	562	19	0.6	3217	23	US-09-614-150-11341	Sequence 11341, A
491	19	0.6	571	24	US-09-634-306B-321654	Sequence 321654,	563	19	0.6	3217	61	US-60-173-464-9197	Sequence 9197, Ap
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494	19	0.6	571	38	US-10-027-632-321655	Sequence 321655,	566	19	0.6	3235	60	US-60-167-217-11369	Sequence 11369, A
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496	19	0.6	579	12	US-08-823-745-190	Sequence 190, App	c 568	19	0.6	3861	18	US-09-428-944-892	Sequence 892, App
497	19	0.6	579	13	US-08-993-002A-1575	Sequence 1575, Ap	569	19	0.6	4042	65	US-60-213-847-202	Sequence 202, App
498	19	0.6	585	24	US-09-634-306B-212537	Sequence 212537,	c 570	19	0.6	4275	58	US-60-145-138-37	Sequence 37, Appl
499	19	0.6	585	38	US-10-027-632-212537	Sequence 212537,	c 571	19	0.6	4275	58	US-60-146-394-47	Sequence 47, Appl
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501	19	0.6	590	69	US-60-255-592-2841	Sequence 2841, Ap	573	19	0.6	4710	17	US-09-340-623-9150	Sequence 9150, Ap
502	19	0.6	593	29	US-09-758-473-482	Sequence 482, App	574	19	0.6	4710	33	US-09-898-888-9150	Sequence 9150, Ap
503	19	0.6	593	42	US-10-222-939-482	Sequence 482, App	575	19	0.6	4710	33	US-09-898-888A-9150	Sequence 9150, Ap
504	19	0.6	597	60	US-60-162-247-1168	Sequence 1168, Ap	c 576	19	0.6	4717	18	US-09-428-944-1384	Sequence 1384, Ap
505	19	0.6	601	25	US-09-654-617-187282	Sequence 187282,	c 577	19	0.6	5189	1	PCT-US99-22855-2241	Sequence 2241, Ap
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507	19	0.6	601	35	US-09-948-933-5069	Sequence 5069, Ap	579	19	0.6	5557	65	US-60-213-847-392	Sequence 392, App
508	19	0.6	620	61	US-60-172-376-2815	Sequence 2815, Ap	c 580	19	0.6	5581	28	US-09-702-134-15506	Sequence 15506, A
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511	19	0.6	625	24	US-09-634-306B-226909	Sequence 226909,	c 583	19	0.6	6316	22	US-09-560-875A-4587	Sequence 4587, Ap
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514	19	0.6	625	38	US-10-027-632-226910	Sequence 226910,	586	19	0.6	6445	28	US-09-702-134-10631	Sequence 10631, A
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516	19	0.6	634	60	US-60-162-247-1637	Sequence 1637, Ap	588	19	0.6	7031	24	US-09-620-392-20621	Sequence 20621, A
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519	19	0.6	649	33	US-09-882-227-317	Sequence 317, App	591	19	0.6	7163	17	US-09-359-922-257	Sequence 257, App
520	19	0.6	666	28	US-09-708-427-24169	Sequence 24169, A	592	19	0.6	7163	17	US-09-359-922-257	Sequence 257, App
521	19	0.6	677	63	US-60-196-718-2252	Sequence 2252, Ap	593	19	0.6	7163	34	US-09-919-003-257	Sequence 257, App
522	19	0.6	677	63	US-60-196-718-2253	Sequence 2253, Ap	c 594	19	0.6	8095	24	US-09-620-392-42020	Sequence 42020, A
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525	19	0.6	734	60	US-60-162-247-573	Sequence 573, App	597	19	0.6	10204	24	US-09-620-392-42152	Sequence 42152, A
526	19	0.6	744	63	US-60-197-872-46936	Sequence 46936, A	598	19	0.6	10204	28	US-09-702-134-1874	Sequence 1874, Ap
527	19	0.6	759	18	US-09-406-292A-1947	Sequence 1947, Ap	599	19	0.6	10204	31	US-09-815-264-69896	Sequence 69896, A
528	19	0.6	868	33	US-09-861-478-7055	Sequence 7055, Ap	600	19	0.6	10757	19	US-09-514-000-235	Sequence 235, App
529	19	0.6	876	21	US-09-540-209B-1452	Sequence 1452, Ap	601	19	0.6	10917	33	US-09-871-107-1	Sequence 1, Appl1
530	19	0.6	912	10	US-08-621-425-23	Sequence 23, Appl	602	19	0.6	10917	41	US-10-195-963-1	Sequence 1, Appl1
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612	19	0.6	13633	59	US-60-150-584-306	Sequence 306, App	18	0.6	115	46	US-09-020-591-3447	Sequence 3447, Ap
613	19	0.6	14306	65	US-60-213-177-392	Sequence 392, App	18	0.6	124	26	US-09-677-367-502	Sequence 502, App
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615	19	0.6	14346	39	US-10-074-024-505	Sequence 505, App	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
616	19	0.6	15109	67	US-60-230-445-306	Sequence 306, App	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
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632	19	0.6	32768	65	US-60-213-177-245	Sequence 245, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
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634	19	0.6	32768	67	US-60-230-435-535	Sequence 535, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
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c 754	18	0.6	225	20	US-09-534-846B-28014	Sequence 28014, A	c 827	18	0.6	256	13	US-08-992-868-2625	Sequence 2625, Ap
c 755	18	0.6	228	13	US-08-922-315-3126	Sequence 3126, Ap	c 828	18	0.6	256	17	US-09-304-517A-154602	Sequence 154602,
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; NUMBER OF SEQ ID NOS: 16  
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US-09-841-739-3

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DB 901 ACAGATCACAGCCCGCCAGGCTCTCATCCGAGAAGTGTCTGATCAAGGAGCTTGTCTGAAGGC 960  
QY 961 TTGTTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCTCAAGAACCCCTCTCTTT 1020  
DB 961 TTGTTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCTCAAGAACCCCTCTCTTT 1020  
QY 1021 GTGCTCATCATACCTTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT 1140  
DB 1021 GTGCTCATCATACCTTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT 1140  
QY 1081 ACGCTGTCCATACCTTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT 1140  
DB 1081 ACGCTGTCCATACCTTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT 1140  
QY 1141 GTGCTTCAAGTGTACTTTCATTCGGAGCTGGACCACTGTGGAGACCTAGCTCTGGAGGCT 1200  
DB 1141 GTGCTTCAAGTGTACTTTCATTCGGAGCTGGACCACTGTGGAGACCTAGCTCTGGAGGCT 1200  
QY 1201 GTGTTTCCACAAAGTTTGTATTCGAACTGCAGGATGTGTCCAGGCTGAATGAGGATGTC 1260  
DB 1201 GTGTTTCCACAAAGTTTGTATTCGAACTGCAGGATGTGTCCAGGCTGAATGAGGATGTC 1260  
QY 1261 CTGCTGCAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1320  
DB 1261 CTGCTGCAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1320  
QY 1321 TTTCTTTCACAAAGTCTTCCAGGAGTACAGCAGGAGCAAGACTCAGCAGTTTATTGAGC 1380  
DB 1321 TTTCTTTCACAAAGTCTTCCAGGAGTACAGCAGGAGCAAGACTCAGCAGTTTATTGAGC 1380  
QY 1381 TCTCATAGCCAGAGGAGTGTGACCAAGGGAATGTTTACTTGCAGAAATGTTTCCATT 1440  
DB 1381 TCTCATAGCCAGAGGAGTGTGACCAAGGGAATGTTTACTTGCAGAAATGTTTCCATT 1440  
QY 1441 TCGGACATACATCCACTTATAGCAGCTGTCTCGGTCACACTGTGGGTCTATCTGTGAA 1500  
DB 1441 TCGGACATACATCCACTTATAGCAGCTGTCTCGGTCACACTGTGGGTCTATCTGTGAA 1500  
QY 1501 GCCACCAATGGCTGTATGAAGCAGCTTCGACAGCTGTATCAACGCTGCTCTCGGA 1560  
DB 1501 GCCACCAATGGCTGTATGAAGCAGCTTCGACAGCTGTATCAACGCTGCTCTCGGA 1560  
QY 1561 CTTTCCAACGCCAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
DB 1561 CTTTCCAACGCCAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
QY 1621 ACTGAGCAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCAT 1680  
DB 1621 ACTGAGCAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCAT 1680  
QY 1681 TTATATCTAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAA 1740  
DB 1681 TTATATCTAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAA 1740  
QY 1741 GGTAAAAAGCTTATATATCAACTCAGGGAACATCCCGGATTTACTTATTTGACTTCTTTGAA 1800  
DB 1741 GGTAAAAAGCTTATATATCAACTCAGGGAACATCCCGGATTTACTTATTTGACTTCTTTGAA 1800  
QY 1801 CATTTGCCAATGTGCAAGTGTCTGGACTTCAATTAACCTGGACTTTTATGGGGAGCT 1860  
DB 1801 CATTTGCCAATGTGCAAGTGTCTGGACTTCAATTAACCTGGACTTTTATGGGGAGCT 1860  
QY 1861 ATGCTTCTTCTGGGAAAGGCTGCAAGACACAGTGTGAATCCACATGGAAGAGGCCCA 1920  
DB 1861 ATGCTTCTTCTGGGAAAGGCTGCAAGACACAGTGTGAATCCACATGGAAGAGGCCCA 1920  
QY 1921 GAAACCTATATCCAGCAGGCTGTATCTTTCTTCAACTGGAAGCAGGAAATTCAGG 1980

Db 1921 GAAACCTACATCCACAGGGCTGTATCTTTGTTCTTCAACTGGAGGAGTAATTCAGG 1980  
QY 1981 ACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTTCAAGTAAGCAAGATATACATATCG 2040  
Db 1981 ACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTTCAAGTAAGCAAGATATACATATCG 2040  
QY 2041 GGGAAATATTCAGCTCTGCCAAGCCTCAGGCTCAAAATAAAGAGATGTGCTGGTGTG 2100  
Db 2041 GGGAAATATTCAGCTCTGCCAAGCCTCAGGCTCAAAATAAAGAGATGTGCTGGTGTG 2100  
QY 2101 GCTGGAAGCTCAGTTTGGTCTCAGCAGCTGTGAAGAACATTTATCTCTCATGTGGAA 2160  
Db 2101 GCTGGAAGCTCAGTTTGGTCTCAGCAGCTGTGAAGAACATTTATCTCTCATGTGGAA 2160  
QY 2161 GCCAGTCCCTCACCATAGAAGATGAGGCGACATCACATCTGTAAACAACTGAAACCC 2220  
Db 2161 GCCAGTCCCTCACCATAGAAGATGAGGCGACATCACATCTGTAAACAACTGAAACCC 2220  
QY 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGT 2280  
Db 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGT 2280  
QY 2281 AACTTGAAGAACTTACAAAGCTCATATGGGATACATTAAGATGAATGAAGATGCT 2340  
Db 2281 AACTTGAAGAACTTACAAAGCTCATATGGGATACATTAAGATGAATGAAGATGCT 2340  
QY 2341 ATAAAACTAGCTGAAGGCTGAAACCTGAAAGAGATCTGTTATTTTCATTTGACCCAC 2400  
Db 2341 ATAAAACTAGCTGAAGGCTGAAACCTGAAAGAGATCTGTTATTTTCATTTGACCCAC 2400  
QY 2401 TTGCTGACATTTGGAGAGGAAATGATATACATAGTCAAGTCTCTGTCAAGTGAACCCCTG 2460  
Db 2401 TTGCTGACATTTGGAGAGGAAATGATATACATAGTCAAGTCTCTGTCAAGTGAACCCCTG 2460  
QY 2461 GACCTTGAAGAAATCAATTAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
Db 2461 GACCTTGAAGAAATCAATTAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
QY 2521 GCTCAGAACTTTCAAAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAATATACCTG 2580  
Db 2521 GCTCAGAACTTTCAAAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAATATACCTG 2580  
QY 2581 GAAAAGATGGAATGAAGCTCTTCATGAAGTGAATGATGATGATGATGATGATGATGATG 2640  
Db 2581 GAAAAGATGGAATGAAGCTCTTCATGAAGTGAATGATGATGATGATGATGATGATGATG 2640  
QY 2641 CTCACCGCACTGATGCTGCCCTGGGCTGCTGAGCTCAAGGAGCCTGAGCAGCCTGTG 2700  
Db 2641 CTCACCGCACTGATGCTGCCCTGGGCTGCTGAGCTCAAGGAGCCTGAGCAGCCTGTG 2700  
QY 2701 AAACATTTGGAGAGGTCGCCAAGCTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACA 2760  
Db 2701 AAACATTTGGAGAGGTCGCCAAGCTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACA 2760  
QY 2761 GATACAGAGATAGAAATTTAGTGATTTTGGTGAAGAACCTCTGAAAACCTTCCAG 2820  
Db 2761 GATACAGAGATAGAAATTTAGTGATTTTGGTGAAGAACCTCTGAAAACCTTCCAG 2820  
QY 2821 CAGTTCAATTTGGCGGAAATCGTGTGAGCAGTGATGATGATGATGATGATGATGATGATG 2880  
Db 2821 CAGTTCAATTTGGCGGAAATCGTGTGAGCAGTGATGATGATGATGATGATGATGATGATG 2880  
QY 2881 TTTGAAATCTTAAGCAATTTAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2940  
Db 2881 TTTGAAATCTTAAGCAATTTAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2940  
QY 2941 CCAGCAATTTAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 3000  
Db 2941 CCAGCAATTTAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 3000  
QY 3001 AGGCTGTGTTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060  
Db 3001 AGGCTGTGTTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060

QY 3061 CTAGTAACGTCT 3072  
Db 3061 CTAGTAACGTCT 3072

RESULT 4  
PCT-US00-29643-1  
; Sequence 1. Application PC/TUS0029643  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-136W01  
; CURRENT APPLICATION NUMBER: PCT/US00/29643  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)...(3107)  
PCT-US00-29643-1

Query Match 100.0%; Score 3072; DB 1; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAATTTTCATTAAGGACAAATAGCCGAGCCCTATTCAAGAAATGGAAATGACTGTTATA 60  
Db 36 ATGAATTTTCATTAAGGACAAATAGCCGAGCCCTATTCAAGAAATGGAAATGACTGTTATA 95  
QY 61 AAGCAAAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAGTAAACATC 120  
Db 96 AAGCAAAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAGTAAACATC 155  
QY 121 ATTTGCTGGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTGTTGAAA 180  
Db 156 ATTTGCTGGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTGTTGAAA 215  
QY 181 AAGGGTTCAAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240  
Db 216 AAGGGTTCAAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 275  
QY 241 TTTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTTGGACGAT 300  
Db 276 TTTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTTGGACGAT 335  
QY 301 TTGGGCTCAGGATTTAAAGGACTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTT 360  
Db 336 TTGGGCTCAGGATTTAAAGGACTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTT 395  
QY 361 GGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCTTCACAGAACTGTCTGTGG 420  
Db 396 GGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCTTCACAGAACTGTCTGTGG 455  
QY 421 AGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCCTGACAGGT 480  
Db 456 AGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCCTGACAGGT 515  
QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGAGCAAGTCCACTCTGCTGCGAG 540  
Db 516 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGAGCAAGTCCACTCTGCTGCGAG 575  
QY 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAAATTCGTC 600  
Db 576 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAAATTCGTC 635

Qy 601 TTCTTCCCTCCCTCAGCAGGCGCCAGGCTGAGCTTTTGAACCCCTGTGATCAACTC 660  
Db 636 TTCCTTCCCTCCCTCAGCAGGCGCCAGGCTGAGCTTTTGAACCCCTGTGATCAACTC 695  
Qy 661 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATPGGCCATGCTGCTGAAGCTGGG 720  
Db 696 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATPGGCCATGCTGCTGAAGCTGGG 755  
Qy 721 CAGAGGGTCTTTTCCCTTCTTGATGGCTACAAATGAATTCAGGCCCCAGAACTGCCCGAA 780  
Db 756 CAGAGGGTCTTTTCCCTTCTTGATGGCTACAAATGAATTCAGGCCCCAGAACTGCCCGAA 815  
Qy 781 ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACC 840  
Db 816 ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACC 875  
Qy 841 ACTGAGTCCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATG 900  
Db 876 ACTGAGTCCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATG 935  
Qy 901 ACAGNAGACAGGCCCGCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC 960  
Db 936 ACAGNAGACAGGCCCGCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC 995  
Qy 961 TTGTTGCTCCAAATTCAGAAATCAGAGTGCCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Db 996 TTGTTGCTCCAAATTCAGAAATCAGAGTGCCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1055  
Qy 1021 GTGGTFCATCCTGTGCAATCCAGATGGGTGAAAGTGGAGTTCCTCACTCTCACACACAACA 1080  
Db 1056 GTGGTFCATCCTGTGCAATCCAGATGGGTGAAAGTGGAGTTCCTCACTCTCACACACAACA 1115  
Qy 1081 ACGCTGTTCCTACATCCTTATGATCTGTGTGATACAGAAAAACAACACAAACATAAAGGT 1140  
Db 1116 ACGCTGTTCCTACATCCTTATGATCTGTGTGATACAGAAAAACAACACAAACATAAAGGT 1175  
Qy 1141 GTGGTGCAGTGCCTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT 1200  
Db 1176 GTGGTGCAGTGCCTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT 1235  
Qy 1201 GTGTTCTCCCAAGTTTGATTTTCGAAGTCGAGGATGTGCCAGCTGAATGAGGATGTC 1260  
Db 1236 GTGTTCTCCCAAGTTTGATTTTCGAAGTCGAGGATGTGCCAGCTGAATGAGGATGTC 1295  
Qy 1261 CTGCTGACACTGGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1320  
Db 1296 CTGCTGACACTGGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1355  
Qy 1321 TTCTTTACAAAGTCATTCAGGAGTACACAGCAGCAGCACTCAGCAGTTTATTGACG 1380  
Db 1356 TTCTTTACAAAGTCATTCAGGAGTACACAGCAGCAGCACTCAGCAGTTTATTGACG 1415  
Qy 1381 TCTCATGAGCAGAGGAGTGCACCAAGGGAAATGGTTACTTGCAGAAAATGGTTCCATT 1440  
Db 1416 TCTCATGAGCAGAGGAGTGCACCAAGGGAAATGGTTACTTGCAGAAAATGGTTCCATT 1475  
Qy 1441 TCGGACATTTACATCCACTTATAGAGCCTGCTCCGGTACACCTGTGGGTCTATCTGTGGAA 1500  
Db 1476 TCGGACATTTACATCCACTTATAGAGCCTGCTCCGGTACACCTGTGGGTCTATCTGTGGAA 1535  
Qy 1501 GCCACAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1560  
Db 1536 GCCACAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1595  
Qy 1561 CTTTCCATTCGCAAGAGGCCCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
Db 1596 CTTTCCATTCGCAAGAGGCCCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1655  
Qy 1621 ACTGAGCAAGAAATCTTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680  
Db 1656 ACTGAGCAAGAAATCTTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715  
Qy 1681 TTATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAA 1740

Db 1716 TTATP TCAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAA 1775  
Qy 1741 GGTAF AAGCTTATATCAACTCAGGGAACATCCCGGATTACTTATTTGACTTCTTTGAA 1800  
Db 1776 GGTAF AAGCTTATATCAACTCAGGGAACATCCCGGATTACTTATTTGACTTCTTTGAA 1835  
Qy 1801 CATTT ECCCCAATTTGCAAGTCTCTGGACTTCAATTAACATGGACTTTTATGGGGAGCT 1860  
Db 1836 CATTT ECCCCAATTTGCAAGTCTCTGGACTTCAATTAACATGGACTTTTATGGGGAGCT 1895  
Qy 1861 ATGCG TCATGGGAAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
Db 1896 ATGCG TCATGGGAAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1955  
Qy 1921 GAAAC TACATTTCCACAGGCGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 1980  
Db 1956 GAAAC TACATTTCCACAGGCGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 2015  
Qy 1981 ACTCT GAGGTTCACAGCTCCGGATTTTCAGCAAGTGTGATTAAGCAAGATATCACATATCTG 2040  
Db 2016 ACTCT GAGGTTCACAGCTCCGGATTTTCAGCAAGTGTGATTAAGCAAGATATCACATATCTG 2075  
Qy 2041 GGGAA PNTATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATPAAAGAGATGTGCTGGTGTG 2100  
Db 2076 GGGAA PNTATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATPAAAGAGATGTGCTGGTGTG 2135  
Qy 2101 GCTGGA AGCCTTCAGTCTTGGTCTCCTCAGCACCTGTAAAGAACATTTATCTCTCATGGTGAA 2160  
Db 2136 GCTGGA AGCCTTCAGTCTTGGTCTCCTCAGCACCTGTAAAGAACATTTATCTCTCATGGTGAA 2195  
Qy 2161 GCCAGT XCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAAACC 2220  
Db 2196 GCCAGT XCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAAACC 2255  
Qy 2221 TTGAGT TTTCAATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2280  
Db 2256 TTGAGT TTTCAATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2315  
Qy 2281 AACTTG AGAACCTTACAAAGCTCATATGATGAATCAATATAAGATGAATGAAGAGATGCT 2340  
Db 2316 AACTTG AGAACCTTACAAAGCTCATATGATGAATCAATATAAGATGAATGAAGAGATGCT 2375  
Qy 2341 ATAAAC TAGCTGAGGCGCTGAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCAC 2400  
Db 2376 ATAAAC TAGCTGAGGCGCTGAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCAC 2435  
Qy 2401 TTGCTG ACATTTGAGAGGGNAATGGATTACATAGTCAAGTCTCTGTCNAAGTGAACCCCTG 2460  
Db 2436 TTGCTG ACATTTGAGAGGGNAATGGATTACATAGTCAAGTCTCTGTCNAAGTGAACCCCTG 2495  
Qy 2461 GACCTG AGAAATTCATTAAGTCTCCTGCTGCTGCTGCTGCAAAATGCAAGTGAATACTTA 2520  
Db 2496 GACCTG AGAAATTCATTAAGTCTCCTGCTGCTGCTGCTGCAAAATGCAAGTGAATACTTA 2555  
Qy 2521 GCTCAG TCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATACCTG 2580  
Db 2556 GCTCAG TCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATACCTG 2615  
Qy 2581 GAAAAAG TGGAAATGAAGCTCTTTCATGACTGATCGACAGAGTGAAGCTGCTGAACAG 2640  
Db 2616 GAAAAAG TGGAAATGAAGCTCTTTCATGACTGATCGACAGAGTGAAGCTGCTGAACAG 2675  
Qy 2641 CTCACCG ACTGATGCTGCCCTGGGGCTGTGACCTGCAAGCAGCCTGAGCAGCTGTG 2700  
Db 2676 CTCACCG ACTGATGCTGCCCTGGGGCTGTGACCTGCAAGCAGCCTGAGCAGCTGTG 2735  
Qy 2701 AAACATTT GAGGAGGTCCCAACACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2760  
Db 2736 AAACATTT GAGGAGGTCCCAACACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2795  
Qy 2761 GATACAG ATTAGAAATTTAGGTGCAATTTTTCGAAAGAACCTCTGAAAACTTCCAG 2820

Db 2796 GATACAGAGATTAGAAATTTAGGTGCAATTTTGGAAAGAACCCCTCTGAAAAAATCCAG 2855  
QY 2821 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTCCATGGGTGA 2880  
Db 2856 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTCCATGGGTGA 2915  
QY 2881 TTTGAGAATCTTAAGCAATTTAGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGAT 2940  
Db 2916 TTTGAGAATCTTAAGCAATTTAGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGAT 2975  
QY 2941 CCAGCATTTAGTCAGAAAATTTAGCAAGTGTATCCAGTTAACTTTCTGCAAGAGCT 3000  
Db 2976 CCAGCATTTAGTCAGAAAATTTAGCAAGTGTATCCAGTTAACTTTCTGCAAGAGCT 3035  
QY 3001 AGGCTTTGTTGGTGCAATTTTATGATGATGATCTCAGTGTATTTACAGGTGCTTTTAAA 3060  
Db 3036 AGGCTTTGTTGGTGCAATTTTATGATGATGATCTCAGTGTATTTACAGGTGCTTTTAAA 3095  
QY 3061 CTAGTAACGTCT 3072  
Db 3096 CTAGTAACGTCT 3107

RESULT 5

US-09-697-089-1  
; Sequence 1, Application US/09697089  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-136001  
; CURRENT APPLICATION NUMBER: US/09/697,089  
; PRIORITY FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)...(3107)  
US-09-697-089-1

Query Match 100.0%; Score 3072; DB 27; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATTTTCATAAAGCAATAGCCGAGCCCTTATTCAGAGATGGGATGACTGTTATA 60  
Db 36 ATGAATTTTCATAAAGCAATAGCCGAGCCCTTATTCAGAGATGGGATGACTGTTATA 95  
QY 61 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAATTAACATC 120  
Db 96 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAATTAACATC 155  
QY 121 ATTGCTGGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180  
Db 156 ATTGCTGGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 215  
QY 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGAGTGAACATATCTCTA 240  
Db 216 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGAGTGAACATATCTCTA 275  
QY 241 TTTTCAGGACTTGAATGGCAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 300  
Db 276 TTTTCAGGACTTGAATGGCAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 335  
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATCCCTT 360

Db 336 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATCCCTT 395  
QY 361 GTTGAAGATTTGACATTTATTTTAACTTTGAAAGCACTTTCACAGAACTCTCTCTGTGG 420  
Db 396 GTTGAAGATTTGACATTTATTTTAACTTTGAAAGCACTTTCACAGAACTCTCTCTGTGG 455  
QY 421 AGGAAGGACCAACACCATCACCGCTGGAGCAGTGTGACCTGAATGGGCTCTCTGAGGCT 480  
Db 456 AGGAAGGACCAACACCATCACCGCTGGAGCAGTGTGACCTGAATGGGCTCTCTGAGGCT 515  
QY 481 CTTTCAGAGCCCTGTGATCATTTGAAGGGAATCTGCAAGGCAAGTTCACACTCTGTCGAG 540  
Db 516 CTTTCAGAGCCCTGTGATCATTTGAAGGGAATCTGCAAGGCAAGTTCACACTCTGTCGAG 575  
QY 541 CGCATTTGCTGCTCTGGGCTCCGAAAGTCAAGGCTCTCACCAGTTCAAAATTCGTC 600  
Db 576 CGCATTTGCTGCTCTGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAATTCGTC 635  
QY 601 TTTCTCTCGTCTCAGCAGGCCCCAGGCTGAGCTTTTGTAAACCCCTCTGTGATCAACTC 660  
Db 636 TTTCTCTCGTCTCAGCAGGCCCCAGGCTGAGCTTTTGTAAACCCCTCTGTGATCAACTC 695  
QY 661 CTGGATATACCTGGCACAATCAGAGGAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 720  
Db 696 CTGGATATACCTGGCACAATCAGAGGAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 755  
QY 721 CAGAGGTTCTTTCTTCTTCTGATGGCTACAATGAATTCAGCCCAAGCTGCCCAGAA 780  
Db 756 CAGAGGTTCTTTCTTCTTCTGATGGCTACAATGAATTCAGCCCAAGCTGCCCAGAA 815  
QY 781 ATCGAAGCCCTGATAAAGGAAACCCGCTTCAAGAACATGGTCTGCTACCCTACC 840  
Db 816 ATCGAAGCCCTGATAAAGGAAACCCGCTTCAAGAACATGGTCTGCTACCCTACC 875  
QY 841 ACTGAGTCCCTCAGCAGCAGATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGATATG 900  
Db 876 ACTGAGTCCCTCAGCAGCAGATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGATATG 935  
QY 901 ACAGAGACAGGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTCTGTAAGGC 960  
Db 936 ACAGAGACAGGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTCTGTAAGGC 995  
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGCTTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Db 996 TTGTTGCTCCAAATTCAGAAATCCAGGCTTTGAGGAATCTCATGAAGACCCCTCTCTTT 1055  
QY 1021 GTGGTCATCAGTTGTGCAATCCAGATGGGTGAAAGTGTGAGTTCACACTCTCAGACAAACA 1080  
Db 1056 GTGGTCATCAGTTGTGCAATCCAGATGGGTGAAAGTGTGAGTTCACACTCTCAGACAAACA 1115  
QY 1081 AGGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAATTAAGT 1140  
Db 1116 AGGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAATTAAGT 1175  
QY 1141 GTGGCTGCAAGTGTCTTATTCGGAGCCTGGACACTGTGGAGACTAGCTCTGGAGGCT 1200  
Db 1176 GTGGCTGCAAGTGTCTTATTCGGAGCCTGGACACTGTGGAGACTAGCTCTGGAGGCT 1235  
QY 1201 GTGGTCTCCACAGTTTGTATTTCCAACTGAGGATGTGTCAGGCTGATGAGGATGTC 1260  
Db 1236 GTGGTCTCCACAGTTTGTATTTCCAACTGAGGATGTGTCAGGCTGATGAGGATGTC 1295  
QY 1261 GTGGTGTGACAGTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1320  
Db 1296 GTGGTGTGACAGTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1355  
QY 1321 TTTCTTTCAGAGTCTTATTCAGGAGTACAGCAGGAGCAAGACTCAGCAGTTTATTTAGG 1380  
Db 1356 TTTCTTTCAGAGTCTTATTCAGGAGTACAGCAGGAGCAAGACTCAGCAGTTTATTTAGG 1415  
QY 1381 TCTCATGAGCCAGAGGAGTGTACCAAGGGAATGTTACTTTCAGAAAAATGTTTCCAT 1440  
Db 1416 TCTCATGAGCCAGAGGAGTGTACCAAGGGAATGTTACTTTCAGAAAAATGTTTCCAT 1475



QY 1441 TCGACATTAACATCCACTTATAGACGCTGCTCCGGGTACACCTGTGGGTGCATCTGTGGAA 1500  
Db 1476 TCGGACATTAACATCCACTTATAGACGCTGCTCCGGGTACACCTGTGGGTGCATCTGTGGAA 1535  
QY 1501 GCCACAGGCGCTGTATGAAGACCTCGCAGCAGTGTATCAACACGCGCTGCCCTTCGCGA 1560  
Db 1536 GCCACAGGCGCTGTATGAAGACCTCGCAGCAGTGTATCAACACGCGCTGCCCTTCGCGA 1595  
QY 1561 CTTTCCATCCCAAGAGCGCTCTGTGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
Db 1596 CTTTCCATCCCAAGAGCGCTCTGTGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1655  
QY 1621 ACTGAGCAAGAAATCTGAAGCATATAACATCAATTCCTTTGTAGAGTGTGCATCCAT 1680  
Db 1656 ACTGAGCAAGAAATCTGAAGCATATAACATCAATTCCTTTGTAGAGTGTGCATCCAT 1715  
QY 1681 TTATATCAAGAGAGTACATCAATCAGCCCTGAGCCCAAGAAATTTGAGCTTTCTTTCAA 1740  
Db 1716 TTATATCAAGAGAGTACATCAATCAGCCCTGAGCCCAAGAAATTTGAGCTTTCTTTCAA 1775  
QY 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 1800  
Db 1776 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 1835  
QY 1801 CATTGGCCCAATGTGCAAGTGTCTGGACTTCATTAACTGACCTTTTATGGGGAGCT 1860  
Db 1836 CATTGGCCCAATGTGCAAGTGTCTGGACTTCATTAACTGACCTTTTATGGGGAGCT 1895  
QY 1861 ATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
Db 1896 ATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1955  
QY 1921 GAAACCTTACATCCAGCAGGGCTGTATCTTTGTCTTCAACTGGAAGCAGGAATTCAGG 1980  
Db 1956 GAAACCTTACATCCAGCAGGGCTGTATCTTTGTCTTCAACTGGAAGCAGGAATTCAGG 2015  
QY 1981 ACTCTGAGGTGCACACTCCCGGATTTTCAGCAAGTTTGAATAAGCAAGATATCATATCTG 2040  
Db 2016 ACTCTGAGGTGCACACTCCCGGATTTTCAGCAAGTTTGAATAAGCAAGATATCATATCTG 2075  
QY 2041 GGGAAATATTCAGCTCTGCGCACAGGCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTG 2100  
Db 2076 GGGAAATATTCAGCTCTGCGCACAGGCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTG 2135  
QY 2101 GCTGGAAGCCTCAGTTTGGTCCCTCAGCACCCTGTAAGAACATTTATCTCTCATGGTGGAA 2160  
Db 2136 GCTGGAAGCCTCAGTTTGGTCCCTCAGCACCCTGTAAGAACATTTATCTCTCATGGTGGAA 2195  
QY 2161 GCCAGTCCCTCACCATAGAGATGAGAGCAGCATCACATCTCTAACAACCTGABAACC 2220  
Db 2196 GCCAGTCCCTCACCATAGAGATGAGAGCAGCATCACATCTGTAAACAACCTGABAACC 2255  
QY 2221 TTGAGTATTCATGACCTACAGATCAACGCGCTGCCGGGTGCTGACTGACAGCTTGGGT 2280  
Db 2256 TTGAGTATTCATGACCTACAGATCAACGCGCTGCCGGGTGCTGACTGACAGCTTGGGT 2315  
QY 2281 AACTTGAAGACCTTACAAAGCTCATAATGGATAACAATAAGATGAATGAAGAAGATGCT 2340  
Db 2316 AACTTGAAGACCTTACAAAGCTCATAATGGATAACAATAAGATGAATGAAGAAGATGCT 2375  
QY 2341 AATAACTAGCTGAAGGCCTGAAAAACCTCGAAGAAGATGTGTTTATTTCAATTTGACCCAC 2400  
Db 2376 AATAACTAGCTGAAGGCCTGAAAAACCTCGAAGAAGATGTGTTTATTTCAATTTGACCCAC 2435  
QY 2401 TTGTCTGACATTTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAGGTGAACCCCTGT 2460  
Db 2436 TTGTCTGACATTTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAGGTGAACCCCTGT 2495  
QY 2461 GACCTTGAAGAAATTCAAATTTAGTCTCCTGCTGCTTGTCTCAAAATGAGGTGAAAAATCCTA 2520  
Db 2496 GACCTTGAAGAAATTCAAATTTAGTCTCCTGCTGCTTGTCTCAAAATGAGGTGAAAAATCCTA 2555

QY 2521 GCTCAIAAATCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATTACCTG 2580  
Db 2556 GCTCAIAAATCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATTACCTG 2615  
QY 2581 GAAAAI.GATGGAATGAAGCTCTTTCATGAACCTGATCGACAGGATGAACGCTGTAGAACAG 2640  
Db 2616 GAAAAI.GATGGAATGAAGCTCTTTCATGAACCTGATCGACAGGATGAACGCTGTAGAACAG 2675  
QY 2641 CTCACI.GCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCCTGAGCAGCCTGTTG 2700  
Db 2676 CTCACI.GCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCCTGAGCAGCCTGTTG 2735  
QY 2701 AAACAT.TTGAGAGAGGTCCACAACTCGTCAAGCTTGGGTGAAAACTGGAGACTCACA 2760  
Db 2736 AAACAT.TTGAGAGAGGTCCACAACTCGTCAAGCTTGGGTGAAAACTGGAGACTCACA 2795  
QY 2761 GATACA.ZAGATTAAGATTTTAGTGCATTTTGGAAAGAACCTCTGAAAACTTCCAG 2820  
Db 2796 GATACA.ZAGATTAAGATTTTAGTGCATTTTGGAAAGAACCTCTGAAAACTTCCAG 2855  
QY 2821 CAGTTG.IATTTGGCGGGAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGTA 2880  
Db 2856 CAGTTG.IATTTGGCGGGAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGTA 2915  
QY 2881 TTTGAG.IATCTTAAGCAATTTAGTGTGTTTTTTGACTTTTAGTACTAAAGAAATTTCTACCTGAT 2940  
Db 2916 TTTGAG.IATCTTAAGCAATTTAGTGTGTTTTTTGACTTTTAGTACTAAAGAAATTTCTACCTGAT 2975  
QY 2941 CCAGCA.TAGTCAGAAAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAGCT 3000  
Db 2976 CCAGCA.TAGTCAGAAAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAGCT 3035  
QY 3001 AGCTTC.TTGGGTGCGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA 3060  
Db 3036 AGCTTC.TTGGGTGCGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA 3095  
QY 3061 CTAGTA.TGCT 3072  
Db 3096 CTAGTA.TGCT 3107

RESULT 6

US-09-841-739-1

; Sequence 1, Application US/09841739  
; GENERAL INFORMATION:  
; APPLICANT: Ber.in. John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; NUMBER OF SEQ. D NOS: 16  
; SOFTWARE: Fast; EQ for Windows Version 4.0  
; SEQ. ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)...(3107)  
US-09-841-739-1

Query Match 100.0%; Score 3072; DB 32; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAATTT.ATAAAGACAAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATA 60  
Db 36 ATCAATTT.ATAAAGACAAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATA 95



QY 61 AAGCAATCACAGATGACCTATTGTGTAATGTAATGTTCTGAATCGGAGAAAGTAACATC 120  
DB 96 AAGCAATCACAGATGACCTATTGTGTAATGTAATGTTCTGAATCGGAGAAAGTAACATC 155  
QY 121 ATTGCTCGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 180  
DB 156 ATTGCTCGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 215  
QY 181 AAGGTTTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240  
DB 216 AAGGTTTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 275  
QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAAAGGACTTGGACGAT 300  
DB 276 TTTCAGGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAAAGGACTTGGACGAT 335  
QY 301 TTGGCTCAGGATTTAAGGACTTGTACCATACCCATCTTTCTGAACCTTTTATCCCTT 360  
DB 336 TTGGCTCAGGATTTAAGGACTTGTACCATACCCATCTTTCTGAACCTTTTATCCCTT 395  
QY 361 GGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCTTCACAGAACTGTCTGTGG 420  
DB 396 GGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCTTCACAGAACTGTCTGTGG 455  
QY 421 AGGAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCCTCTCTGACGGCT 480  
DB 456 AGGAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCCTCTCTGACGGCT 515  
QY 481 CTTACAGGCCCTGCATATTGAGGGGAATCTGGCAAAAGGCAAGTCCACTCTGCTGCAG 540  
DB 516 CTTACAGGCCCTGCATATTGAGGGGAATCTGGCAAAAGGCAAGTCCACTCTGCTGCAG 575  
QY 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 600  
DB 576 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 635  
QY 601 TTCTTCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTAAACCTCTGTGATCAACTC 660  
DB 636 TTCTTCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTAAACCTCTGTGATCAACTC 695  
QY 661 CTGGATATACCTGGCAATCAGGAAGCAGACATTTATGGCCATGCTGTGAAGCTGGG 720  
DB 696 CTGGATATACCTGGCAATCAGGAAGCAGACATTTATGGCCATGCTGTGAAGCTGGG 755  
QY 721 CAGAGGGTTCTTTTCTCTGATGCTACAATGAATTAAGGCCCGAGAACTGCCCAGAA 780  
DB 756 CAGAGGGTTCTTTTCTCTGATGCTACAATGAATTAAGGCCCGAGAACTGCCCAGAA 815  
QY 781 ATCGAAGCCCTGATAAAGGAAACCCAGCTTCAAGAATGATGTCATCTCACCCTACC 840  
DB 816 ATCGAAGCCCTGATAAAGGAAACCCAGCTTCAAGAATGATGTCATCTCACCCTACC 875  
QY 841 ACTGAGTGGCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGTGGGGATATG 900  
DB 876 ACTGAGTGGCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGTGGGGATATG 935  
QY 901 ACAGAAGCAGGCGCCAGGCTCTCATCCGAGAGTCTGATCAAGGAGCTTGTCTGAAGC 960  
DB 936 ACAGAAGCAGGCGCCAGGCTCTCATCCGAGAGTCTGATCAAGGAGCTTGTCTGAAGC 995  
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
DB 996 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1055  
QY 1021 GTGGTCATCATTTGTCATTCAGATGGGTGAAAGTGTTCACCTCTCAGACACAAACA 1080  
DB 1056 GTGGTCATCATTTGTCATTCAGATGGGTGAAAGTGTTCACCTCTCAGACACAAACA 1115  
QY 1081 ACCTGCTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT 1140  
DB 1116 ACCTGCTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT 1175  
QY 1141 GTGGCTGCAAGTGACTTTCATTTGGAGCCTGGACCCTGTGGAGACCTAGTCTGGAGG 1200

DB 1176 GTGGCTGCAAGTGACTTTCATTCGGAGCCTGGACCCTGTGGAGACCTAGTCTGGAGGT 1235  
QY 1201 GTGTTCTCCCAACAAGTTTTCATTTCCGAACCTGCAGGATGCTGCCAGCGTGAATGAGGATGTC 1260  
DB 1236 GTGTTCTCCCAACAAGTTTTCATTTCCGAACCTGCAGGATGCTGCCAGCGTGAATGAGGATGTC 1295  
QY 1261 CTGCTGACAACCTGGGCTCCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAA 1320  
DB 1296 CTGCTGACAACCTGGGCTCCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAA 1355  
QY 1321 TTCTTTCAACAAGTTCATTTCCAGGAGTACACAGCAGGAGAGACTCAGCAGTTTATTGACG 1380  
DB 1356 TTCTTTCAACAAGTTCATTTCCAGGAGTACACAGCAGGAGAGACTCAGCAGTTTATTGACG 1415  
QY 1381 TCTCATGACCCAGAGGAGGTGACCAAGGGAATGTTTACTTGCAGAAAAATGGTTTCCATT 1440  
DB 1416 TCTCATGACCCAGAGGAGGTGACCAAGGGAATGTTTACTTGCAGAAAAATGGTTTCCATT 1475  
QY 1441 TCGGACATTTACATCCACTTTATAGCAGCCTGCTCCGGTACACCTTGTGGGTCTATCTGTGAA 1500  
DB 1476 TCGGACATTTACATCCACTTTATAGCAGCCTGCTCCGGTACACCTTGTGGGTCTATCTGTGAA 1535  
QY 1501 GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA 1560  
DB 1536 GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA 1595  
QY 1561 CTTTCCATCGCCAAGAGGCTCTCTCGGACAGGAACTTTGCAAAAGTGTGAAAAACACC 1620  
DB 1596 CTTTCCATCGCCAAGAGGCTCTCTCGGACAGGAACTTTGCAAAAGTGTGAAAAACACC 1655  
QY 1621 ACTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680  
DB 1656 ACTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715  
QY 1681 TTATATCAAGAGATACATCCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 1740  
DB 1716 TTATATCAAGAGATACATCCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 1775  
QY 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTTTACCTTCTTTTGA 1800  
DB 1776 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTTTACCTTCTTTTGA 1835  
QY 1801 CATTTGCCCAATTTGTCAGTGTCTGGACTTCATTTAAACTGGACTTTTATGGGGAGCT 1860  
DB 1836 CATTTGCCCAATTTGTCAGTGTCTGGACTTCATTTAAACTGGACTTTTATGGGGAGCT 1895  
QY 1861 ATGGCTTCATGGGAAAAGGCTGCAGAAACACAGGTGGAAATCCACATGAAGAGGCCCA 1920  
DB 1896 ATGGCTTCATGGGAAAAGGCTGCAGAAACACAGGTGGAAATCCACATGAAGAGGCCCA 1955  
QY 1921 GAAACCTACATTTCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAG 1980  
DB 1956 GAAACCTACATTTCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAG 2015  
QY 1981 ACTCTGAGGTCACACTCCGGGATTTTCAGCAAGTTTCAATAAGCAAGATATCATATCTG 2040  
DB 2016 ACTCTGAGGTCACACTCCGGGATTTTCAGCAAGTTTCAATAAGCAAGATATCATATCTG 2075  
QY 2041 GGGAAATATTCAGCTCTGCCACAGCCCTCAGGCTCAAAATAAAGAGATGTGCTGTGTG 2100  
DB 2076 GGGAAATATTCAGCTCTGCCACAGCCCTCAGGCTCAAAATAAAGAGATGTGCTGTGTG 2135  
QY 2101 GCTGGAAGCCTCAGTTTGTCTCAGCAGCTGTAAAGCAATTTATTTCTCTCATGGTGA 2160  
DB 2136 GCTGGAAGCCTCAGTTTGTCTCAGCAGCTGTAAAGCAATTTATTTCTCTCATGGTGA 2195  
QY 2161 GCCAGTCCCTCACCATAGAAGATGAGGCACATCACATCTGTAAACACCTGAAAC 2220  
DB 2196 GCCAGTCCCTCACCATAGAAGATGAGGCACATCACATCTGTAAACACCTGAAAC 2255  
QY 2221 TTGAGTATTTCAGCTTACAGATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTTGGT 2280



Db 901 ACAGAAACAGACGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGGCTTGCTGAAGGC 960  
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGTGTCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Db 961 TTGTTGCTCCAAATTCAGAAATCCAGTGTCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
QY 1021 GTGGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACCTCTCACACACAACA 1080  
Db 1021 GTGGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACCTCTCACACACAACA 1080  
QY 1081 ACCTGTTCATACCTCTCTATGATCTGTTGATACAGAAAAACAACACAAAAATAAGGT 1140  
Db 1081 ACCTGTTCATACCTCTCTATGATCTGTTGATACAGAAAAACAACACAAAAATAAGGT 1140  
QY 1141 GTGGCTGCAAGTGACATTCATTCGGAGCCTGGACACTGTGGAGACCTAGCTCTGGAGGCT 1200  
Db 1141 GTGGCTGCAAGTGACATTCATTCGGAGCCTGGACACTGTGGAGACCTAGCTCTGGAGGCT 1200  
QY 1201 GTGTTCTCCACAAGTTTGATTTGCAACTGCAGGATGTGCCAGCGTGAATGAGGATGTC 1260  
Db 1201 GTGTTCTCCACAAGTTTGATTTGCAACTGCAGGATGTGCCAGCGTGAATGAGGATGTC 1260  
QY 1261 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAGGCCAAAGTATAA 1320  
Db 1261 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAGGCCAAAGTATAA 1320  
QY 1321 TTCTTTCACAAGTCATTCAGGAGTACACAGCAGGAGGAGACTCAGCAGTTATTGACG 1380  
Db 1321 TTCTTTCACAAGTCATTCAGGAGTACACAGCAGGAGGAGACTCAGCAGTTATTGACG 1380  
QY 1381 TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGAGAAAAATGGTTTCCATT 1440  
Db 1381 TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGAGAAAAATGGTTTCCATT 1440  
QY 1441 TCGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTGCGAA 1500  
Db 1441 TCGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTGCGAA 1500  
QY 1501 GCCACAGGGCTCTTATGAAGCACCCTCGCAGCAGTGTATCAACACGCTGCCCTTCGGA 1560  
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QY 1561 CTTTCCATCGCCAAAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC 1620  
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QY 1621 ACTGACCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680  
Db 1621 ACTGACCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680  
QY 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTCGAAGCTTCTTTCAA 1740  
Db 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTCGAAGCTTCTTTCAA 1740  
QY 1741 GGTAAAGCTTATATCAACTCAGGAACATCCCGATTAATTTGACTTCTTTGAA 1800  
Db 1741 GGTAAAGCTTATATCAACTCAGGAACATCCCGATTAATTTGACTTCTTTGAA 1800  
QY 1801 CATTTGCCCAATTTGCAAGTGTCTGAGACTTCATTAACCTGACTTTTATGGGGAGCT 1860  
Db 1801 CATTTGCCCAATTTGCAAGTGTCTGAGACTTCATTAACCTGACTTTTATGGGGAGCT 1860  
QY 1861 ATGGCTTCATGGGAAAGGCTGCAGAAACACAGAGTGGGAATCCACATGGAAGGCCCA 1920  
Db 1861 ATGGCTTCATGGGAAAGGCTGCAGAAACACAGAGTGGGAATCCACATGGAAGGCCCA 1920  
QY 1921 GAAACCTACATTCCTCCAGCAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAG 1980  
Db 1921 GAAACCTACATTCCTCCAGCAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAG 1980  
QY 1981 ACTCTGGAGGTACACTCCGGGATTTGACAGAGTTGAAATGAAGCAAGATATCACATATCG 2040  
Db 1981 ACTCTGGAGGTACACTCCGGGATTTGACAGAGTTGAAATGAAGCAAGATATCACATATCG 2040

QY 2041 GGGAAAATATTGAGCTCTGCCAAGCCCTCAGGCTCAAAATAAGAGATGTGCTGCTGTG 2100  
Db 2041 GGGAAAATATTGAGCTCTGCCAAGCCCTCAGGCTCAAAATAAGAGATGTGCTGCTGTG 2100  
QY 2101 GCTGGAAGCCTCAGTTTGGTCTCTCAGCCTCTGTAGAACAATTTATTTCTCTCATGTTG 2160  
Db 2101 GCTGGAAGCCTCAGTTTGGTCTCTCAGCCTCTGTAGAACAATTTATTTCTCTCATGTTG 2160  
QY 2161 GCCAGTCCCTCACCATTAGAAGATGAGAGCACAATCAGATCTGTAAACAACCTGAAACC 2220  
Db 2161 GCCAGTCCCTCACCATTAGAAGATGAGAGCACAATCAGATCTGTAAACAACCTGAAACC 2220  
QY 2221 TTGAGTATTTCATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTTGG 2280  
Db 2221 TTGAGTATTTCATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTTGG 2280  
QY 2281 AACTTGAAGAACCCTTACAAGCTCAATAATGGATTAACATAAGATGAATGAAGAATGCT 2340  
Db 2281 AACTTGAAGAACCCTTACAAGCTCAATAATGGATTAACATAAGATGAATGAAGAATGCT 2340  
QY 2341 ATAAACTAGCTGAAGCCCTGAAAAACCTGAAAAACCTCAAGAAGATGTTTATTTCATTTG 2400  
Db 2341 ATAAACTAGCTGAAGCCCTGAAAAACCTGAAAAACCTCAAGAAGATGTTTATTTCATTTG 2400  
QY 2401 TTGCTGTACATTTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGT 2460  
Db 2401 TTGCTGTACATTTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGT 2460  
QY 2461 GACCTTTGAAGAAATTCATTTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
Db 2461 GACCTTTGAAGAAATTCATTTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
QY 2521 GCTCAGAAATTCACAAATTTGGTCAAACTGAGCAATCTTGTATTATTCAGAAAAATACCTG 2580  
Db 2521 GCTCAGAAATTCACAAATTTGGTCAAACTGAGCAATCTTGTATTATTCAGAAAAATACCTG 2580  
QY 2581 GAAAAAGATGGAATCAAGCTCTTCATGAACATGATCAGAGGATGAACGCTGTAGAACAG 2640  
Db 2581 GAAAAAGATGGAATCAAGCTCTTCATGAACATGATCAGAGGATGAACGCTGTAGAACAG 2640  
QY 2641 CTCACCGCACTGATGCTGCCCTGGGCTGTGAGTGTGAGGAGCCTGAGCAGCCTGTG 2700  
Db 2641 CTCACCGCACTGATGCTGCCCTGGGCTGTGAGTGTGAGGAGCCTGAGCAGCCTGTG 2700  
QY 2701 AAACATTTGGAGGAGTCCCAACATCTGCAAGCTTTGGGTTGAAAAACTGGAGACTCACA 2760  
Db 2701 AAACATTTGGAGGAGTCCCAACATCTGCAAGCTTTGGGTTGAAAAACTGGAGACTCACA 2760  
QY 2761 GATACAGATTTAGAAATTTTAGTGCAATTTTGGGAAAGAACCTCTGAAAAACTTTCCAG 2820  
Db 2761 GATACAGATTTAGAAATTTTAGTGCAATTTTGGGAAAGAACCTCTGAAAAACTTTCCAG 2820  
QY 2821 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGAGGTGTA 2880  
Db 2821 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGAGGTGTA 2880  
QY 2881 TTTGAGAAATTTAGGCAATTTAGTGTGTTTTTGTGACTTTTAGTACTTAAAGAAATTTCTAC 2940  
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QY 2941 CCAGCAATTTAGTCCAGAAACTTAGCCCAAGTGTATCCAAGTTAACTTTCTGCAAGAGCT 3000  
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QY 3001 AGGCTTTGTTGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA 3060  
Db 3001 AGGCTTTGTTGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA 3060  
QY 3061 CTAGTAACCTGCT 3072  
Db 3061 CTAGTAACCTGCT 3072

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RESULT 8
US-10-156-733-14
; Sequence 14, Application US/10156733
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; TITLE OF INVENTION: FACTOR AN ICE-PROTEASE ACTIVATING
; FILE REFERENCE: 480140.477
; CURRENT APPLICATION NUMBER: US/10/156.733
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-733-14

Query Match      95.0%; Score 2919; DB 41; Length 3219;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAAAGGACAATAGCGAGCCCTTATTAAAGAAATGGGAATGACTGTTATA 60
Db 145 ATGAATTTCAAAAGGACAATAGCGAGCCCTTATTAAAGAAATGGGAATGACTGTTATA 204
QY 61 AAGCAATACAGATGACCTATTGCTATGGAATGCTTCAATCCGGAAGAGTAACATC 120
Db 205 AAGCAATACAGATGACCTATTGCTATGGAATGCTTCAATCCGGAAGAGTAACATC 264
QY 121 ATTGCTCGGAGAAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTGAAA 180
Db 265 ATTGCTCGGAGAAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTGAAA 324
QY 181 AAGGTTTCAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAAGGAGTGAACCTATCCTCTA 240
Db 325 AAGGTTTCAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAAGGAGTGAACCTATCCTCTA 384
QY 241 TTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGAT 300
Db 385 TTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGAT 444
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTT 360
Db 445 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTT 504
QY 361 GGTGAAGATATTGACATTTATTTAACTTGAAGACCTTTCAGAACCTGCTGTGG 420
Db 505 GGTGAAGATATTGACATTTATTTAACTTGAAGACCTTTCAGAACCTGCTGTGG 564
QY 421 AGGAAGGACCAACACCATCAGCGGTGGAGCAGCTGACCCCTGAATGGCTCCTGAGGCT 480
Db 565 AGGAAGGACCAACACCATCAGCGGTGGAGCAGCTGACCCCTGAATGGCTCCTGAGGCT 624
QY 481 CTTACAGCCCTGATCATTTGAAGGGGAATCTGGCAAAGCAAGTCCACTCTGCTGCAG 540
Db 625 CTTACAGCCCTGATCATTTGAAGGGGAATCTGGCAAAGCAAGTCCACTCTGCTGCAG 684
QY 541 CGCATTTGCATGCTGTGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC 600
Db 685 CGAATTTGCATGCTGTGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC 744
QY 601 TTCTTCCCTGCTCAGCAGGCGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660
Db 745 TTCTTCCCTGCTCAGCAGGCGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 804
QY 661 CTGATATACCTGGCACATCAGAAAGCAGACATTCATGGCCATGCTGCAAGCTGGG 720
Db 805 CTGATATACCTGGCACATCAGAAAGCAGACATTCATGGCCATGCTGCAAGCTGGG 864
QY 721 CAGAGGTTCTTTCTTCTGATGGCTACATGAATCAAGCCCGCAGAACTGCCAGAA 780
Db 145 CAGAGGTTCTTTCTTCTGATGGCTACATGAATCAAGCCCGCAGAACTGCCAGAA 2004
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Db 865 CAGAGGGTTCTTTCTTCTGATGGCTACATGAATTCAGCCCGCAGAACTGCCAGAA 924
QY 781 ATCGAAGCCCTGATAAAGGAAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACC 840
Db 925 ATCGAAGCCCTGATAAAGGAAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACC 984
QY 841 ACTGAATGCTGAGGACATACGGCAGTTTGGTGCCTCGTACTGCTGAGGTGGGGATATG 900
Db 985 ACTGAATGCTGAGGACATACGGCAGTTTGGTGCCTCGTACTGCTGAGGTGGGGATATG 1044
QY 901 ACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGC 960
Db 1045 ACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGC 1104
QY 961 TTGTTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
Db 1105 TTGTTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1164
QY 1021 GTGTCTATCACTTGTGCAATCCAGATGGTGAAGTGAAGTGTCCACTCTCACACAAACA 1080
Db 1165 GTGTCTATCACTTGTGCAATCCAGATGGTGAAGTGAAGTGTCCACTCTCACACAAACA 1224
QY 1081 ACGCTGTCCCATACCTTCTATGATCTGTGATACAGAAAACACACAAACATAAAGGT 1140
Db 1225 ACGCTGTCCCATACCTTCTATGATCTGTGATACAGAAAACACACAAACATAAAGGT 1284
QY 1141 GTGCTTCAAGTGTACTTTCGAGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT 1200
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QY 1201 GTGTCTTCCACAAAGTTTGAATTTCCAACTGCAGGATGTGCCAGCGTGAATGAGGATGTC 1260
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QY 1261 CTGCTGTCACAACTGGGCTCCTCTGTAAATATATACAGTCAAGAGGTTCAGCCAAAGTATAAA 1320
Db 1405 CTGCTGTCACAACTGGGCTCCTCTGTAAATATATACAGTCAAGAGGTTCAGCCAAAGTATAAA 1464
QY 1321 TTTCTTTTACAAAGTTCATCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGTTTATTGACG 1380
Db 1465 TTTCTTTTACAAAGTTCATCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGTTTATTGACG 1524
QY 1381 TCTCATCAGCCAGAGGAGTGCACCAAGGGAAATGGTTACTTGCAGAAATGTTTCCATT 1440
Db 1525 TCTCATCAGCCAGAGGAGTGCACCAAGGGAAATGGTTACTTGCAGAAATGTTTCCATT 1584
QY 1441 TCGGACATACACTTATAGCAGCTGCTCCGGTACACTGTGGTCACTCTGTGGAA 1500
Db 1585 TCGGACATACACTTATAGCAGCTGCTCCGGTACACTGTGGTCACTCTGTGGAA 1644
QY 1501 GCCACCAATGGCTGTATGAACACCTCGCAGCAGTGTATCAACACGCGTGCCTTCTCGGA 1560
Db 1645 GCCACCAATGGCTGTATGAACACCTCGCAGCAGTGTATCAACACGCGTGCCTTCTCGGA 1704
QY 1561 CTTTCCAATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACC 1620
Db 1705 CTTTCCAATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACC 1764
QY 1621 ACTGAGCTAGAAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Db 1765 ACTGAGCTAGAAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1824
QY 1681 TTATATCTAGAGACTACATCCAAATCAGCCTGAGCCAGAAATTTGAAGCTTCTCTTCAA 1740
Db 1825 TTATATCTAGAGACTACATCCAAATCAGCCTGAGCCAGAAATTTGAAGCTTCTCTTCAA 1884
QY 1741 GGTAAAGCTTATATATCAACTCAGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 1800
Db 1885 GGTAAAGCTTATATATCAACTCAGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 1944
QY 1801 CATTTGCCAATTTGTGCAAGTGTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCT 1860
Db 1945 CATTTGCCAATTTGTGCAAGTGTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCT 2004
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Qy	1861	ATGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGAAGAGGCCCA	1920
Db	2005	ATGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGAAGAGGCCCA	2064
Qy	1921	GAACCTACATCCCAAGCGGCTGATCTTTGTTCTCACTGGAACAGGAATTCAGG	1980
Db	2065	GAACCTACATCCCAAGCGGCTGATCTTTGTTCTCACTGGAACAGGAATTCAGG	2124
Qy	1981	ACTCGAGGTCACACTCCGGGATTTCAACAAGTTGAATAAGCAAGATATCACATATCTG	2040
Db	2125	ACTCGAGGTCACACTCCGGGATTTCAACAAGTTGAATAAGCAAGATATCACATATCTG	2184
Qy	2041	GGGAAATATTCAGCTCTGCCACAAGCTTCAGGCTGCAAAATAAGAGATGTGCTGGTG	2100
Db	2185	GGGAAATATTCAGCTCTGCCACAAGCTTCAGGCTGCAAAATAAGAGATGTGCTGGTG	2244
Qy	2101	GCTGGAAGCCTCAGTTTGGTCTCAGCACCCTGTAAGAACAATTTATCTCTCATGCTGGA	2160
Db	2245	GCTGGAAGCCTCAGTTTGGTCTCAGCACCCTGTAAGAACAATTTATCTCTCATGCTGGA	2304
Qy	2161	GCCAGTCCCTCCACATAGAAGATGAGAGGCACATCACATCTGTAAACAACTGAAAC	2220
Db	2305	GCCAGTCCCTCCACATAGAAGATGAGAGGCACATCACATCTGTAAACAACTGAAAC	2364
Qy	2221	TTGAGTATTCATGACCTACAGAATCAACGGCTGCCGGGTGCTGACTGACGACTGGGT	2280
Db	2365	TTGAGTATTCATGACCTACAGAATCAACGGCTGCCGGGTGCTGACTGACGACTGGGT	2424
Qy	2281	AACCTTGAAGAACCTTCAAAAGCTCAATATGGATAACATAAAGATCAATTAAGAAGATGCT	2340
Db	2425	AACCTTGAAGAACCTTCAAAAGCTCAATATGGATAACATAAAGATCAATTAAGAAGATGCT	2484
Qy	2341	ATAAACTAGCTGAAGCCCTGAAAACTGAAAGAAGATGTGTTATTTTCATTGACCCAC	2400
Db	2485	ATAAACTAGCTGAAGCCCTGAAAACTGAAAGAAGATGTGTTATTTTCATTGACCCAC	2544
Qy	2401	TTGTCTCACATTCGAGAGGAATGGAATACATAGTCACAGTCTCTGTCGAAGTGAACCTGT	2460
Db	2545	TTGTCTCACATTCGAGAGGAATGGAATACATAGTCACAGTCTCTGTCGAAGTGAACCTGT	2604
Qy	2461	GACCTTGAAGAAATCAATTAGTCTCCTGCTTCTGCTGCTGCTGCTGCAAAATCCCTA	2520
Db	2605	GACCTTGAAGAAATCAATTAGTCTCCTGCTGCTGCTGCTGCAAAATCCCTA	2664
Qy	2521	GCTCAGAAATCTTCAAAATTTGGTCAAACTGACATCTCTTGATTTATCAGAAAATACCTG	2580
Db	2665	GCTCAGAAATCTTCAAAATTTGGTCAAACTGACATCTCTTGATTTATCAGAAAATACCTG	2724
Qy	2581	GAAAAGATGGAATGAAGCTCTTCATGAACATGATCGACAGATGAACGCTCTAGAACAG	2640
Db	2725	GAAAAGATGGAATGAAGCTCTTCATGAACATGATCGACAGATGAACGCTCTAGAACAG	2784
Qy	2641	CTCACCCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTG	2700
Db	2785	CTCACCCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTG	2844
Qy	2701	AAACATTTGAGAGAGTCCCAACATCTGTCAGCTTTGGTTGAAAACCTGGAGACTCACA	2760
Db	2845	AAACATTTGAGAGAGTCCCAACATCTGTCAGCTTTGGTTGAAAACCTGGAGACTCACA	2904
Qy	2761	GATACAGAAATAGAATTTTAGTGTCATTTTGTGAAAAGAACCCCTCTGAAAACCTCCAG	2820
Db	2905	GATACAGAAATAGAATTTTAGTGTCATTTTGTGAAAAGAACCCCTCTGAAAACCTCCAG	2964
Qy	2821	CAGTTGAATTTGGCGGAAATCGGTGAGCAGTGATGATGGCTTGCCCTTCATGGGTGTA	2880
Db	2965	CAGTTGAATTTGGCGGAAATCGGTGAGCAGTGATGATGGCTTGCCCTTCATGGGTGTA	3024
Qy	2881	TTTGAGAACTCTTAAGCAATTAGTGTGTTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGAT	2940
Db	3025	TTTGAGAACTCTTAAGCAATTAGTGTGTTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGAT	3084

[illegible]











		: APPLICANT: Liu, Chenghua		
		: APPLICANT: Dmanac, Radoje T.		
		: TITLE OF INVENTION: Novel Contigs Obtained		
		: TITLE OF INVENTION: From Various Libraries		
		: FILE REFERENCE: 785		
		: CURRENT APPLICATION NUMBER: US/09/922,279A		
		: CURRENT FILING DATE: 2001-08-03		
		: PRIOR APPLICATION NUMBER: 09/491,404		
		: PRIOR FILING DATE: 2000-01-25		
		: NUMBER OF SEQ ID NOS: 3796		
		: SOFTWARE: pt_sp_genes Version 1.0		
		: SEQ ID NO 1319		
		: LENGTH: 3545		
		: TYPE: DNA		
		: ORGANISM: Homo sapiens		
		: FEATURE:		
		: NAME/KEY: sig_peptide		
		: LOCATION: (781)...(916)		
		: OTHER INFORMATION: this location contains the signal peptide sequence,		
		: OTHER INFORMATION: MLWGGKALTKFKFVFLRLSRAOGLFETLCDQLDIPGTR, Run with SignalP		
		: NAME/KEY: misc_feature		
		: LOCATION: (679)...(3279)		
		: OTHER INFORMATION: similar to g13688110 in the genepept database release 114,		
		: OTHER INFORMATION: Run with FASTX 3.3c00, default parameters		
		US-09-922-279A-1319		
		Query Match 95.0%; Score 2919; DB 34; Length 3545;		
		Best Local Similarity 99.9%; Pred. No. 0;		
		Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	1	ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA	60	
Db	232	ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA	291	
QY	61	AAGCAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGATTAACATC	120	
Db	292	AAGCAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGATTAACATC	351	
QY	121	ATTTGCTCGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA	180	
Db	352	ATTTGCTCGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA	411	
QY	181	AAGGTTTCAGAGTCCGTAAACCTCTTTCTTAATCCCTTTAAGSAGTGAACATCTCTA	240	
Db	412	AAGGTTTCAGAGTCCGTAAACCTCTTTCTTAATCCCTTTAAGSAGTGAACATCTCTA	471	
QY	241	TTTCAGGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAGGAGCTTGGACGAT	300	
Db	472	TTTCAGGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAGGAGCTTGGACGAT	531	
QY	301	TTGGCTCAGGATTTAAGGACTTGTACCATACCCCATCTTTCTGAACATTTTATCCCTT	360	
Db	532	TTGGCTCAGGATTTAAGGACTTGTACCATACCCCATCTTTCTGAACATTTTATCCCTT	591	
QY	361	GGTGAAGATATTGACATATTTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG	420	
Db	592	GGTGAAGATATTGACATATTTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG	651	
QY	421	AGSAGGACCAACACCATACCGCGTGGAGAGCTGTACCCCTGAATGGCCCTCTGACGGCT	480	
Db	652	AGSAGGACCAACACCATACCGCGTGGAGAGCTGTACCCCTGAATGGCCCTCTGACGGCT	711	
QY	481	CTTCAGAGCCCTGCATATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG	540	
Db	712	CTTCAGAGCCCTGCATATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG	771	
QY	541	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC	600	
Db	772	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC	831	
QY	601	TTCTTCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC	660	
Db	832	TTCTTCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC	891	

QY	661	CTGGATATACCTGGCACAATCAGGAAGACAGACATTCATGGCCATGCTGCTGAAGCTGCGG	720
Db	892	CTGGATATACCTGGCACAATCAGGAAGACAGACATTCATGGCCATGCTGCTGAAGCTGCGG	951
QY	721	CAGAGGGTCTCTTTCCCTTCTTGATGGCTACAAATCAAGAGTCAAGAGTCAAGAGTCAAG	780
Db	952	CAGAGGGTCTCTTTCCCTTCTTGATGGCTACAAATCAAGAGTCAAGAGTCAAGAGTCAAG	1011
QY	781	ATCGAAGCCCTGTATAAAGGAAAACACCGCTTCAAGAACATGTCATCGTCACCACTACC	840
Db	1012	ATCGAAGCCCTGTATAAAGGAAAACACCGCTTCAAGAACATGTCATCGTCACCACTACC	1071
QY	841	ACTGAGTCCCTGAGGACATACGCGCAGTCTTGAGTCCCTGACTGCTGAGGTGGGGATATG	900
Db	1072	ACTGAGTCCCTGAGGACATACGCGCAGTCTTGAGTCCCTGACTGCTGAGGTGGGGATATG	1131
QY	901	ACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGAGTCTGCTGAAGGC	960
Db	1132	ACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGAGTCTGCTGAAGGC	1191
QY	961	TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGACCCCTCTCTTT	1020
Db	1192	TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGACCCCTCTCTTT	1251
QY	1021	GTGTCATCATCTTGTCAAATCCAGATGGGTGAAAGTGAAGTTCCTACTCTCACACACAACA	1080
Db	1252	GTGTCATCATCTTGTCAAATCCAGATGGGTGAAAGTGAAGTTCCTACTCTCACACACAACA	1311
QY	1081	ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAACAACAACATATAAGGT	1140
Db	1312	ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAACAACAACATATAAGGT	1371
QY	1141	GTGCTCAAGTGAAGTCTTTCGAGGCTGGACCACTGTGGAGACCTGAGTCTCTGGAGGT	1200
Db	1372	GTGCTCAAGTGAAGTCTTTCGAGGCTGGACCACTGTGGAGACCTGAGTCTCTGGAGGT	1431
QY	1201	GTGTTCTTCCACAAAGTTTGATTTTCCAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC	1260
Db	1432	GTGTTCTTCCACAAAGTTTGATTTTCCAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC	1491
QY	1261	CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGATATAA	1320
Db	1492	CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGATATAA	1551
QY	1321	TTCTTTTCAAAAGTCAATTCAGGAGTACACAGCAGGAGAGACCTCAGCAGTTTATTGACG	1380
Db	1552	TTCTTTTCAAAAGTCAATTCAGGAGTACACAGCAGGAGAGACCTCAGCAGTTTATTGACG	1611
QY	1381	TCTCATGAGCCAGAGGAGTGAACCAAGGGAATGTTTACTTGCAGAAAATGGTTTCCATT	1440
Db	1612	TCTCATGAGCCAGAGGAGTGAACCAAGGGAATGTTTACTTGCAGAAAATGGTTTCCATT	1671
QY	1441	TCGGACATTTACATCCACTTATAGACGCTGCTCCGGTACACCTGCTGGGTCTATCTGGAA	1500
Db	1672	TCGGACATTTACATCCACTTATAGACGCTGCTCCGGTACACCTGCTGGGTCTATCTGGAA	1731
QY	1501	GCCACAGGGCTGTTATGAAGCAGCTGCAGCAGTGTATCAACAGCGCTGCCCTCTCGGA	1560
Db	1732	GCCACAGGGCTGTTATGAAGCAGCTGCAGCAGTGTATCAACAGCGCTGCCCTCTCGGA	1791
QY	1561	CTTTTCCATCGCAAGAGGCGCTCTCTGGAGACAGGAATCTTTTGCAAGTGTCAAAAACACC	1620
Db	1792	CTTTTCCATCGCAAGAGGCGCTCTCTGGAGACAGGAATCTTTTGCAAGTGTCAAAAACACC	1851
QY	1621	ACTGAGCAAGAAATTTCTGAAAGCCATAAATCAATTTCTTTGTAGAGTGTGGCATCCAT	1680
Db	1852	ACTGAGCAAGAAATTTCTGAAAGCCATAAATCAATTTCTTTGTAGAGTGTGGCATCCAT	1911
QY	1681	TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAA	1740
Db	1912	TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAA	1971

QY	661	CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGG	720
Db	892	CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGG	951
QY	721	CAGAGGGTCTTTTCTCTTGTATGCTACAATGAATTCAGAGCCAGAACTGCCAGAA	780
Db	952	CAGAGGGTCTTTTCTCTTGTATGCTACAATGAATTCAGAGCCAGAACTGCCAGAA	1011
QY	781	ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGCTCATCGTCACCATACC	840
Db	1012	ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGCTCATCGTCACCATACC	1071
QY	841	ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATG	900
Db	1072	ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATG	1131
QY	901	ACAGAAGACAGCCGCCAGGCTCTATCCAGAGAAGTCTGATCAAGAGCTTGTGTAAGGC	960
Db	1132	ACAGAAGACAGCCGCCAGGCTCTATCCAGAGAAGTCTGATCAAGAGCTTGTGTAAGGC	1191
QY	961	TTGTTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT	1020
Db	1192	TTGTTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT	1251
QY	1021	GTGGTCATCATTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACAAACA	1080
Db	1252	GTGGTCATCATTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACAAACA	1311
QY	1081	AGCTGTTCCATACCTTCTATGATCTGTGATACAGAAAACAAACACAAACATAAGGT	1140
Db	1312	AGCTGTTCCATACCTTCTATGATCTGTGATACAGAAAACAAACACAAACATAAGGT	1371
QY	1141	GTGGTCGAAGTGACTTTCATTCGGGCTGGACCTGTGGACCTAGCTCTGGAGGT	1200
Db	1372	GTGGTCGAAGTGACTTTCATTCGGGCTGGACCTGTGGATACCTAGCTCTGGAGGT	1431
QY	1201	GTGTTCTCCACAAAGTTTGAATTCGAACTGCAGGATGTGCCAGCGTGAATGAGGATGC	1260
Db	1432	GTGTTCTCCACAAAGTTTGAATTCGAACTGCAGGATGTGCCAGCGTGAATGAGGATGC	1491
QY	1261	CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAA	1320
Db	1492	CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAA	1551
QY	1321	TTCTTTCAAGTCAATCCAGGATACAGCAGGACGAAGACTCAGCAGTTTATTGAGC	1380
Db	1552	TTCTTTCAAGTCAATCCAGGATACAGCAGGACGAAGACTCAGCAGTTTATTGAGC	1611
QY	1381	TCTCATGACGACAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTTCCAT	1440
Db	1612	TCTCATGACGACAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTTCCAT	1671
QY	1441	TCGGACATTTACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCAATCTGGAA	1500
Db	1672	TCGGACATTTACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCAATCTGGAA	1731
QY	1501	GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACAGGCTGCTTCTCGGA	1560
Db	1732	GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACAGGCTGCTTCTCGGA	1791
QY	1561	CTTTCCATCGCCAAAGGGCTCTCTGGAGACAGGAATCTTTTGCAAGTGTGAAAAACACC	1620
Db	1792	CTTTCCATCGCCAAAGGGCTCTCTGGAGACAGGAATCTTTTGCAAGTGTGAAAAACACC	1851
QY	1621	ACTGACAGAAATTTCTGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Db	1852	ACTGACAGAAATTTCTGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1911
QY	1681	TTATATCAGAGAGTACATCCAAATCAGCCCTGAGCCAGCAAGATTTGAAGCTTTCTTCAA	1740
Db	1912	TTATATCAGAGAGTACATCCAAATCAGCCCTGAGCCCTGAGCCAGCAAGATTTGAAGCTTTCTTCAA	1971



QY 362 GTGAAGATATTGACATTAATTTTAACTTGAAAGACACCTTCAGAACCTGTCCCTGTGA 421  
|||||  
Db 500 GTGAAGATATTGACATTAATTTTAACTTGAAAGACACCTTCAGAACCTGTCCCTGTGA 559  
QY 422 GGAAGGACCAACACATACCGGTGGAGCAGCTGACCCGTGAATGGCCCTCCGAGGCTC 481  
Db 560 GGAAGGACCAACACATACCGGTGGAGCAGCTGACCCGTGAATGGCCCTCCGAGGCTC 619  
QY 482 TTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGC 541  
Db 620 TTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGC 679  
QY 542 GCATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAAATGCTGCT 601  
Db 680 GAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAAATGCTGCT 739  
QY 602 TCTTCTCCGCTCAGCAGGGCCAGGTGGAGCTTTTGAACCCCTCTGTGATCAACTCC 661  
Db 740 TCTTCTCCGCTCAGCAGGGCCAGGTGGAGCTTTTGAACCCCTCTGTGATCAACTCC 799  
QY 662 TGSATATACCTGSCACAANTCAGSAGCAGACATTCATGGCCATGCTGTGAAGCTGCGGC 721  
Db 800 TGSATATACCTGSCACAANTCAGSAGCAGACATTCATGGCCATGCTGTGAAGCTGCGGC 859  
QY 722 AGAGGGTCTCTTTCTCTTGATGGCTACAATGAATTCAGGCCCCAGAACTGCCAGAAA 781  
Db 860 AGAGGGTCTCTTTCTCTTGATGGCTACAATGAATTCAGGCCCCAGAACTGCCAGAAA 919  
QY 782 TCGAGCCCTGATAAGAGAAAACACCGCTTCAAGAACATGTGTCACTCACCCTACCA 841  
Db 920 TCGAGCCCTGATAAGAGAAAACACCGCTTCAAGAACATGTGTCACTCACCCTACCA 979  
QY 842 CTGAGTGCCTGAGGACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGGATATCA 901  
Db 980 CTGAGTGCCTGAGGACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGGATATCA 1039  
QY 902 CAGAAGACAGCCAGGCTCTCATCCGAGAACTGCTGATCAAGGAGCTTGCTGAAGGCT 961  
Db 1040 CAGAAGACAGCCAGGCTCTCATCCGAGAACTGCTGATCAAGGAGCTTGCTGAAGGCT 1099  
QY 962 TGTGTCTCAAAATTCAGAAATCCAGTGTCTGAGGAATCTCATGAAGACCCCTCTCTTG 1021  
Db 1100 TGTGTCTCAAAATTCAGAAATCCAGTGTCTGAGGAATCTCATGAAGACCCCTCTCTTG 1159  
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Db 3200 TAGTAAGTCT 3210

RESULT 14  
US-09-864-921-96  
; Sequence 96, Application US/09864921  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian

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; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 337 AAGCAAAATCACAGATGACCTATTGTTATGGATGTTCTGAATCGCGAAGAAATTAACATC 396

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DB 397 ATTTGCTCGGAAGGTGGAGCAGATGCTGTAGAGGATCATTCACATGATGTTTGA 456

QY 181 AAGGGTTACAGAGTCTGTAACTCTTTCTTAAATCCCTTAAGGAGTGAACCTATCTCTA 240
DB 457 AAGGGTTACAGAGTCTGTAACTCTTTCTTAAATCCCTTAAGGAGTGAACCTATCTCTA 516

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DB 517 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 576

QY 301 TTGGCTCAGGATTTAAGGACTTGTACCATACCCCATCTTTCTGAATTTTATCCCTT 360
DB 577 TTGGCTCAGGATTTAAGGACTTGTACCATACCCCATCTTTCTGAATTTTATCCCTT 636

QY 361 GGTGAAGATATGACATTAATTTTAACTTGAAGACCTTTCACAGACCTGCTCTGTGG 420
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QY 1460 ATAGTAGCCTGCTCGGTACACCTGTGGGTATCTGTGTGAAGCCACACAGGGCTGTATGA 1519  
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Db 1736 ATAGTAGCCTGCTCGGTACACCTGTGGGTATCTGTGTGAAGCCACACAGGGCTGTATGA 1795  
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QY 1520 AGCACTCCGACAGTGTATCAACACGGCTGCTCTTCGGACTTTTCATCTGCCAAGAGGC 1579  
|||||  
Db 1796 AGCACTCCGACAGTGTATCAACACGGCTGCTCTTCGGACTTTTCATCTGCCAAGAGGC 1855  
|||||  
QY 1580 CTCTCTGGAGACAGGAATCTTTTCAAAAGTGTGAAAAACACCACTGAGCAAGAAATTCCTGA 1639  
|||||  
Db 1856 CTCTCTGGAGACAGGAATCTTTTCAAAAGTGTGAAAAACACCACTGAGCAAGAAATTCCTGA 1915  
|||||  
QY 1640 AAGCATTAACATCAATCTCTTGTAGAGTGTGGATCCATTTATATCAAGAGAGTACAT 1699  
|||||  
Db 1916 AAGCATTAACATCAATCTCTTGTAGAGTGTGGATCCATTTATATCAAGAGAGTACAT 1975  
|||||  
QY 1700 CCAATTCAGCCCTGAGCCAAAGATTTTGAAGCTTTCTTCAAGGTAAAGCTTTATATCA 1759  
|||||  
Db 1976 CCAATTCAGCCCTGAGCCAAAGATTTTGAAGCTTTCTTCAAGGTAAAGCTTTATATCA 2035  
|||||  
QY 1760 ACTCA3GGAAACATCCCGATTACTTATTGTACTTTCTTTGAACATTTGCCCCAATTTGCA 1819  
|||||  
Db 2036 ACTCA3GGAAACATCCCGATTACTTATTGTACTTTCTTTGAACATTTGCCCCAATTTGCA 2095  
|||||  
QY 1820 GTGCT3TGAGCTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGG 1879  
|||||  
Db 2096 GTGCC3TGAGCTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGG 2155  
|||||  
QY 1880 CTGCA3AAGACACAGTGGAAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCA 1939  
|||||  
Db 2156 CTGCA3AAGACACAGTGGAAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCA 2215  
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QY 1940 GGGCT3TATCTTTGTTTCAACTGGAAGCAGGAATTCAGGACTCTGGAAGGTCAACACTCC 1999  
|||||  
Db 2216 GGGCT3TATCTTTGTTTCAACTGGAAGCAGGAATTCAGGACTCTGGAAGGTCAACACTCC 2275  
|||||  
QY 2000 GGGAT3TCAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGGAATAATTCAGCTCTG 2059  
|||||  
Db 2276 GGGAT3TCAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGGAATAATTCAGCTCTG 2335  
|||||  
QY 2060 CCACATGGCTCAGGCTGCAATAAAGAGATGCTGGTGGCTGGAAGCCCTCAGTTGG 2119  
|||||  
Db 2336 CCACATGGCTCAGGCTGCAATAAAGAGATGCTGGTGGCTGGAAGCCCTCAGTTGG 2395  
|||||  
QY 2120 TGCTCTGCACCTGTGAACATTTATTTCTCATGGTGGAGCCAGTCCCTCACCATAG 2179  
|||||  
Db 2396 TGCTCTGCACCTGTGAACATTTATTTCTCATGGTGGAGCCAGTCCCTCACCATAG 2455  
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QY 2180 AAGATCAGAGGCACATCATCTGTAAACAACTGAAACCTTTGAGTATTCATGACCTAC 2239  
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Db 2456 AAGATCAGAGGCACATCATCTGTAAACAACTGAAACCTTTGAGTATTCATGACCTAC 2515  
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QY 2240 AGAATCAGAGGCCTGGGTGGTCTGACTGACAGCTTTGGGTAACTTGAAGAACCCTTACAA 2299  
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Db 2516 AGAATCAGAGGCCTGGGTGGTCTGACTGACAGCTTTGGGTAACTTGAAGAACCCTTACAA 2575  
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QY 2300 AGCTCTAATAGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCC 2359  
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Db 2576 AGCTCTAATAGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCC 2635  
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QY 2360 TGAATACTCTGAAGAAGATGCTTTTATTTTCAATTTGACCCACCTGTCTGACATTTGAGAGG 2419  
|||||  
Db 2636 TGAATACTCTGAAGAAGATGCTTTTATTTTCAATTTGACCCACCTGTCTGACATTTGAGAGG 2695  
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QY 2420 GAATGGATACATAGCTCAAGCTCTGTCAAGTGAACCTGTGACCTTGAGAAATTCAT 2479  
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Db 2696 GAATGGATACATAGCTCAAGCTCTGTCAAGTGAACCTGTGACCTTGAGAAATTCAT 2755  
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QY 2480 TAGTCTCTGTGCTGTCTGCAAAATGCAAGTGAATAATCTTAGCTCAGATCTTCAAAAT 2539  
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Db 2756 TAGTCTCCCTGCTGTGCTGCAAAATGCAGTGAATAATCTAGCTCAGAAATCTTCAAAAT 2815  
QY 2540 TGGTCAAACTGAGCATCTTGGATTTATCAGAAAATFACCTGGAAAAGATGGAATGAAG 2599  
Db 2816 TGGTCAAACTGAGCATCTTGGATTTATCAGAAAATFACCTGGAAAAGATGGAATGAAG 2875  
QY 2600 CTCCTCATGAACGTGATGCGACAGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGC 2659  
Db 2876 CTCCTCATGAACGTGATGCGACAGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGC 2935  
QY 2660 CTTGGGGCTGTGACGTGCGAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAGTCC 2719  
Db 2936 CTTGGGGCTGTGACGTGCGAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAGTCC 2995  
QY 2720 CACAACCTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAAATTT 2779  
Db 2996 CACAACCTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAAATTT 3055  
QY 2780 TAGGTGCATTTTTTGGAAAGAACCCCTCTGAAAACCTCCAGCAGTTGAAATTTGGCGGAA 2839  
Db 3056 TAGGTGCATTTTTTGGAAAGAACCCCTCTGAAAACCTCCAGCAGTTGAAATTTGGCGGAA 3115  
QY 2840 ATCGTGTGAGCAGTATGATGGCTTGCCTTCATGGGTGTATTTGAGAATCTTAAGCAAT 2899  
Db 3116 ATCGTGTGAGCAGTATGATGGCTTGCCTTCATGGGTGTATTTGAGAATCTTAAGCAAT 3175  
QY 2900 TAGTGTTTTTTGTACTTTACTATAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAC 2959  
Db 3176 TAGTGTTTTTTGTACTTTACTATAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAC 3235  
QY 2960 TTAGCCAACTGTTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGCAAT 3019  
Db 3236 TTAGCCAACTGTTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGCAAT 3295  
QY 3020 TTGATGATGATGATCTCAGTGTATTACAGTGCCTTTTAACTAGTAACTGCT 3072  
Db 3296 TTGATGATGATGATCTCAGTGTATTACAGTGCCTTTTAACTAGTAACTGCT 3348

RESULT 16  
PCT-US01-14826-66  
; Sequence 66, Application PC/TUS0114826  
; GENERAL INFORMATION:  
; APPLICANT: Hysed, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-103  
; CURRENT APPLICATION NUMBER: PCT/US01/14826  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/577,408  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: 09/677,298<151> 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,781<151> 2000-10-24  
; PRIOR APPLICATION NUMBER: 09/715,869<151> 2000-11-17  
; PRIOR APPLICATION NUMBER: 09/775,330<151> 2001-02-01  
; NUMBER OF SEQ ID NOS: 864  
; SOFTWARE: Custom  
; SEQ ID NO 66  
; LENGTH: 3260  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)...(3226)  
PCT-US01-14826-66

Query Match 90.0%; Score 2765; DB 1; Length 3260;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3065; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2 TGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGAATGAGCTGTATAA 61  
Db 156 TGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGAATGAGCTATTATAA 215

QY 62 AGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGATAACATCA 121  
Db 216 AGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGATAACATCA 275  
QY 122 TTTGCTGCAGAAAGTGGAGCAGGATGCTGTAGAGGGATCATTCACATGATTTTGAATA 181  
Db 276 TTTGCTGCAGAAAGTGGAGCAGGATGCTGTAGAGGGATCATTCACATGATTTTGAATA 335  
QY 182 AGGGTTTCAGAGTCCCTGTAACCTCTTTTAAATCCCTTAAAGGAGTGAACATATCCTCTAT 241  
Db 336 AGGGTTTCAGAGTCCCTGTAACCTCTTTTAAATCCCTTAAAGGAGTGAACATATCCTCTAT 395  
QY 242 TTCAGAGCTTGAATGGACAAAGTCTTTTTTCATCAGACATCAGAAAGAGACTTTGGACGATT 301  
Db 396 TTCAGAGCTTGAATGGACAAAGTCTTTTTTCATCAGACATCAGAAAGAGACTTTGGACGATT 455  
QY 302 TGGCTCAGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTTG 361  
Db 456 TGGCTCAGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTTG 515  
QY 362 GTGAAGATATGACATTTATTTTAACTTGAAAAGCACCCTTCACAGAACCTGCTCTGTGA 421  
Db 516 GTGAAGATATGACATTTATTTTAACTTGAAAAGCACCCTTCACAGAACCTGCTCTGTGA 575  
QY 422 GGAAGGACCAACACCATCATCCGCGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 481  
Db 576 GGAAGGACCAACACCATCATCCGCGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 635  
QY 482 TTCAGAGCCCTTGCAATTTGAAGGGAAATCTGGGAAAGAGCAAGTCCACTCTGCTGCAGC 541  
Db 636 TTCAGAGCCCTTGCAATTTGAAGGGAAATCTGGGAAAGAGCAAGTCCACTCTGCTGCAGC 695  
QY 542 GCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTGACCAAGTTTCAAAATTCGTCT 601  
Db 696 GAATTCCTCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTGACCAAGTTTCAAAATTCGTCT 755  
QY 602 TCTTCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTTTGAACCCCTCTGTGATCAACTCC 661  
Db 756 TCTTCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTTTGAACCCCTCTGTGATCAACTCC 815  
QY 662 TGGATATACCTGGCACAATCAGAAAGCAGACATTTATGCGCATGCTGTGAAGCTGGGC 721  
Db 816 TGGATATACCTGGCACAATCAGAAAGCAGACATTTATGCGCATGCTGTGAAGCTGGGC 875  
QY 722 AGAGGGTCTTTTCTTCTGTGAGTGTACAATGAATTCAGGCCCCAGAACTGCCAGAAA 781  
Db 876 AGAGGGTCTTTTCTTCTGTGAGTGTACAATGAATTCAGGCCCCAGAACTGCCAGAAA 935  
QY 782 TCGAAGCCCTGATAAAGGAAAACACCGCTTCAAGAACATGGTTCATCGTCAACCACTACCA 841  
Db 936 TCGAAGCCCTGATAAAGGAAAACACCGCTTCAAGAACATGGTTCATCGTCAACCACTACCA 995  
QY 842 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATGA 901  
Db 996 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATGA 1055  
QY 902 CAGAAGACAGCCCGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGTGAAGGCT 961  
Db 1056 CAGAAGACAGCCCGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGTGAAGGCT 1115  
QY 962 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1021  
Db 1116 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1175  
QY 1022 TGGTCAATCACTTGTGCAATCCAGATGGGTGAAGTGAAGTGTCCACTCTCACACACAAACAA 1081  
Db 1176 TGGTCAATCACTTGTGCAATCCAGATGGGTGAAGTGAAGTGTCCACTCTCACACACAAACAA 1235  
QY 1082 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGGTG 1141  
Db 1236 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGGTG 1295  
QY 1142 TGGCTGCAAGTGACTTTCATTGCGAGCCTTGACCACCTGTGGAGACCTAGCTCTGGAGGGTG 1201

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Db 1296 TGGCTGCAAGTGACTTCATTCCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGGTG 1355  
Qy 1202 TGTCTCCCAACAAGTTTGATTTCCGAAGTGCAGATGTGTCCAGCGTGAATGAGGATGCC 1261  
Db 1356 TGTCTCCCAACAAGTTTGATTTCCGAAGTGCAGATGTGTCCAGCGTGAATGAGGATGCC 1415  
Qy 1262 TGTGACAACTCGGGCTCTCTGTGTAATATACAGTCTCAAGGTTCAAGCCAAAGTATAAT 1321  
Db 1416 TGTGACAACTCGGGCTCTCTGTGTAATATACAGTCTCAAGGTTCAAGCCAAAGTATAAT 1475  
Qy 1322 TCTTTCAAGTTCATTCAGAGTACACAGCAGGACGAGTGTACTTCGACAAATGTTTATGAGGT 1381  
Db 1476 TCTTTCAAGTTCATTCAGAGTACACAGCAGGACGAGTGTACTTCGACAAATGTTTATGAGGT 1535  
Qy 1382 CTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTCGACAAATGTTTCCATTTT 1441  
Db 1536 CTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTCGACAAATGTTTCCATTTT 1595  
Qy 1442 CGGACATTTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTTCATCTGTGGAAG 1501  
Db 1596 CGGACATTTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTTCATCTGTGGAAG 1655  
Qy 1502 CCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGAC 1561  
Db 1656 CCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGAC 1715  
Qy 1562 TTTCCATCGCCAAAGAGCCTCTCTGGAGACAGGATCTTTGCCAAGTGTGAANAACACCA 1621  
Db 1716 TTTCCATCGCCAAAGAGCCTCTCTGGAGACAGGATCTTTGCCAAGTGTGAANAACACCA 1775  
Qy 1622 CTGAGCAAGAAATCTGAAGCCATAAATCAATCTCTTTGTAGAGTGTGGCATCCATT 1681  
Db 1776 CTGAGCAAGAAATCTGAAGCCATAAATCAATCTCTTTGTAGAGTGTGGCATCCATT 1835  
Qy 1682 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAAG 1741  
Db 1836 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAAG 1895  
Qy 1742 GTAAAGCTTATATATCAACTCAGGGAACATCCCGCATTTACTTATTTGACTTCTTTGAAC 1801  
Db 1896 GTAAAGCTTATATATCAACTCAGGGAACATCCCGCATTTACTTATTTGACTTCTTTGAAC 1955  
Qy 1802 ATTTGCCAAATTTGTGCAAGTCTCTGGACTTCATTAACTGGACTTTTATGGGGGAGCTA 1861  
Db 1956 ATTTGCCAAATTTGTGCAAGTCTCTGGACTTCATTAACTGGACTTTTATGGGGGAGCTA 2015  
Qy 1862 TGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGGAATCCACATGGAAGAGGCCCCAG 1921  
Db 2016 TGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGGAATCCACATGGAAGAGGCCCCAG 2075  
Qy 1922 AAACCTACATTCAGCAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGA 1981  
Db 2076 AAACCTACATTCAGCAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGA 2135  
Qy 1982 CTCTGGAGTCCACACTCCGGGATTTACAGCAAGTTGATTAAGCAAGATATACATATCTGG 2041  
Db 2136 CTCTGGAGTCCACACTCCGGGATTTACAGCAAGTTGATTAAGCAAGATATACATATCTGG 2195  
Qy 2042 GGAAATATTCAGCTCTGCCACAGCCCTCAGCGTGCAAATTAAGAGATGTCTGGTGTGG 2101  
Db 2196 GGAAATATTCAGCTCTGCCACAGCCCTCAGCGTGCAAATTAAGAGATGTCTGGTGTGG 2255  
Qy 2102 CTGGAAGCCTCAGTTGGTCTCTCAGCACCCTGTAAAGACATTTATCTCTCATGTGTGAAG 2161  
Db 2256 CTGGAAGCCTCAGTTGGTCTCTCAGCACCCTGTAAAGACATTTATCTCTCATGTGTGAAG 2315  
Qy 2162 CCAGTCCCTCACCATGAAGATGAGAGGCACATCAGATCTGTAAACAACTGAAAACCT 2221  
Db 2316 CCAGTCCCTCACCATGAAGATGAGAGGCACATCAGATCTGTAAACAACTGAAAACCT 2375  
Qy 2222 TGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTA 2281  
|||||

Db 2376 TGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTA 2435  
Qy 2282 ACTTGTAGAACCTTACAAAGCTCATATGATGATAACATAAAGATGAATGAAGAAGATGCTA 2341  
Db 2436 ACTTGTAGAACCTTACAAAGCTCATATGATGATAACATAAAGATGAATGAAGAAGATGCTA 2495  
Qy 2342 TAAAA TAGCTGAAGGGCTGAAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACCCACT 2401  
Db 2496 TAAAA TAGCTGAAGGGCTGAAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACCCACT 2555  
Qy 2402 TGTCTGACATTTGGAGAGGGAATGGATTACATAGTCAAGTCTCTCTCAAGTGAACCCCTGTG 2461  
Db 2556 TGTCTGACATTTGGAGAGGGAATGGATTACATAGTCAAGTCTCTCTCAAGTGAACCCCTGTG 2615  
Qy 2462 ACCTTGAAGAAATTCATTTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2521  
Db 2616 ACCTTGAAGAAATTCATTTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2675  
Qy 2522 CTCAGATCTTTCACAAATTTGGTCAAACTGAGCATTTCTTTGATTTTATCAGAAAAATTTACCTGG 2581  
Db 2676 CTCAGATCTTTCACAAATTTGGTCAAACTGAGCATTTCTTTGATTTTATCAGAAAAATTTACCTGG 2735  
Qy 2582 AAAAG VTGGAATGAAGCTCTTCATGAACHTGATCGACAGGATGAACGTGTAGAACAGC 2641  
Db 2736 AAAAG VTGGAATGAAGCTCTTCATGAACHTGATCGACAGGATGAACGTGTAGAACAGC 2795  
Qy 2642 TCACCGTACTGATGCTGCCCTGGGGCTGTGACGTGCBAAGCAGCTGAGCAGCCTGTGA 2701  
Db 2796 TCACCGTACTGATGCTGCCCTGGGGCTGTGACGTGCBAAGCAGCTGAGCAGCCTGTGA 2855  
Qy 2702 AACATTGGAGAGGTGCCAACTCGTCAAGCTTGGTGTGAAAACHTGGAGACTCAGAG 2761  
Db 2856 AACATTGGAGAGGTGCCAACTCGTCAAGCTTGGTGTGAAAACHTGGAGACTCAGAG 2915  
Qy 2762 ATACAGTATTAGTGCATTTTGGTGCATTTTGGAAAGAACCCCTCTGAAAAACTTCCAGC 2821  
Db 2916 ATACAGTATTAGTGCATTTTGGTGCATTTTGGAAAGAACCCCTCTGAAAAACTTCCAGC 2975  
Qy 2822 AGTTGAATTTGGCGGGAAATCGTGTGACAGTGTGATGATGCTGCTTCAATGGGTGTAT 2881  
Db 2976 AGTTGAATTTGGCGGGAAATCGTGTGACAGTGTGATGATGCTGCTTCAATGGGTGTAT 3035  
Qy 2882 TTGAGAAICTTTAAGCAATTAGTGTGTTTTTGTAGTCTTAGTACTTAAAGAAATTTCTACTGTATC 2941  
Db 3036 TTGAGAAICTTTAAGCAATTAGTGTGTTTTTGTAGTCTTAGTACTTAAAGAAATTTCTACTGTATC 3095  
Qy 2942 CAGCATTTGTGAGAAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTA 3001  
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Qy 3002 GGCTTGTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3061  
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Qy 3062 TAGTAACGCT 3072  
Db 3216 TAGTAACGCT 3226

RESULT 17  
US-09-667-298-66  
; Sequence 66, Application US/09667298  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Zhou, Ping  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wan, Jian-Rui  
; APPLICANT: Chen, Rui-hong

APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: Novel Nucleic Acids and  
FILE REFERENCE: 792CIP2A  
CURRENT APPLICATION NUMBER: US/09/667,298  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/577,408  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 178  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 66  
LENGTH: 3260  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (29)..(3229)  
US-09-667-298-66

Query Match 90.0%; Score 2765; DB 26; Length 3260;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3065; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TGAATTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTATTATAA 61  
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QY 62 AGCAATACAGATGACCTATTGTATGGAATGTTCTGAAATCGGAATCGGAAGAATGAACATCA 121  
Db 216 AGCAATACAGATGACCTATTGTATGGAATGTTCTGAAATCGGAAGAATGAACATCA 275  
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Db 756 TCTTCTCCCTCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCC 815  
QY 662 TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 721  
Db 816 TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 875  
QY 722 AGAGGGTCTTTCTTCTTGTGCTGCTACAAATGAATTCAGAGCCCAAGAACTGCCAGAA 781  
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Db 876 AGAGGGTCTTTCTTCTTGTATGGCTACAATGAATTCAGAGCCCAAGAACTGCCAGAA 935  
QY 782 TCGAAGCCCTGATAAAGGAAAAACCCCGCTTCAAGAAATCGTCTCATCGTCAACCACTACCA 841  
Db 936 TCGAAGCCCTGATAAAGGAAAAACCCCGCTTCAAGAAATCGTCTCATCGTCAACCACTACCA 995  
QY 842 CTGAGTGCCTTGAGGCACATACGGCAGTTTGGTGCCCTGACTGTGAGGTGGGGATATGA 901  
Db 996 CTGAGTGCCTTGAGGCACATACGGCAGTTTGGTGCCCTGACTGTGAGGTGGGGATATGA 1055  
QY 902 CAGAAGACAGGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 961  
Db 1056 CAGAAGACAGGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 1115  
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Db 1236 CGCTGTTCATACCTTCTATGATCTGTGTATACAGAAAAACAAACACAAATAAAGGTG 1295  
QY 1142 TGGCTGCAAGTGAATTCGAGGCTCGACCACTGTGAGACCTAGCTGTGGAGGTG 1201  
Db 1296 TGGCTGCAAGTGAATTCGAGGCTCGACCACTGTGAGACCTAGCTGTGGAGGTG 1355  
QY 1202 TGTCTCCCAACAAGTTTGAATTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGCC 1261  
Db 1356 TGTCTCCCAACAAGTTTGAATTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGCC 1415  
QY 1262 TGGTGAACATGGGCTCTCTGTAAATATACAGCTCAAAGTTTCAAGCCAAAGTATTAAT 1321  
Db 1416 TGGTGAACATGGGCTCTCTGTAAATATACAGCTCAAAGTTTCAAGCCAAAGTATTAAT 1475  
QY 1322 TCTTTTCAAGTTCATCCAGGAGTACACAGCAGCAAGACCTCAGCAGTTTATTGACGT 1381  
Db 1476 TCTTTTCAAGTTCATCCAGGAGTACACAGCAGCAAGACCTCAGCAGTTTATTGACGT 1535  
QY 1382 CTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTTGCAGAAAATGGTTTCCATTT 1441  
Db 1536 CTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTTGCAGAAAATGGTTTCCATTT 1595  
QY 1442 CGACATTTACATCCATTTATAGAGCCTGTCCGGTACACCTGTGGGTCTATCTGTGGAAG 1501  
Db 1596 CGACATTTACATCCATTTATAGAGCCTGTCCGGTACACCTGTGGGTCTATCTGTGGAAG 1655  
QY 1502 CCACAGGCTGTATTGAAGCCTCCGACAGTGTATCAACAGCGCTGCTTCTCGGAC 1561  
Db 1656 CCACAGGCTGTATTGAAGCCTCCGACAGTGTATCAACAGCGCTGCTTCTCGGAC 1715  
QY 1562 TTTTCCATTCGCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1621  
Db 1716 TTTTCCATTCGCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1775  
QY 1622 CTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681  
Db 1776 CTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1835  
QY 1682 TATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAAG 1741  
Db 1836 TATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAAG 1895  
QY 1742 GTAAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAAAC 1801  
Db 1896 GTAAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAAAC 1955  
QY 1802 ATTTGCCCAATTTGCAAGTGTCTGGACATTCATTAACATGGACATTTTATGGGGAGCTA 1861  
Db 1956 ATTTGCCCAATTTGCAAGTGTCTGGACATTCATTAACATGGGCTTTTATGGGGAGCTA 2015  
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QY 1862 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGAGTGGGAATCCACATCGAAGAGGCCCCAG 1921
Db 2016 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGAGTGGGAATCCACATCGAAGAGGCCCCAG 2075
QY 1922 AAACCTACATCCCGAGGCGGTGATCTTTCTTCAACTGGAAGCAGGAAATTCAGGA 1981
Db 2076 AAACCTACATCCCGAGGCGGTGATCTTTCTTCAACTGGAAGCAGGAAATTCAGGA 2135
QY 1982 CTCGAGGTACACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTGG 2041
Db 2136 CTCGAGGTACACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTGG 2195
QY 2042 GGAATAATTCAGCTCTGCACAAGCCTCAGGCTGCAATAAAGAGATGCTGCTGGTGG 2101
Db 2196 GGAATAATTCAGCTCTGCACAAGCCTCAGGCTGCAATAAAGAGATGCTGCTGGTGG 2255
QY 2102 CTGGAAGCCTCAGTTGGTCCCTCAGCACCTGTAAAGCAATTTATCTCTCATGTTGGAG 2161
Db 2256 CTGGAAGCCTCAGTTGGTCCCTCAGCACCTGTAAAGCAATTTATCTCTCATGTTGGAG 2315
QY 2162 CCAGTCCCTCACCATAGAAGATGAGGCGCATCATCTCTTAACAACCTGAAACCT 2221
Db 2316 CCAGTCCCTCACCATAGAAGATGAGGCGCATCATCTCTTAACAACCTGAAACCT 2375
QY 2222 TCAGTATTCATCACTACAGATCAACGCTGCCGGTGGTCTGACTGACAGCTTGGGTA 2281
Db 2376 TCAGTATTCATCACTACAGATCAACGCTGCCGGTGGTCTGACTGACAGCTTGGGTA 2435
QY 2282 ACTTGAAGAACCTTACAAGCTCATTAATGGATPAACATAAAGATGAATGAAGAAGATGCTA 2341
Db 2436 ACTTGAAGAACCTTACAAGCTCATTAATGGATPAACATAAAGATGAATGAAGAAGATGCTA 2495
QY 2342 TAAACTAGCTGAAGGCTGAAACCTGAAGAAGATGTTTATTTATTTGACCCACT 2401
Db 2496 TAAACTAGCTGAAGGCTGAAACCTGAAGAAGATGTTTATTTATTTGACCCACT 2555
QY 2402 TCTCTGACATTTGGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAAGTGAACCTGTG 2461
Db 2556 TCTCTGACATTTGGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAAGTGAACCTGTG 2615
QY 2462 ACCTTGAAGAAATTCAAATTAAGTCTCTGCTGCTGTCGCAAAATGCAAGTGAACCTGTG 2521
Db 2616 ACCTTGAAGAAATTCAAATTAAGTCTCTGCTGCTGTCGCAAAATGCAAGTGAACCTGTG 2675
QY 2522 CTCAGAATCTTCACAAATTTGGTCAAACTGAGCATTTTGATTTATCAGAAAATTAACCTGG 2581
Db 2676 CTCAGAATCTTCACAAATTTGGTCAAACTGAGCATTTTGATTTATCAGAAAATTAACCTGG 2735
QY 2582 AAAAGATGGAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACGTGCTAGAACAGC 2641
Db 2736 AAAAGATGGAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACGTGCTAGAACAGC 2795
QY 2642 TCACCGCACTGATGTCGCCCTGGGGCTGTGACGTGCAAGGCGCTGACAGCCTGTTGA 2701
Db 2796 TCACCGCACTGATGTCGCCCTGGGGCTGTGACGTGCAAGGCGCTGACAGCCTGTTGA 2855
QY 2702 AACATTTGGAGGAGTCCCAACACTCGTCAAGCTTTGGGTTGAAAACTGGAGACTCACAG 2761
Db 2856 AACATTTGGAGGAGTCCCAACACTCGTCAAGCTTTGGGTTGAAAACTGGAGACTCACAG 2915
QY 2762 ATACAGAGATTAAGATTTTATGATGATTTTGGAAAAACCCCTCTGAAAACTTCCAGC 2821
Db 2916 ATACAGAGATTAAGATTTTATGATGATTTTGGAAAAACCCCTCTGAAAACTTCCAGC 2975
QY 2822 AGTTGAATTTGGCGGAATTCGTGTGACAGTGAATGGCTTCCCTTCATGGGTGAT 2881
Db 2976 AGTTGAATTTGGCGGAATTCGTGTGACAGTGAATGGCTTCCCTTCATGGGTGAT 3035
QY 2882 TTGAGAATCTTAAGCAATTAAGTGTGTTTTTTGACTTTTAGTAAAGAAATTTTACCTGATC 2941
Db 3036 TTGAGAATCTTAAGCAATTAAGTGTGTTTTTTGACTTTTAGTAAAGAAATTTTACCTGATC 3095
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QY 2942 CAGCATTAGTCAGAAAACTTAGCCAAGTGTATATCAAGTTAACTTTTCGCAAGAGCTA 3001
Db 3096 CAGCATTAGTCAGAAAACTTAGCCAAGTGTATATCAAGTTAACTTTTCGCAAGAGCTA 3155
QY 3002 GGCTTGTGGGTGGCAATTTGATGATGATCTCAGTGTGTTATTACAGTGCTTTTAAAC 3061
Db 3156 GGCTTGTGGGTGGCAATTTGATGATGATCTCAGTGTGTTATTACAGTGCTTTTAAAC 3215
QY 3062 TAGTAACTGCT 3072
Db 3216 TAGTAACTGCT 3226

RESULT 18
US-09-697-089-6
; Sequence 6, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Burbin, John
; APPLICANT: Jobison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT APPLICANT NUMBER: US/09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-697-089-6

Query Match 85.7%; Score 2634; DB 27; Length 3612;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCCTTTTCATCAGACATCAGAAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 322
Db 734 GTCCTTTTCATCAGACATCAGAAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 793
QY 323 TGTACCTACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATTTGACATTTAT 382
Db 794 TGTACCTACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATTTGACATTTAT 853
QY 383 TTAACCTTGAAGAAGCACTTCACAGAACCTGCTGTGGAGGAGGACCAACACCATCACC 442
Db 854 TTAACCTTGAAGAAGCACTTCACAGAACCTGCTGTGGAGGAGGACCAACACCATCACC 913
QY 443 GCGTGGTGCAGTGAACCTGAAATGGCTCCTGTCAGAGCTTTCAGAGCCCTGCATCAT 502
Db 914 GCGTGGTGCAGTGAACCTGAAATGGCTCCTGTCAGAGCTTTCAGAGCCCTGCATCAT 973
QY 503 AAGGGGATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGCT 562
Db 974 AAGGGGATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGCT 1033
QY 563 CCGGAAAATGCAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTCTCCGTCTCAGCAGG 622
Db 1034 CCGGAAAATGCAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTCTCCGTCTCAGCAGG 1093
QY 623 CCAGGGTGGACTTTTGAACCCCTGTCGATCAACTCTCGATATACCTGGCAACAATCA 682
Db 1094 CCAGGGTGGACTTTTGAACCCCTGTCGATCAACTCTCGATATACCTGGCAACAATCA 1153
QY 683 GGAAGCAACATTCATGCCATGCTGCTGAAGCTGGCAGAGGCTTTCTTCTCTCTG 742
Db 1154 GGAAGCAACATTCATGCCATGCTGCTGAAGCTGGCAGAGGCTTTCTTCTCTCTG 1213
QY 743 ATGGCTAACATGAATTAAGCCCAAGCTGCCAGAAATCGAAGCCCTGATAAAGGAA 802
Db 1214 ATGGCTAACATGAATTAAGCCCAAGCTGCCAGAAATCGAAGCCCTGATAAAGGAA 1273
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Qy	803	ACCACCGCTTCAAGAAACATGGTCATGTCACCACTACCACCTGAGTGCCTGAGGCACATAC	862
Db	1274	ACCACCGCTTCAAGAAACATGGTCATGTCACCACTACCACCTGAGTGCCTGAGGCACATAC	1333
Qy	863	GGCAGTTGGTGGCCCTGACTGCTGAGGTGGGGATATACACAGAAGACAGCCGCCAGGCTC	922
Db	1334	GGCAGTTGGTGGCCCTGACTGCTGAGGTGGGGATATACACAGAAGACAGCCGCCAGGCTC	1393
Qy	923	TCATCCGAGAAGTGCATCAAGGAGCTTGCCTGAAGGCTTGTGTCCAAAATTCAGAAAT	982
Db	1394	TCATCCGAGAAGTGCATCAAGGAGCTTGCCTGAAGGCTTGTGTCCAAAATTCAGAAAT	1453
Qy	983	CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGGTCATCACTTGTGCAATCC	1042
Db	1454	CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGGTCATCACTTGTGCAATCC	1513
Qy	1043	AGATGGGTGAAGTGAGTTCCCACTCTCACACACAACCAACGCTGTTCATACCTTCTATG	1102
Db	1514	AGATGGGTGAAGTGAGTTCCCACTCTCACACACAACCAACGCTGTTCATACCTTCTATG	1573
Qy	1103	ATCTGTTGATACAGAAAAACAACACATAAAGGTGTGGCTGCAAGTGACTTCATTC	1162
Db	1574	ATCTGTTGATACAGAAAAACAACACATAAAGGTGTGGCTGCAAGTGACTTCATTC	1633
Qy	1163	GGAGCCTGGACACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCACAAGTTTGATT	1222
Db	1634	GGAGCCTGGACACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCACAAGTTTGATT	1693
Qy	1223	TCGAACCTGCAGGATGTGTCAGCGTGAATGAGGATGTCTCTGTGACAACTGGGCTCTCT	1282
Db	1694	TCGAACCTGCAGGATGTGTCAGCGTGAATGAGGATGTCTCTGTGACAACTGGGCTCTCT	1753
Qy	1283	GTAATATACAGCTCAAGGTTCAAGCCAAAGATATAAATCTTTCAACAAGTCATTCAGG	1342
Db	1754	GTAATATACAGCTCAAGGTTCAAGCCAAAGATATAAATCTTTCAACAAGTCATTCAGG	1813
Qy	1343	AGTACACAGCAGCAGCAAGACACTCACAGTTTATTCACCTCTCATGACCCAGAGAGGTGA	1402
Db	1814	AGTACACAGCAGCAGCAGCAGCAGCTCAGCAGTTTATTCACCTCTCATGACCCAGAGAGGTGA	1873
Qy	1403	CCAAGGGGAATGGTTACTTTCGAAAAATGGTTTCCATTTTCGACATTCATCCACTTATA	1462
Db	1874	CCAAGGGGAATGGTTACTTTCGAAAAATGGTTTCCATTTTCGACATTCATCCACTTATA	1933
Qy	1463	GCAGCCTGCTCCGGTACACGCTGGGTCACTGTGGAAGCACACAGGGCTGTTATGAAGC	1522
Db	1934	GCAGCCTGCTCCGGTACACGCTGGGTCACTGTGGAAGCACACAGGGCTGTTATGAAGC	1993
Qy	1523	ACCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGACTTTTCATTCGCCAAGAGGCTC	1582
Db	1994	ACCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGACTTTTCATTCGCCAAGAGGCTC	2053
Qy	1583	TCTGGAGACAGGAATCTTTGCAAGGTGTGAAAAACCAACCACTGAGCAAGAAATCTCGAAG	1642
Db	2054	TCTGGAGACAGGAATCTTTGCAAGGTGTGAAAAACCAACCACTGAGCAAGAAATCTCGAAG	2113
Qy	1643	CCATAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA	1702
Db	2114	CCATAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA	2173
Qy	1703	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT	1762
Db	2174	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT	2233
Qy	1763	CAGGAAACATCCCCGATTACTTATTGACTTTCTTTGAACTTTGCCAATTTGCCAAGT	1822
Db	2234	CAGGAAACATCCCCGATTACTTATTGACTTTCTTTGAACTTTGCCAATTTGCCAAGT	2293
Qy	1823	CTCTGAGCTTCATTAACCTGGACTTTTATGGGGGAGCTATGGCTTCATGGGAAAAGCTG	1882
Db	2294	CCCTGAGCTTCATTAACCTGGACTTTTATGGGGGAGCTATGGCTTCATGGGAAAAGCTG	2353

Qy	1883	CAGAAGACACAGGTGGAATCCACATGGAAAGAGGCCCCAGAAACCTTACATTTCCCAGCAGGG	194
Db	2354	CAGAAGACACAGGTGGAATCCACATGGAAAGAGGCCCCAGAAACCTTACATTTCCCAGCAGGG	2413
Qy	1943	CTGTATCTTTGTTCCTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGGG	2002
Db	2414	CTGTATCTTTGTTCCTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGGG	2473
Qy	2003	ATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTCGGGGAAAAATATTCAGCTCTGCCA	2062
Db	2474	ATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTCGGGGAAAAATATTCAGCTCTGCCA	2533
Qy	2063	CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC	2122
Db	2534	CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC	2593
Qy	2123	TCAGCACTCTAAGACATTTATCTCTCATGGTGGAGCCAGTCCCCTCACCATAGAG	2182
Db	2594	TCAGCACTCTAAGACATTTATCTCTCATGGTGGAGCCAGTCCCCTCACCATAGAG	2653
Qy	2183	ATGAGAGGCACATCACATCTGTAAACAAACCTTGAAACCTTGGAGTTTCATGACCTACAGA	2242
Db	2654	ATGAGAGGCACATCACATCTGTGTAAACAAACCTTGAAACCTTGGAGTTTCATGACCTACAGA	2713
Qy	2243	ATCAACGGCTGCCGGTGGTCTGACTGACGTGAGCGTGGGTAACTTGAAGAACCTTACAAAGC	2302
Db	2714	ATCAACGGCTGCCGGTGGTCTGACTGACGTGAGCGTGGGTAACTTGAAGAACCTTACAAAGC	2773
Qy	2303	TCATAATGGATACATAAAGATCAATGAAGAGAGTGCATAAACCTAGCTGAAGGCTCGA	2362
Db	2774	TCATAATGGATACATAAAGATCAATGAAGAGAGTGCATAAACCTAGCTGAAGGCTCGA	2833
Qy	2363	AAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACCCACCTTGTCTGACATTTGGAGAGGAA	2422
Db	2834	AAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACCCACCTTGTCTGACATTTGGAGAGGAA	2893
Qy	2423	TGGATTACATAGTCAAGTCTCTCTCAAGTGAACCCGTGACCTTGAAGAAATTCAAATTAG	2482
Db	2894	TGGATTACATAGTCAAGTCTCTCTCAAGTGAACCCGTGACCTTGAAGAAATTCAAATTAG	2953
Qy	2483	TCTCCTGCTGTTGCTGCAAAATGACGTGAAATCCTAGCTCAGAACTTTCACAAATTTGG	2542
Db	2954	TCTCCTGCTGTTGCTGCAAAATGACGTGAAATCCTAGCTCAGAACTTTCACAAATTTGG	3013
Qy	2543	TCAAACCTGAGCATTTCTGATTTATCAGAAAAATACCTGGAAGAGATGGAATGAAGCTC	2602
Db	3014	TCAAACCTGAGCATTTCTGATTTATCAGAAAAATACCTGGAAGAGATGGAATGAAGCTC	3073
Qy	2603	TTCAATGAACCTGATCGACAGATGAAGTGTCTAGAACAGCTCACCCGACTGATGTGCCCT	2662
Db	3074	TTCAATGAACCTGATCGACAGATGAAGTGTCTAGAACAGCTCACCCGACTGATGTGCCCT	3133
Qy	2663	GGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGAGGTCCTCCAC	2722
Db	3134	GGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGAGGTCCTCCAC	3193
Qy	2723	AACTCTGCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGAATTTTAG	2782
Db	3194	AACTCTGCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGAATTTTAG	3253
Qy	2783	GTGCATTTTTTGGAAAGAACCCCTCTGAAAACTTCCAGCGTTGAATTTGGCGGGAATC	2842
Db	3254	GTGCATTTTTTGGAAAGAACCCCTCTGAAAACTTCCAGCGTTGAATTTGGCGGGAATC	3313
Qy	2843	GTGTGACAGTGTGATGGCTTGCCTTTCATGGGTGTATTTGAGAACTCTTAAGCAATTTAG	2902
Db	3314	GTGTGACAGTGTGATGGCTTGCCTTTCATGGGTGTATTTGAGAACTCTTAAGCAATTTAG	3373
Qy	2903	TGTTTTTTTGACTTTTAGTACTAAAGAAATTTCTACCTGATGTCACGATTTAGTCAGAAACTTA	2962
Db	3374	TGTTTTTTTGACTTTTAGTACTAAAGAAATTTCTACCTGATGTCACGATTTAGTCAGAAACTTA	3433
Qy	2963	GCCAAGTGTTATCCAAAGTTAACTTTTTTCTGCAAGAAAGCTAGGCTGTTGGGTGGCAATTTG	3022

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Db 3434 GCCAAGTGTATCCAAAGTAACTTTTCGCAAGAGCTAGGCTTGTGGGGGCAATTG 3493  
Qy 3023 ATGATGATGATCTCAGTGTATTACAG 3049  
Db 3494 ATGATGATGATCTCAGTGTATTACAG 3520

RESULT 19  
US-09-841-739-6  
; Sequence 6, Application US/09841739  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 3612  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-6

Query Match 85.7%; Score 2634; DB 32; Length 3612;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 263 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGAGGATTTGGCTCAGGATTTAAAGGACT 322  
Db 734 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGAGGATTTGGCTCAGGATTTAAAGGACT 793  
Qy 323 TGTACATACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATATT 382  
Db 794 TGTACATACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATATT 853  
Qy 383 TTAACCTTCAAAAGACCTTACAGAACCTGCTGTGGAGGAAGGACCAACACCATCAC 442  
Db 854 TTAACCTTCAAAAGACCTTACAGAACCTGCTGTGGAGGAAGGACCAACACCATCAC 913  
Qy 443 GCGTGGAGCAGCTGACCTGAATGGCTCTCTGAGGCTCTTTCAGAGCCCTGCATCAT 502  
Db 914 GCGTGGAGCAGCTGACCTGAATGGCTCTCTGAGGCTCTTTCAGAGCCCTGCATCAT 973  
Qy 503 AAGGGATCTGGCAAGGAGTCCACTCTGCTGCGAGCGCATTTGCCATGCTCTGGGCT 562  
Db 974 AAGGGATCTGGCAAGGAGTCCACTCTGCTGCGAGGATTTGCCATGCTCTGGGCT 1033  
Qy 563 CCGGAAGTGAAGCTCTGACCAAGTTCAAATTCGCTTCTTCCGCTCTCAGCAGG 622  
Db 1034 CCGGAAGTGAAGCTCTGACCAAGTTCAAATTCGCTTCTTCCGCTCTCAGCAGG 1093  
Qy 623 CCCAGGTTGAGCTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCAATCA 682  
Db 1094 CCCAGGTTGAGCTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCAATCA 1153  
Qy 683 GGAAGCAGACATTCATGCGCATGCTGTGAAGCTGCGGCGAGGTTCTTTTCTCTT 742  
Db 1154 GGAAGCAGACATTCATGCGCATGCTGTGAAGCTGCGGCGAGGTTCTTTTCTCTT 1213  
Qy 743 ATGGCTACAATGAATTCGAAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAA 802  
Db 1214 ATGGCTACAATGAATTCGAAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAA 1273  
Qy 803 ACCACCGTTCAAGAACATGTCATGTCACCACTACCACTGAGTGGCTGAGGCACATAC 862  
Db 1274 ACCACCGTTCAAGAACATGTCATGTCACCACTACCACTGAGTGGCTGAGGCACATAC 1333

Qy 863 GGCAGTTTGTGGCTGACTCTGAGGTGGGGATATACAGAGACAGCGCCAGGCTC 922  
Db 1334 GGCAGTTTGTGGCTGACTCTGAGGTGGGGATATACAGAGACAGCGCCAGGCTC 1393  
Qy 923 TCATC TGAGAAAGTGTGATCAAGGAGCTTGTGAAGGCTTGTGCTCCAAATTCAGAAAT 982  
Db 1394 TCATC TGAGAAAGTGTGATCAAGGAGCTTGTGAAGGCTTGTGCTCCAAATTCAGAAAT 1453  
Qy 983 CCAGG TCGTTGAGGAATCTCATGAAGACCCCTCTCTTTTGTGGTTCATCATCTTGTGCAATCC 1042  
Db 1454 CCAGG TCGTTGAGGAATCTCATGAAGACCCCTCTCTTTTGTGGTTCATCATCTTGTGCAATCC 1513  
Qy 1043 AGATG TGTGAAGTGTGAGTTCACACTCTCACACACAAACAGCTGTTCATACCTTCTATG 1102  
Db 1514 AGATG TGTGAAGTGTGAGTTCACACTCTCACACACAAACAGCTGTTCATACCTTCTATG 1573  
Qy 1103 ATCTG TGCATACAGAAAACAAACACAAACATAAAGGTGTGCTGCAAGTGCATTCATTC 1162  
Db 1574 ATCTG TGCATACAGAAAACAAACACAAACATAAAGGTGTGCTGCAAGTGCATTCATTC 1633  
Qy 1163 GGAGC TGGACACACTGTGGAGACCTAGCTCTGGAGGCTGTGTTCTCCCAAGTTTGAT 1222  
Db 1634 GGAGC TGGACACACTGTGGAGACCTAGCTCTGGAGGCTGTGTTCTCCCAAGTTTGAT 1693  
Qy 1223 TCGAAC TGCAGGATGTGCCAGCGTGAATGAGGATGTCCTGCTGACAACTGGGCTCTCT 1282  
Db 1694 TCGAAC TGCAGGATGTGCCAGCGTGAATGAGGATGTCCTGCTGACAACTGGGCTCTCT 1753  
Qy 1283 GTAAATATACAGCTCAAAGTTCAAGCCAAAGTATAAATCTTTTCAACAGTCATTCACAG 1342  
Db 1754 GTAAATATACAGCTCAAAGTTCAAGCCAAAGTATAAATCTTTTCAACAGTCATTCACAG 1813  
Qy 1343 AGTACA TAGCAGGAGGAGACTCAGCAGTTTATTGACCTCTCATGAGCAGAGGAGTGA 1402  
Db 1814 AGTACA TAGCAGGAGGAGACTCAGCAGTTTATTGACCTCTCATGAGCAGAGGAGTGA 1873  
Qy 1403 CCAAGG TGAATGGTTACTTTGAGAAAATGGTTTCCATTTGAGACATTCATCCACTTATA 1462  
Db 1874 CCAAGG TGAATGGTTACTTTGAGAAAATGGTTTCCATTTGAGACATTCATCCACTTATA 1933  
Qy 1463 GCAGCC TGTCCCGGTACACCTGTGGGTCTCTGTGGAAGCCACAGGCTGTGTTGAAGC 1522  
Db 1934 GCAGCC TGTCCCGGTACACCTGTGGGTCTCTGTGGAAGCCACAGGCTGTGTTGAAGC 1993  
Qy 1523 ACCTCG TAGCAGTCTATCAACACGCTGCCCTCTCGGACTTTCCATCGCCAGAGGCTC 1582  
Db 1994 ACCTCG TAGCAGTCTATCAACACGCTGCCCTCTCGGACTTTCCATCGCCAGAGGCTC 2053  
Qy 1583 TCTGGATACAGGAATCTTGCAAAAGTGTGAAGAACACACACTGAGCAGAAAATTCGAAAG 1642  
Db 2054 TCTGGATACAGGAATCTTGCAAAAGTGTGAAGAACACACACTGAGCAGAAAATTCGAAAG 2113  
Qy 1643 CCATTAATCATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702  
Db 2114 CCATTAATCATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 2173  
Qy 1703 AATCAG CCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762  
Db 2174 AATCAG CCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 2233  
Qy 1763 CAGGGAATATCCCCGATTAATTTGACTTCTTTTGAACATTTGCCCAATTTGTGCAAGTG 1822  
Db 2234 CAGGGAATATCCCCGATTAATTTGACTTCTTTTGAACATTTGCCCAATTTGTGCAAGTG 2293  
Qy 1823 CTCTGGA TTTCAATTAAGCTGACCTTTTATGGGGAGCTGATGGCTTCATGGGAAAAGGCTG 1882  
Db 2294 CCCTGGA TTTCAATTAAGCTGACCTTTTATGGGGAGCTGATGGCTTCATGGGAAAAGGCTG 2353  
Qy 1883 CAGAAGATACAGGTTGAATCCACATGGAAGAGCCCAAGAACCTACATTTCCAGCAGG 1942  
Db 2354 CAGAAGATACAGGTTGAATCCACATGGAAGAGCCCAAGAACCTACATTTCCAGCAGG 2413  
Qy 1943 CTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGACTCTGAGGCTCACATCCGGG 2002

|||||  
Db 2414 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTCGAGGTCAACATCCGGG 2473  
QY 2003 ATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTCGGGGAAATATTCAGCTCTGCCA 2062  
Db 2474 ATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTCGGGGAAATATTCAGCTCTGCCA 2533  
QY 2063 CAAGCCTCAGGCTGCAATTAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTGGTCC 2122  
Db 2534 CAAGCCTCAGGCTGCAATTAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTGGTCC 2593  
QY 2123 TCAGCAGCTGTGAAGCAATTTATCTCATGTGTGGTGAAGCCAGTCCCTCACCATAGAG 2182  
Db 2594 TCAGCAGCTGTGAAGCAATTTATCTCATGTGTGGTGAAGCCAGTCCCTCACCATAGAG 2653  
QY 2183 ATGAGAGGCACATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACAGA 2242  
Db 2654 ATGAGAGGCACATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACAGA 2713  
QY 2243 ATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGTAACTTGAAGAACCTTCAAAAGC 2302  
Db 2714 ATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGTAACTTGAAGAACCTTCAAAAGC 2773  
QY 2303 TCATATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGCCCTGA 2362  
Db 2774 TCATATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGCCCTGA 2833  
QY 2363 AAAACCTGAAGAGATGTTTATTTATTTGACCTTGTGACCTTGTCTGACATTTGAGAGGNA 2422  
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QY 2423 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCTGTGACCTTGAAGAAATTCATATAG 2482  
Db 2894 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCTGTGACCTTGAAGAAATTCATATAG 2953  
QY 2483 TCTCTGCTGCTGTGCAAAATGCAAGTGAATCCTAGCTCAGATTTTCAATTTGG 2542  
Db 2954 TCTCTGCTGCTGTGCAAAATGCAAGTGAATCCTAGCTCAGATTTTCAATTTGG 3013  
QY 2543 TCMAACTGAGCATCTTGATTTATCAGAAATTTACCTGAAAAAGATGGAATGAAGTC 2602  
Db 3014 TCMAACTGAGCATCTTGATTTATCAGAAATTTACCTGAAAAAGATGGAATGAAGTC 3073  
QY 2603 TTTCATGAATGATGACAGGATGAACGTGTAGAACAGCTCACCGCATGTGCTGCCCT 2662  
Db 3074 TTTCATGAATGATGACAGGATGAACGTGTAGAACAGCTCACCGCATGTGCTGCCCT 3133  
QY 2663 GGGGTGTGACGTGAAGCAGCCTGAGAGCCTGTGAAACATTTGGAGGAGTCCAC 2722  
Db 3134 GGGGTGTGACGTGAAGCAGCCTGAGAGCCTGTGAAACATTTGGAGGAGTCCAC 3193  
QY 2723 AACTGCTCAAGCTTGGTTGAAAACTGGAGACTCACAGATACAGATTAGAATTTAG 2782  
Db 3194 AACTGCTCAAGCTTGGTTGAAAACTGGAGACTCACAGATACAGATTAGAATTTAG 3253  
QY 2783 GTGCATTTTTTGGAAAGAACCTCTGAAAACTCCAGCAGTTGAATTTGGGGGAAATC 2842  
Db 3254 GTGCATTTTTTGGAAAGAACCTCTGAAAACTCCAGCAGTTGAATTTGGGGGAAATC 3313  
QY 2843 GTGTGAGCAGTATGATGGCTTGCTTCAATGGGTGTATTTGAGATCTTAAAGCAATTAG 2902  
Db 3314 GTGTGAGCAGTATGATGGCTTGCTTCAATGGGTGTATTTGAGATCTTAAAGCAATTAG 3373  
QY 2903 TGTTTTTGACATTTAGTACTAAGATTTCTTACCTGATCCAGCATAGTCAGAAACTTA 2962  
Db 3374 TGTTTTTGACATTTAGTACTAAGATTTCTTACCTGATCCAGCATAGTCAGAAACTTA 3433  
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATTTG 3022  
Db 3434 GCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATTTG 3493  
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049  
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Db 3494 ATGATGATGATCTCAGTGTATTACAG 3520  
RESULT 20  
PCT-US00-29643-4  
; Sequence 4, Application PC/TUS0029643  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-136W01  
; CURRENT APPLICATION NUMBER: PCT/US00/29643  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 3615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3612)  
PCT-US00-29643-4  
Query Match 85.7%; Score 2634; DB 1; Length 3615;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 263 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322  
Db 734 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 793  
QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATATT 382  
Db 794 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATATT 853  
QY 383 TTAACCTTGAAGAGCACCCTTACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACC 442  
Db 854 TTAACCTTGAAGAGCACCCTTACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACC 913  
QY 443 GCGTGAGCAGCTGACCCTTGAATGGCTCTCTCAGAGCTCTTCAGAGCCCTGCATCATTTG 502  
Db 914 GCGTGAGCAGCTGACCCTTGAATGGCTCTCTCAGAGCTCTTCAGAGCCCTGCATCATTTG 973  
QY 503 AAGGGGAATCTGGCAAGCAAGTCCACTCTCTGCGAGGCGATTTGCCATGCTCTGGGGCT 562  
Db 974 AAGGGGAATCTGGCAAGCAAGTCCACTCTCTGCGAGGCAATTTGCCATGCTCTGGGGCT 1033  
QY 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTTCCCTCCTCAGCAGG 622  
Db 1034 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTTCCCTCCTCAGCAGG 1093  
QY 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATFACCTGCACAATCA 682  
Db 1094 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATFACCTGCACAATCA 1153  
QY 683 GGAAGCAGACATTCATGCGCATGTGTGAAGCTGCGGAGAGGGTCTTTTCTCTCTTG 742  
Db 1154 GGAAGCAGACATTCATGCGCATGTGTGAAGCTGCGGAGAGGGTCTTTTCTCTCTTG 1213  
QY 743 ATGGCTACAAATTCAGCCCAAGACTGCCAGAAATCAAGCCCTGATTAAGGAA 802  
Db 1214 ATGGCTACAAATTCAGCCCAAGACTGCCAGAAATCAAGCCCTGATTAAGGAA 1273  
QY 803 ACCACCGCTTCAAGAACATGTGCTCACCACCTACCACTCAGTGCCTTGAGGACATAC 862  
Db 1274 ACCACCGCTTCAAGAACATGTGCTCACCACCTACCACTCAGTGCCTTGAGGACATAC 1333  
QY 863 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAAGACACGCCGCCAGCTC 922  
Db 1334 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAAGACACGCCGCCAGCTC 1393



Qy	923	TCATCCGAGAAGTGTGATCTAAGGAGCTGTGCTGAAGGCTGTGCTCTCCAAATTCAGAAAT	982
Db	1394	TCATCCGAGAAGTGTGATCAAGGAGCTGTCTGAAGGCTGTGCTCTCCAAATTCAGAAAT	1453
Qy	983	CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGTGTCATCACATTGTGCAATCC	1042
Db	1454	CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGTGTCATCACATTGTGCAATCC	1513
Qy	1043	AGATGGGTGAAGTGAAGTTCCTCTCACACAAACAACGCTGTTCATACCTTCTTATG	1102
Db	1514	AGATGGGTGAAGTGAAGTTCCTCTCACACAAACAACGCTGTTCATACCTTCTTATG	1573
Qy	1103	ATCTGTTGATACAGAAAAACAACAACAATAAAGGTGTGGCTGCAAGTCACTTCATTC	1162
Db	1574	ATCTGTTGATACAGAAAAACAACAACAATAAAGGTGTGGCTGCAAGTCACTTCATTC	1633
Qy	1163	GGAGCCTGGACCACTGTGGAGACCTTAGCTCTGGAGGGTGTGTTCTCCACAAGTTTGATT	1222
Db	1634	GGAGCCTGGACCACTGTGGAGACCTTAGCTCTGGAGGGTGTGTTCTCCACAAGTTTGATT	1693
Qy	1223	TCGAAGTCGAGGATGTGCCAGGTGAATGAGGATGTCCCTGCTGACAACTGGGCTCCTCT	1282
Db	1694	TCGAAGTCGAGGATGTGCCAGGTGAATGAGGATGTCCCTGCTGACAACTGGGCTCCTCT	1753
Qy	1283	GTAATATACAGCTCAAGAGTTCAAGCCAAAGATATAAATCTTTACAAAGTCATTCAGG	1342
Db	1754	GTAATATACAGCTCAAGAGTTCAAGCCAAAGATATAAATCTTTACAAAGTCATTCAGG	1813
Qy	1343	AGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCATGAGCGACGAGGAGTGA	1402
Db	1814	AGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCATGAGCGACGAGGAGTGA	1873
Qy	1403	CCAAGGGGAATGTTACTTTCGAAAAATGGTTTCCATTTCGAGACATACATCCACTTATA	1462
Db	1874	CCAAGGGGAATGTTACTTTCGAAAAATGGTTTCCATTTCGAGACATACATCCACTTATA	1933
Qy	1463	GCAGCTGTCCGGTACACTGTGGGTGATCTGTGGAGCCACACAGGCGTGTATTGAGC	1522
Db	1934	GCAGCTGTCCGGTACACTGTGGGTGATCTGTGGAGCCACACAGGCGTGTATTGAGC	1993
Qy	1523	ACCTCGCAGCAGTGTATCAACAGGCGTGCCTTCTCGGACTTTCGATCCGCAAGAGGCGTC	1582
Db	1994	ACCTCGCAGCAGTGTATCAACAGGCGTGCCTTCTCGGACTTTCGATCCGCAAGAGGCGTC	2053
Qy	1583	TCGAGAGACAGGAATCTTTGCAAAAGTGTGA AAAACACACACTGAGCAGAGAAATTCGAAAG	1642
Db	2054	TCGAGAGACAGGAATCTTTGCAAAAGTGTGA AAAACACACACTGAGCAGAGAAATTCGAAAG	2113
Qy	1643	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA	1702
Db	2114	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA	2173
Qy	1703	AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCACT	1762
Db	2174	AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCACT	2233
Qy	1763	CAGGGAACATCCCCGATTAATTTATTTGACTCTTTTGAACATTTGCCCAATTTGTCGAAGTG	1822
Db	2234	CAGGGAACATCCCCGATTAATTTATTTGACTCTTTTGAACATTTGCCCAATTTGTCGAAGTG	2293
Qy	1823	CTCTGCACTTCATTAAGCTGGACTTTTATGGGGAGCTATTGGCTTCATGGGAAAAGCGTG	1882
Db	2294	CCCTGGACTTCATTAAGCTGGACTTTTATGGGGAGCTATTGGCTTCATGGGAAAAGCGTG	2353
Qy	1883	CAGAGACACAGGTGGAAATCCACATGGAGAGGCCCCAGAAACCTTACATTTCCCAGCAGGG	1942
Db	2354	CAGAGACACAGGTGGAAATCCACATGGAGAGGCCCCAGAAACCTTACATTTCCCAGCAGGG	2413
Qy	1943	CTGTATCTTTGTTCTTCAACTGGAGCAGGAATTCAGGACTCTCGAGGTCACTCCGCGG	2002
Db	2414	CTGTATCTTTGTTCTTCAACTGGAGCAGGAATTCAGGACTCTCGAGGTCACTCCGCGG	2473

Qy	2003	ATTTCT	AGCAAGTTGAAT	TAAGCAAGATAT	CACATATCT	TGGGGGAAAATAT	TTACAGCTCTGCCA	2062
Db	2474	ATTTTC	AGCAAGTTGAAT	TAAGCAAGATAT	CAGATATCT	TGGGGGAAAATAT	TTACAGCTCTGCCA	2533
Qy	2063	CAAGC	TTCAAGGCTGCAAA	TAAAGAGATG	TGCTGGTG	TGGCTGGAAGCCT	TCAGTTTGGTTC	2122
Db	2534	CAAGC	TTCAAGGCTGCAAA	TAAAGAGATG	TGCTGGTG	TGGCTGGAAGCCT	TCAGTTTGGTTC	2593
Qy	2123	TCAGC	TCCTCTAAGAAACAT	TTATTTCT	CATGGTGGAAAGC	CAGTCCCCT	TCACCATAGAA	2182
Db	2594	TCAGC	TCCTCTAAGAAACAT	TTATTTCT	CATGGTGGAAAGC	CAGTCCCCT	TCACCATAGAA	2653
Qy	2183	ATGAG	GGCACATCACAT	CTGTAACAAAC	CTCGAAACCT	TTGAGTAT	TCATGACCTACAGA	2242
Db	2654	ATGAG	GGCACATCACAT	CTGTAACAAAC	CTCGAAACCT	TTGAGTAT	TCATGACCTACAGA	2713
Qy	2243	ATCAA	GGCTGCCGGTG	GTCTGAC	TGCAGAC	CTTGGGTAACT	TTGAAGAACCTTCAAAAGC	2302
Db	2714	ATCAA	GGCTGCCGGTG	GTCTGAC	TGCAGAC	CTTGGGTAACT	TTGAAGAACCTTCAAAAGC	2773
Qy	2303	TCATAP	TGGATACAT	TAAAGATGAAT	TGAAGAGAT	GTCTATAAACT	AGCTCAAGGCCTGA	2362
Db	2774	TCATAP	TGGATACAT	TAAAGATGAAT	TGAAGAGAT	GTCTATAAACT	AGCTCAAGGCCTGA	2833
Qy	2363	AAAAC	TGAAGAGATG	TGTTTATTT	TCATTTG	AGCCCACTT	GTCTGCACATTTGGAGAGGAA	2422
Db	2834	AAAAC	TGAAGAGATG	TGTTTATTT	TCATTTG	AGCCCACTT	GTCTGCACATTTGGAGAGGAA	2893
Qy	2423	TGGAT	TACATPAGTCAAG	TCCTCTG	TCAAGTGA	AACCTGTGAC	CTTTGAAGAAATTCAAATAG	2482
Db	2894	TGGAT	TACATPAGTCAAG	TCCTCTG	TCAAGTGA	AACCTGTGAC	CTTTGAAGAAATTCAAATAG	2953
Qy	2483	TCCTCT	CTCTGCTTGT	CTGCAAA	TGCAAGT	GAAATCCT	AGCTCAGAAATCTTCACAAATTTGG	2542
Db	2954	TCCTCT	CTCTGCTTGT	CTGCAAA	TGCAAGT	GAAATCCT	AGCTCAGAAATCTTCACAAATTTGG	3013
Qy	2543	TCAAAC	AGACATCTCTTGAT	TTATAT	TCAGAAAT	TACCTG	GGAAAAAGATGGAAATGAAGCTC	2602
Db	3014	TCAAAC	AGACATCTCTTGAT	TTATAT	TCAGAAAT	TACCTG	GGAAAAAGATGGAAATGAAGCTC	3073
Qy	2603	TTCATG	TACTGATCGACAG	GATGAAC	GTGCTAG	AACACAGCT	CACCCGACATGATGTCGCCCT	2662
Db	3074	TTCATG	TACTGATCGACAG	GATGAAC	GTGCTAG	AACACAGCT	CACCCGACATGATGTCGCCCT	3133
Qy	2663	GGGGCT	TTGACGTG	CGCAAGG	CAGCCTG	GAGCAGC	CTGTTGAAACATTTGGAGGAGGTGCCAC	2722
Db	3134	GGGGCT	TTGACGTG	CGCAAGG	CAGCCTG	GAGCAGC	CTGTTGAAACATTTGGAGGAGGTGCCAC	3193
Qy	2723	AACTCG	CAAGCTTGGGTT	TGAAAACT	GTGGAGACT	CACAGAT	CACAGATATAGAAATTTTAT	2782
Db	3194	AACTCG	CAAGCTTGGGTT	TGAAAACT	GTGGAGACT	CACAGAT	CACAGATATAGAAATTTTAT	3253
Qy	2783	GTGCAT	TTTTTGGAAAGAAC	CCCTCT	CGAAAACT	CCACAGT	TTGAAATTTGGCGGGAATC	2842
Db	3254	GTGCAT	TTTTTGGAAAGAAC	CCCTCT	CGAAAACT	CCACAGT	TTGAAATTTGGCGGGAATC	3313
Qy	2843	GTGTGAC	CAGTGATGGAT	TGGCTT	GGCTTCAT	TGGGTGAT	TTTTCAGAAATCTTAAAGCAATTTAG	2902
Db	3314	GTGTGAC	CAGTGATGGAT	TGGCTT	GGCTTCAT	TGGGTGAT	TTTTCAGAAATCTTAAAGCAATTTAG	3373
Qy	2903	TGTTTTT	TGACTTTAGT	CTAAGAAAT	TTTCTAC	CTGTAT	TCCAGCAATTTAGTCAGAAACATTTA	2962
Db	3374	TGTTTTT	TGACTTTAGT	CTAAGAAAT	TTTCTAC	CTGTAT	TCCAGCAATTTAGTCAGAAACATTTA	3433
Qy	2963	GCCAAAGT	TTTATCCAAAGT	TTAACTTT	TCTGCCAAG	AGAGCTAG	GCTTGTGTGGGTGGCAATTTTG	3022
Db	3434	GCCAAAGT	TTTATCCAAAGT	TTAACTTT	TCTGCCAAG	AGAGCTAG	GCTTGTGTGGGTGGCAATTTTG	3493
Qy	3023	ATGATGA	AGATCT	CAAGTGT	TATTTAC	AG	3049	
Db	3494	ATGATGA	AGATCT	CAAGTGT	TATTTAC	AG	3520	



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RESULT 21
PCT-US00-29643-6/c
; Sequence 6, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-6

Query Match      85.7%; Score 2634; DB 1; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCTTTTTCATCAGACATCAGAAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
DB 2882 GTCTTTTTCATCAGACATCAGAAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 2823
QY 323 TGTACCATACCCCATCTTTTCTGAACATTTATCCCTTGGTGAAGATATTGACATATTT 392
DB 2822 TGTACCATACCCCATCTTTTCTGAACATTTATCCCTTGGTGAAGATATTGACATATTT 2763
QY 383 TTAACCTTGAAGAACCTTTCACAGAACCTCTCTCTGTGGAGGAGGACCAACACCATCAC 442
DB 2762 TTAACCTTGAAGAACCTTTCACAGAACCTCTCTCTGTGGAGGAGGACCAACACCATCAC 2703
QY 443 GCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGACAGCTCTTTCAGAGCCCTGTCATCAT 502
DB 2702 GCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGACAGCTCTTTCAGAGCCCTGTCATCAT 2643
QY 503 AAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGAGGCGCATTGCATGCTCTGGGGCT 562
DB 2642 AAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGAGGCGCAATTTGCCATGCTCTGGGGCT 2583
QY 563 CCGGAAGTGCAGAGCTGACCAACTTCAAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 622
DB 2582 CCGGAAGTGCAGAGCTGACCAACTTCAAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 2523
QY 623 CCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 682
DB 2522 CCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 2463
QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAGTGGCGCAGAGGGTCTCTCTCTCTCTCT 742
DB 2462 GGAAGCAGACATTCATGGCCATGCTGCTGAAGTGGCGCAGAGGGTCTCTCTCTCTCTCT 2403
QY 743 ATGGCTACAAATGAATTCAGAGCCCAAGCTGCCCAAAATTCGAGCCCTGATAAAGGAA 802
DB 2402 ATGGCTACAAATGAATTCAGAGCCCAAGCTGCCCAAAATTCGAGCCCTGATAAAGGAA 2343
QY 803 ACCACCGCTTCAAGAACATGGTTCATCGTACCACCTACCCTGAGTGGCTGAGGCACATAC 862
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QY 863 GGAGTTTGGTCCCTGACTGCTGAGTGGGGGATATGACAGAAACAGCGCCCGAGGCTC 922
DB 2282 GGAGTTTGGTCCCTGACTGCTGAGTGGGGGATATGACAGAAACAGCGCCCGAGGCTC 2223
QY 923 TCATCCGAGAGTGCATCAGAGGCTTGCCTGAAGGCTTGTGCTCCAAATTCAGAAAT 982
DB 2222 TCATCCGAGAGTGCATCAGAGGCTTGCCTGAAGGCTTGTGCTCCAAATTCAGAAAT 2163
QY 983 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTTGGTGCATCACTTTGTGCAATCC 1042
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Db 2162 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGGTGCATCACTTTGTGCAATCC 2103
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Db 2102 AGATGGTGAAGTGAGTTCCACTCTCACACAAACAGGCTGTTCACATACCTTCTATG 2043
QY 1103 ATCTGTTGATACAGAAAAACAAACAAACATAAAGTGTGGCTGCAAGTGACTTCATTC 1162
Db 2042 ATCTGTTGATACAGAAAAACAAACAAACATAAAGTGTGGCTGCAAGTGACTTCATTC 1983
QY 1163 GGAGCCTGGACCACTCTGGAGACCTAGCTCTCTGGAGGCTGTCTCCACAAAGTTGAT 1222
Db 1982 GGAGCCTGGACCACTCTGGAGACCTAGCTCTCTGGAGGCTGTCTCTCCACAAAGTTGAT 1923
QY 1223 TCGAACTCAGGATGTCTCAGCGTGAATGAGGATCTCTCTGCTGCAACCTGGGCTCTCT 1282
Db 1922 TCGAACTCAGGATGTCTCAGCGTGAATGAGGATCTCTCTGCTGCAACCTGGGCTCTCT 1863
QY 1283 GTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATTTTTCACAAAGTCAATCCAGG 1342
Db 1862 GTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATTTTTCACAAAGTCAATCCAGG 1803
QY 1343 AGTACACAGCAGGACGAGACTCAGCAGTTTATTGACGCTCTCATGAGCCAGAGAGTGA 1402
Db 1802 AGTACACAGCAGGACGAGACTCAGCAGTTTATTGACGCTCTCATGAGCCAGAGAGTGA 1743
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Db 1742 CNAAGGGGAATGGTTACTTTCGACAAAATGGTTTCCATTTTCGGACATATACATCCACTATA 1683
QY 1463 GCAGCTGCTCCGGTACACTGCTGGGTCTCTCTGGAAGCCACAGGCTGTATGAAGC 1522
Db 1682 GCAGCTGCTCCGGTACACTGCTGGGTCTCTCTGGAAGCCACAGGCTGTATGAAGC 1623
QY 1523 ACCTCGCAGCAGTGTATCAACCGGCTCTCTCGGACTTTTCCATTCGCCAAGAGCCCTC 1582
Db 1622 ACCTCGCAGCAGTGTATCAACCGGCTCTCTCGGACTTTTCCATTCGCCAAGAGCCCTC 1563
QY 1583 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACCACCTGAGCAAGAAATTTCTGAAG 1642
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QY 1643 CCATAAACATCAATCTCTTTGAGAGTGTGCATCATTTATATCAAGAGAGTACATCCA 1702
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QY 1703 AATCAGCCCTGAGCCAAAGATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCAACT 1762
Db 1442 AATCAGCCCTGAGCCAAAGATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCAACT 1383
QY 1763 CAGGGAACATCCCGATTAATTTGACTCTTTTGAACATTTGCCCAATTTGTCGAGTG 1822
Db 1382 CAGGGAACATCCCGATTAATTTGACTCTTTTGAACATTTGCCCAATTTGTCGAGTG 1323
QY 1823 CTCGTGACTTCATTAACCTGAGCTTTTATGGGGAGCTATGGCTTCATGTGAAAAGGCTG 1882
Db 1322 CCTGAGCTTCATTAACCTGAGCTTTTATGGGGAGCTATGGCTTCATGTGAAAAGGCTG 1263
QY 1883 CAGAAGACACAGGTGGAATCCACATGAAGAGGCCCCAGAAAACCTTACATTTCCAGCAGGG 1942
Db 1262 CAGAAGACACAGGTGGAATCCACATGAAGAGGCCCCAGAAAACCTTACATTTCCAGCAGGG 1203
QY 1943 CTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGGG 2002
Db 1202 CTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGGG 1143
QY 2003 ATTTACAGCAAGTTGAATAAGCAAGATATACATATCTGGGGAAAAATATTTCAGCTCTGCCA 2062
Db 1142 ATTTACAGCAAGTTGAATAAGCAAGATATACATATCTGGGGAAAAATATTTCAGCTCTGCCA 1083
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCTCAGTTTGGTCC 2122
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Db 1082 CAAGCCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTGGTCC 1023
Qy 2123 TCAGCACCTGTGAAGAACATTTATTTCTCATGGTGAAGAGCCAGTCCCTCCACATAGAAG 2182
Db 1022 TCAGCACCTGTGAAGAACATTTATTTCTCATGGTGAAGAGCCAGTCCCTCCACATAGAAG 963
Qy 2183 ATGAGAGGCACATCATCTCTGTAAACAAACCTGAAACCTTGAGTATTTATGACCTTACAGA 2242
Db 962 ATGAGAGGCACATCATCTGTAAACAAACCTGAAACCTTGAGTATTTATGACCTTACAGA 903
Qy 2243 ATCAACGGCTGCGGGTGTGCTGACTGACAGCTTGGTAACTTGAAGAACCTTACAAAGC 2302
Db 902 ATCAACGGCTGCGGGTGTGCTGACTGACAGCTTGGTAACTTGAAGAACCTTACAAAGC 843
Qy 2303 TCATAATGATTAACATAAAGATGAATGAAGAGATGCTATAAACTAGCTGAAGCCCTGA 2362
Db 842 TCATAATGATTAACATAAAGATGAATGAAGAGATGCTATAAACTAGCTGAAGCCCTGA 783
Qy 2363 AAAACCTGAAGAGATGTGTTTATTTATTTCACTTACCCACTTGTCTACATTTGAGAGGAA 2422
Db 782 AAAACCTGAAGAGATGTGTTTATTTCACTTACCCACTTGTCTACATTTGAGAGGAA 723
Qy 2423 TGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCATTTAG 2482
Db 722 TGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCATTTAG 663
Qy 2483 TCTCTGCTGCTGTGCTGCAAAATGAGTGAATCCTAGCTCAGAACTTTCACAAATTTGG 2542
Db 662 TCTCTGCTGCTGTGCTGCAAAATGAGTGAATCCTAGCTCAGAACTTTCACAAATTTGG 603
Qy 2543 TCAAACTGAGCATCTTGATTTATCAGAAATTAACCTGGAAGAGATGGAATGAAGCTC 2602
Db 602 TCAAACTGAGCATCTTGATTTATCAGAAATTAACCTGGAAGAGATGGAATGAAGCTC 543
Qy 2603 TTCATGAATGATGACAGAGATGAACGTGTAGAACAGCTCACCGCACTGATGCTGCCCT 2662
Db 542 TTCATGAATGATGACAGAGATGAACGTGTAGAACAGCTCACCGCACTGATGCTGCCCT 483
Qy 2663 GGGGCTGTGACGTGCAAGCAGCCTGTGACAGCCTGTTGAAACATTTGGAGGAGGTCCAC 2722
Db 482 GGGGCTGTGACGTGCAAGCAGCCTGTGACAGCCTGTTGAAACATTTGGAGGAGGTCCAC 423
Qy 2723 AACTCGTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAATTTTAG 2782
Db 422 AACTCGTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAATTTTAG 363
Qy 2783 GTGCATTTTGGAAAGAACCTCTGAAAACCTCCAGCAGTTGAATTTGGCGGAAATC 2842
Db 362 GTGCATTTTGGAAAGAACCTCTGAAAACCTCCAGCAGTTGAATTTGGCGGAAATC 303
Qy 2843 GTGTGACGATGATGATGCTTGCCTTCATGGTGTATTTGAGNAATCTTAAGCAATTTAG 2902
Db 302 GTGTGACGATGATGATGCTTGCCTTCATGGTGTATTTGAGNAATCTTAAGCAATTTAG 243
Qy 2903 TGTTTTGTGACTTTAGTACTAAAGAAATTTACCTGATCCAGCATTTAGTCAGAAACCTTA 2962
Db 242 TGTTTTGTGACTTTAGTACTAAAGAAATTTACCTGATCCAGCATTTAGTCAGAAACCTTA 183
Qy 2963 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATTTG 3022
Db 182 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAGCTAGGCTTGTGGTGGCAATTTG 123
Qy 3023 ATGATGATGATCTCAGTGTATTACAG 3049
Db 122 ATGATGATGATCTCAGTGTATTACAG 96
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RESULT 22  
US-09-697-089-4  
; Sequence 4, Application US/09697089  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; APPLICANT: Robison, Keith E.

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; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-136001  
; CURRENT APPLICATION NUMBER: US/09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 3615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CD3  
; LOCATION: (1)...(3612)  
US-09-697-089-4
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Query Match 85.7%; Score 2634; DB 27; Length 3615;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 263 GTCCTTTTCATCAGACATCAGAAGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 322
Db 734 GTCCTTTTCATCAGACATCAGAAGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 793
Qy 323 TGTACCTTACCCCATCTTTCTGAACCTTTATCCCTTTGGTGAAGATATTGACATATT 382
Db 794 TGTACCTTACCCCATCTTTCTGAACCTTTATCCCTTTGGTGAAGATATTGACATATT 853
Qy 383 TTAACCTGAAAGCACCTTTCACAGAACCTGTCTGTGGAGGAAGCAACACCATCACC 442
Db 854 TTAACCTGAAAGCACCTTTCACAGAACCTGTCTGTGGAGGAAGCAACACCATCACC 913
Qy 443 GCGTGGTSCAGCTGACCTGAATGGCTTCTGAGAGCTTTCAGAGCCCTTCATCATTTG 502
Db 914 GCGTGGTSCAGCTGACCTGAATGGCTTCTGAGAGCTTTCAGAGCCCTTCATCATTTG 973
Qy 503 AAGGGGTATCTGGGAAAGCAAGTCCACTGTCTGACAGCATTTGCCATGTCTGGGGCT 562
Db 974 AAGGGGTATCTGGGAAAGCAAGTCCACTGTCTGACAGCAATTTGCCATGTCTGGGGCT 1033
Qy 563 CCGGAAATGTCAAGGCTCTGACCAAGTTCAAAATTCGTTCTCTCTCCGCTTCAGCAGGG 622
Db 1034 CCGGAAATGTCAAGGCTCTGACCAAGTTCAAAATTCGTTCTCTCTCCGCTTCAGCAGGG 1093
Qy 623 CCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCACTCTCGATATACCTGGCACAATCA 682
Db 1094 CCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCACTCTCGATATACCTGGCACAATCA 1153
Qy 683 GGAAGCAACATTCATGCGCATGCTGCTGAAGCTGGCGCAGAGGGTTCTTTCTCTCTTG 742
Db 1154 GGAAGCAACATTCATGCGCATGCTGCTGAAGCTGGCGCAGAGGGTTCTTTCTCTCTTG 1213
Qy 743 ATGCTATTAATGAATTCAGCCCTCAGAACTGCCAGAAATCCAGCCCTGATTAAGAGAA 802
Db 1214 ATGCTATTAATGAATTCAGCCCTCAGAACTGCCAGAAATCCAGCCCTGATTAAGAGAA 1273
Qy 803 ACCACCGTTTCAAGAAACATGCTCATCTGACACTTACCACCTGAGTGCCTGAGGACATAC 862
Db 1274 ACCACCGTTTCAAGAAACATGCTCATCTGACACTTACCACCTGAGTGCCTGAGGACATAC 1333
Qy 863 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATACAGAGACAGCCCGCCAGGCTC 922
Db 1334 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATACAGAGACAGCCCGCCAGGCTC 1393
Qy 923 TCATCCGTAAGTGTCTGATCAAGGCTTGTCTGAGGCTTCTCTCCAAATTCAGAAAT 982
Db 1394 TCATCCGTAAGTGTCTGATCAAGGCTTGTCTGAGGCTTCTCTCCAAATTCAGAAAT 1453
Qy 983 CCAGGTGCTTGAAGAACTCATGAAGACCCCTCTCTTTGTGGTCTATCATCTTGTGCAATCC 1042
Db 1454 CCAGGTGCTTGAAGAACTCATGAAGACCCCTCTCTTTGTGGTCTATCATCTTGTGCAATCC 1513
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QY 1043 AGATGGGTGAAAGTGAGTTCCACTCTCACACAAACACGCTGTTCATACCTTCTATG 1102  
DB 1514 AGATGGGTGAAAGTGAGTTCCACTCTCACACAAACACGCTGTTCATACCTTCTATG 1573  
QY 1103 ATCTGTTGATACAGAAAACAAACACAAATAAAGGTGGCTGCAAGTACTTCATTC 1162  
DB 1574 ATCTGTTGATACAGAAAACAAACACAAATAAAGGTGGCTGCAAGTACTTCATTC 1633  
QY 1163 GGAGCTGACACACTGTGGAGACCTAGCTCTGAGAGGTGTTCTCCCAACAGTTTGATT 1222  
DB 1634 GGAGCTGACACACTGTGGAGACCTAGCTCTGAGAGGTGTTCTCCCAACAGTTTGATT 1693  
QY 1223 TCGAACTCGAGGATGTGTCAGCGTGAATGAGGATGCTCTGCTGCAACAGTGGCTCTCT 1282  
DB 1694 TCGAACTCGAGGATGTGTCAGCGTGAATGAGGATGCTCTGCTGCAACAGTGGCTCTCT 1753  
QY 1283 GTAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTACAAAGTCAATCCAGG 1342  
DB 1754 GTAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTACAAAGTCAATCCAGG 1813  
QY 1343 AGTACACACGACGACGAACTCAGCAGTTTATGACGCTCTCATGAGCCAGAGGAGTGA 1402  
DB 1814 AGTACACACGACGACGAACTCAGCAGTTTATGACGCTCTCATGAGCCAGAGGAGTGA 1873  
QY 1403 CCAAGGGGAATGGTTACTTTCAGAAAATGGTTTCCATTTTCGGACATTTACATCCACTTATA 1462  
DB 1874 CCAAGGGGAATGGTTACTTTCAGAAAATGGTTTCCATTTTCGGACATTTACATCCACTTATA 1933  
QY 1463 GCAGCTGTCGGGTACACCTGTGGGTCACTGTGGAGCCACCAGGGCTGTATGAAGC 1522  
DB 1934 GCAGCTGTCGGGTACACCTGTGGGTCACTGTGGAGCCACCAGGGCTGTATGAAGC 1993  
QY 1523 ACCTGCACAGCTGATCAACAGCGTGCCTTCTCGAGCTTTCATCCGCAAGAGGCCCTC 1582  
DB 1994 ACCTGCACAGCTGATCAACAGCGTGCCTTCTCGAGCTTTCATCCGCAAGAGGCCCTC 2053  
QY 1583 TCTGGAGACAGGAATCTTTGCAAGTGTGAAAACACCACTGAGCAAGAAATTTCTGAAG 1642  
DB 2054 TCTGGAGACAGGAATCTTTGCAAGTGTGAAAACACCACTGAGCAAGAAATTTCTGAAG 2113  
QY 1643 CCATTAACATCAATCTCTTTGTAGAGTGGGCATCCATTTATATCAAGAGATACATCA 1702  
DB 2114 CCATTAACATCAATCTCTTTGTAGAGTGGGCATCCATTTATATCAAGAGATACATCA 2173  
QY 1703 AATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTCAAGGTAAAGCTTATATATCAACT 1762  
DB 2174 AATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTCAAGGTAAAGCTTATATATCAACT 2233  
QY 1763 CAGGGAACATCCCGATTACTTTATTTGACTTCTTTGAACATTTGCCCAATTTGTCAAGTG 1822  
DB 2234 CAGGGAACATCCCGATTACTTTATTTGACTTCTTTGAACATTTGCCCAATTTGTCAAGTG 2293  
QY 1823 CTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATAGCTTCATGGGAAAAGGCTG 1882  
DB 2294 CCCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATAGCTTCATGGGAAAAGGCTG 2353  
QY 1883 CAGAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTCGCCAGCAGG 1942  
DB 2354 CAGAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTCGCCAGCAGG 2413  
QY 1943 CTGTATCTTTGTTCTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTTCACACTCCGGG 2002  
DB 2414 CTGTATCTTTGTTCTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTTCACACTCCGGG 2473  
QY 2003 ATTTGAGCAAGTTGAATAGCAAGATATACATATCTGGGGAATATTTCACTCTGCA 2062  
DB 2474 ATTTGAGCAAGTTGAATAGCAAGATATACATATCTGGGGAATATTTCACTCTGCA 2533  
QY 2063 CAAGCTCAGGCTGCAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC 2122  
DB 2534 CAAGCTCAGGCTGCAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC 2593

QY 2123 TCAGCACCTGTAAAGACATTTATTTCTCATGTGGGAAGCCAGTCCCTCACCATAGAAG 2182  
DB 2594 TCAGCACCTGTAAAGACATTTATTTCTCATGTGGGAAGCCAGTCCCTCACCATAGAAG 2653  
QY 2183 ATGAGAGGCACATCACATCTGTAAACAACTGAAAACCTTGAGTATTTGATGACCTACAGA 2242  
DB 2654 ATGAGAGGCACATCACATCTGTAAACAACTGAAAACCTTGAGTATTTGATGACCTACAGA 2713  
QY 2243 ATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 2302  
DB 2714 ATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 2773  
QY 2303 TCATAATGGATAACATAAAGATGAATGAAGAAGTCTATAAACTAGCTGAAGGCCCTGA 2362  
DB 2774 TCATAATGGATAACATAAAGATGAATGAAGAAGTCTATAAACTAGCTGAAGGCCCTGA 2833  
QY 2363 AAAACCTGAAGAAGATGCTTTTATTTTCAATTTGACCCACTTGTCTGACATTTGAGAGGGAA 2422  
DB 2834 AAAACCTGAAGAAGATGCTTTTATTTTCAATTTGACCCACTTGTCTGACATTTGAGAGGGAA 2893  
QY 2423 TGGATTACATACCTCAAGTCTCTGCAAGTGAACCTGTGACCTTGAAGAAATTTCAATTAG 2482  
DB 2894 TGGATTACATACCTCAAGTCTCTGCAAGTGAACCTGTGACCTTGAAGAAATTTCAATTAG 2953  
QY 2483 TCTCTGCTGCTGTGCAAAATGCAGTGAATAATCCTAGCTCAGATCTTCACAATTTGG 2542  
DB 2954 TCTCTGCTGCTGTGCAAAATGCAGTGAATAATCCTAGCTCAGATCTTCACAATTTGG 3013  
QY 2543 TCAAACTGAGCAATCTTGATTTATCAGAAAATTTACCTGGAAGAAAGATGAAATGAAGCTC 2602  
DB 3014 TCAAACTGAGCAATCTTGATTTATCAGAAAATTTACCTGGAAGAAAGATGAAATGAAGCTC 3073  
QY 2603 TTCATGAACCTGATCAGACGATGAAGTCTAGAACAGCTCACCAGCTGATGCTGCCCT 2662  
DB 3074 TTCATGAACCTGATCAGACGATGAAGTCTAGAACAGCTCACCAGCTGATGCTGCCCT 3133  
QY 2663 GGGGCTGTGACGTGCAAGGACGCTGAGCAGCTGTTGAAACATTTTGGAGGAGTCCCAC 2722  
DB 3134 GGGGCTGTGACGTGCAAGGACGCTGAGCAGCTGTTGAAACATTTTGGAGGAGTCCCAC 3193  
QY 2723 AACTGCTCAAGCTTGGTTGAAAACCTGGAGACTCAGATACAGATACAGATTTAG 2782  
DB 3194 AACTGCTCAAGCTTGGTTGAAAACCTGGAGACTCAGATACAGATACAGATTTAG 3253  
QY 2783 GNGCATTTTTCGAAGAACCCTCTGAAAACCTCCACAGCTTGAATTTGGCGGGAATC 2842  
DB 3254 GNGCATTTTTCGAAGAACCCTCTGAAAACCTCCACAGCTTGAATTTGGCGGGAATC 3313  
QY 2843 GTGTGAGCAGTGTGATGGCTTGGCTTTCATGGGTGTTATTGAGAACTTTAAGCAATTAG 2902  
DB 3314 GTGTGAGCAGTGTGATGGCTTGGCTTTCATGGGTGTTATTGAGAACTTTAAGCAATTAG 3373  
QY 2903 TGTGTTTTGACATTTAGTACTAAAGAAATTTCTACCTGATCCAGATCCAGATTTAGTCAGAAACTTA 2962  
DB 3374 TGTGTTTTGACATTTAGTACTAAAGAAATTTCTACCTGATCCAGATTTAGTCAGAAACTTA 3433  
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTTCTCAAGAAGCTAGGCTTGTGGTGGCAATTTG 3022  
DB 3434 GCCAAGTGTATCCAAAGTTAACTTTTCTCAAGAAGCTAGGCTTGTGGTGGCAATTTG 3493  
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049  
DB 3494 ATGATGATGATCTCAGTGTATTACAG 3520

## RESULT 23

US-09-697-089-12/c  
; Sequence 12, Application US/09697089  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

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; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-697-089-12

Query Match      85.7%; Score 2634; DB 27; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 263 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGAGGACTTTGGCTCAGGATTTAAAGACT 322
Db      |||||
Qy 323 TGTACCATACCCCATCTTTCTGAACCTTTATCCCTTGGTGAAGATATTCACATTTATTT 382
Db      |||||
Qy 2822 TGTACCATACCCCATCTTTCTGAACCTTTATCCCTTGGTGAAGATATTCACATTTATTT 2763
Db      |||||
Qy 383 TTAACCTGAAAAGACCTTCACAGAACCTGTCTGTGGAGGAAGACCAACACCATCACC 442
Db      |||||
Qy 2762 TTAACCTGAAAAGACCTTCACAGAACCTGTCTGTGGAGGAAGACCAACACCATCACC 2703
Db      |||||
Qy 443 GCGTGGAGCAGCTGACCTGAATGGCCTCTCGAGGCTCTTCAGAGCCCTTCGATCATTTG 502
Db      |||||
Qy 2702 GCGTGGAGCAGCTGACCTGAATGGCCTCTCGAGGCTCTTCAGAGCCCTTCGATCATTTG 2643
Db      |||||
Qy 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGTCTCTGGGCT 562
Db      |||||
Qy 2642 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCTGCAGCGCAATTTGCCATGTCTCTGGGCT 2583
Db      |||||
Qy 563 CCGGAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTTCTCGCTCTCAGCAGGG 622
Db      |||||
Qy 2582 CCGGAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTTCTCTCGCTCTCAGCAGGG 2523
Db      |||||
Qy 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 682
Db      |||||
Qy 2522 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 2463
Db      |||||
Qy 683 GGAAGCAGACATTCATGGCCATGCTGTGAAGCTGCGGCGAGAGGGTCTTTCTCTCTTG 742
Db      |||||
Qy 2462 GGAAGCAGACATTCATGGCCATGCTGTGAAGCTGCGGCGAGAGGGTCTTTCTCTCTTG 2403
Db      |||||
Qy 743 ATGGCTACAATGAATTCAGCCCCCAGAACTGCCCCAGAAATCGAAGCCCTGATAAAGGAAA 802
Db      |||||
Qy 2402 ATGGCTACAATGAATTCAGCCCCCAGAACTGCCCCAGAAATCGAAGCCCTGATAAAGGAAA 2343
Db      |||||
Qy 803 ACCACCGCTTCAAGAACATGCTATCCTGTCACCTACCTAGCTGCTGAGGCACATAC 862
Db      |||||
Qy 2342 ACCACCGCTTCAAGAACATGCTATCCTGTCACCTACCTAGCTGCTGAGGCACATAC 2283
Db      |||||
Qy 863 GGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 922
Db      |||||
Qy 2282 GGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 2223
Db      |||||
Qy 923 TCATCCGAGAAATGCTGATCAAGAGCTTGTCTGAAGCTTGTCTCCAAATTCAGAAAT 982
Db      |||||
Qy 2222 TCATCCGAGAAATGCTGATCAAGAGCTTGTCTGAAGCTTGTCTCCAAATTCAGAAAT 2163
Db      |||||
Qy 983 CCAGGTCTTGGAGAAATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTGTGCAATCC 1042
Db      |||||
Qy 2162 CCAGGTCTTGGAGAAATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTGTGCAATCC 2103
Db      |||||
Qy 1043 AGATGGGTGAAGTGAAGTTCACATCTCACAAGAAAGAGCTGTTCATACCTCTATG 1102
Db      |||||
Qy 2102 AGATGGGTGAAGTGAAGTTCACATCTCACAAGAAAGAGCTGTTCATACCTCTCTATG 2043
Db      |||||
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Qy 1103 ATCTG TGTATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGACTTCATTC 1162
Db      |||||
Qy 2042 ATCTG TGTATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGACTTCATTC 1983
Db      |||||
Qy 1163 GGAGC TGGACCACTGTGGAGACCTAGCTCTGTGGAGGTGTGTCTCCACAAAGTTTGAT 1222
Db      |||||
Qy 1982 GGAGC TGGACCACTGTGGAGACCTAGCTCTGTGGAGGTGTGTCTCCACAAAGTTTGAT 1923
Db      |||||
Qy 1223 TCGAA TGCAGGATGTCTCCAGCGTGAATGAGGATGTCTCTGCTGACAACTGGGCTCTCT 1282
Db      |||||
Qy 1922 TCGAA TGCAGGATGTCTCCAGCGTGAATGAGGATGTCTCTGCTGACAACTGGGCTCTCT 1863
Db      |||||
Qy 1283 GTAAA ATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTCAACAAGTCATTCAGG 1342
Db      |||||
Qy 1862 GTAAA ATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTCAACAAGTCATTCAGG 1803
Db      |||||
Qy 1343 AGTAC CAGCAGGACGAAGACTCAGCAGTATTATTGAGCTCTCATGAGCCAGAGGATGA 1402
Db      |||||
Qy 1802 AGTAC CAGCAGGACGAAGACTCAGCAGTATTATTGAGCTCTCATGAGCCAGAGGATGA 1743
Db      |||||
Qy 1403 CCAAGG GCAATGGTTACTTTCAGAAATGTTTCCATTCGGACATTCACATCCACTTATA 1462
Db      |||||
Qy 1742 CCAAGG GCAATGGTTACTTTCAGAAATGTTTCCATTCGGACATTCACATCCACTTATA 1683
Db      |||||
Qy 1463 GCAGCC TGCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCACACAGGGCTGTATTGAAGC 1522
Db      |||||
Qy 1682 GCAGCC TGCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCACACAGGGCTGTATTGAAGC 1623
Db      |||||
Qy 1523 ACTCG AGCAGTGTATCAACACGGCTGCCCTCTCTCGGACTTTCCATCGCCAAAGAGGCTC 1582
Db      |||||
Qy 1622 ACTCG AGCAGTGTATCAACACGGCTGCCCTCTCTCGGACTTTCCATCGCCAAAGAGGCTC 1563
Db      |||||
Qy 1583 TCTGGA ACAGGAACTTTTGCAAAAGTGTGAAAACACACACTTGAGCAAGAAATTCGAAAG 1642
Db      |||||
Qy 1562 TCTGGA ACAGGAACTTTTGCAAAAGTGTGAAAACACACACTTGAGCAAGAAATTCGAAAG 1503
Db      |||||
Qy 1643 CCATAA CATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702
Db      |||||
Qy 1502 CCATAA CATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1443
Db      |||||
Qy 1703 AATCAG CCTGAGCACAAGATTTGAAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762
Db      |||||
Qy 1442 AATCAG CCTGAGCACAAGATTTGAAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1383
Db      |||||
Qy 1763 CAGGGA CATCCCGGATTAATTTGACATCTTTGACATTTGACATTTGCCAATTTGCAAGTG 1822
Db      |||||
Qy 1382 CAGGGA CATCCCGGATTAATTTGACATCTTTTGAACATTTGCCAATTTGCAAGTG 1323
Db      |||||
Qy 1823 CTCTGA CTTCATTTAACTGGACCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
Db      |||||
Qy 1322 CCTTGA CTTCATTTAACTGGACCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1263
Db      |||||
Qy 1883 CAGAAG ACAGGTGGAATCCACATGGAAGAGGCCGCCAGAAACCTACATTTCCAGCAGGG 1942
Db      |||||
Qy 1262 CAGAAG ACAGGTGGAATCCACATGGAAGAGGCCGCCAGAAACCTACATTTCCAGCAGGG 1203
Db      |||||
Qy 1943 CTGTATC TTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTCTGGAGTCACTCCGGG 2002
Db      |||||
Qy 1202 CTGTATC TTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTCTGGAGTCACTCCGGG 1143
Db      |||||
Qy 2003 ATTTCA GAGTTGAATTAAGCAAGATATACATATCTTTGGGAAAATATTTCAGCTCTGCCA 2062
Db      |||||
Qy 1142 ATTTCA GAGTTGAATTAAGCAAGATATACATATCTTTGGGAAAATATTTCAGCTCTGCCA 1083
Db      |||||
Qy 2063 CAAGCTT AGGCTGCAATTAAGAGATGTCTGTGTGGTGGCTGGAGCCTCAGTTTGGTCC 2122
Db      |||||
Qy 1082 CAAGCTT AGGCTGCAATTAAGAGATGTCTGTGTGGTGGCTGGAGCCTCAGTTTGGTCC 1023
Db      |||||
Qy 2123 TCAGCAC TGTAAAGACATTTATCTCTCATGTTGGGAGGAGCAGTCCCTCACCATAGAG 2182
Db      |||||
Qy 1022 TCAGCAC TGTAAAGACATTTATCTCTCATGTTGGGAGGAGCAGTCCCTCACCATAGAG 963
Db      |||||
Qy 2183 ATGAGAG CACATCACATCTGTAAACAACTGAAAACCTTGAGTATTTCATGACCTACAGA 2242
Db      |||||
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(3612)
US-09-841-739-4

Query Match      85.7%; Score 2634; DB 32; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 962 ATGAGAGGCACATCACATCTGTAACAAACCTGAAACACCTTGAGTATTCATGACCTACAGA 903
QY 2243 ATCAACGGCTCGCGGTGCTGCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAGC 2302
Db 902 ATCAACGGCTCGCGGTGCTGCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAGC 843
QY 2303 TCATAATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCTGA 2362
Db 842 TCATAATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCTGA 783
QY 2363 AAAACCTGAAGAAGATGCTGTTTATTCATTTGACCCACTTGTCTGACATTTGAGAGGGAA 2422
Db 782 AAAACCTGAAGAAGATGCTGTTTATTCATTTGACCCACTTGTCTGACATTTGAGAGGGAA 723
QY 2423 TGGATTACATAGTCAAGTCTCTGCTCAAGTGAACCCCTGTGACCTTGAAGAAATTCATTTAG 2482
Db 722 TGGATTACATAGTCAAGTCTCTGCTCAAGTGAACCCCTGTGACCTTGAAGAAATTCATTTAG 663
QY 2483 TCTCTGCTGCTGCTGCTGCAAAATGCAGTGAATAATCCTAGCTCAGAAATCTTCACAAATTTGG 2542
Db 662 TCTCTGCTGCTGCTGCTGCAAAATGCAGTGAATAATCCTAGCTCAGAAATCTTCACAAATTTGG 603
QY 2543 TCAAACTGAGCATTTCTTGATTTATCAGAAATTTACCTGGAAGAAAGATGAAATGAAGCTC 2602
Db 602 TCAAACTGAGCATTTCTTGATTTATCAGAAATTTACCTGGAAGAAAGATGAAATGAAGCTC 543
QY 2603 TTCATGAACCTGATCGACAGGATGAAGTCTAGACAGCTCACCCGACCTGATGCTGCCCT 2662
Db 542 TTCATGAACCTGATCGACAGGATGAAGTCTAGACAGCTCACCCGACCTGATGCTGCCCT 483
QY 2663 GGGGCTGTGACGTGAAGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGTCCAC 2722
Db 482 GGGGCTGTGACGTGAAGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGTCCAC 423
QY 2723 AACTGCTGAAGCTTGGGTTGAAAACCTGGAGACTCACAGATCAGAGATTGAATTTTAG 2782
Db 422 AACTGCTGAAGCTTGGGTTGAAAACCTGGAGACTCACAGATCAGAGATTGAATTTTAG 363
QY 2783 GTGCATTTTGTGAAGAACCTCTGAAAACCTCCAGAGTGAATTTGGCGGGAATC 2842
Db 362 GTGCATTTTGTGAAGAACCTCTGAAAACCTCCAGAGTGAATTTGGCGGGAATC 303
QY 2843 GTGTGACGAGTATGATGGCTTGGCTTCATGGGTGATTTTGAAGATCTTAAGCAATTAG 2902
Db 302 GTGTGACGAGTATGATGGCTTGGCTTCATGGGTGATTTTGAAGATCTTAAGCAATTAG 243
QY 2903 TGTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGATAGTCAGAAACTTA 2962
Db 242 TGTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGATAGTCAGAAACTTA 183
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTAGGCTGTTGGTGGCAATTTG 3022
Db 182 GCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTAGGCTGTTGGTGGCAATTTG 123
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049
Db 122 ATGATGATGATCTCAGTGTATTACAG 96
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RESULT 24
US-09-841-739-4
; Sequence 4, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
```

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(3612)
US-09-841-739-4

Query Match      85.7%; Score 2634; DB 32; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTGGCTCAGGATTTAAAGGACT 322
Db 734 GTCCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTGGCTCAGGATTTAAAGGACT 793
QY 323 TGTACCATACCCCATCTTTTCTGAACTTTATCCCTTGGTGAAGATATTGACATTTATTT 382
Db 794 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTTATTT 853
QY 383 TTAACCTTGAAGAGCAACCTTTCACAGAACCTGTCTGTGAGAGAGGACCACCAACCATCAC 442
Db 854 TTAACCTTGAAGAGCAACCTTTCACAGAACCTGTCTGTGAGAGAGGACCACCAACCATCAC 913
QY 443 GCGTGGAGAGCTGACCCCTGAATGGCTCTGCAGGCTCTTCAGAGCCCTTCATCATTTG 502
Db 914 GCGTGGAGAGCTGACCCCTGAATGGCTCTGCAGGCTCTTCAGAGCCCTTCATCATTTG 973
QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACATCTGCTGAGCGCATTTGCCATGCTCTGGGGCT 562
Db 974 AAGGGGAATCTGGCAAGGCAAGTCCACATCTGCTGAGCGCAATTTGCCATGCTCTGGGGCT 1033
QY 563 CCGGAAGATGCAAGGCTCTGACCAAGTTCAAATTCGCTCTTCTTCCCTCTCAGCAGGG 622
Db 1034 CCGGAAGATGCAAGGCTCTGACCAAGTTCAAATTCGCTCTTCTTCCCTCTCAGCAGGG 1093
QY 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCACTCTCTGGATATACCTGGCACAAATCA 682
Db 1094 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCACTCTCTGGATATACCTGGCACAAATCA 1153
QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAAGCTGGCGCAGAGGGTCTTTTCTCTTTG 742
Db 1154 GGAAGCAGACATTCATGGCCATGCTGCTGAAAGCTGGCGCAGAGGGTCTTTTCTCTTTG 1213
QY 743 ATGGCTACAAATGAATTCAGAGCCCAAGACTGCCAGAAATTCGAAGCCCTGTATAAGGAAA 802
Db 1214 ATGGCTACAAATGAATTCAGAGCCCAAGACTGCCAGAAATTCGAAGCCCTGTATAAGGAAA 1273
QY 803 ACCACCGCTTCAAGRACATGGTCACTGCTCACCACCTACCACCTGAGTCCCTGAGGCACATAC 862
Db 1274 ACCACCGCTTCAAGRACATGGTCACTGCTCACCACCTACCACCTGAGTCCCTGAGGCACATAC 1333
QY 863 GGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 922
Db 1334 GGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 1393
QY 923 TCATCCGAGAAGTGTGTGATCAAGAGGACTTGTGTAAGGCTTGTGTCTCCAAATTCAGAAAT 982
Db 1394 TCATCCGAGAAGTGTGTGATCAAGAGGACTTGTGTAAGGCTTGTGTCTCCAAATTCAGAAAT 1453
QY 983 CCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTTGGCAATCC 1042
Db 1454 CCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTTGGCAATCC 1513
QY 1043 AGATGGTGAAGTGAAGTTCCACTCTCACACACAAACAGCTGTGTCCATACCTTCTATG 1102
Db 1514 AGATGGTGAAGTGAAGTTCCACTCTCACACACAAACAGCTGTGTCCATACCTTCTATG 1573
QY 1103 ATCTGTTGATACAGAAAAACAAACACATAAAGGCTGGCTGCAAGTGAAGTCTTCTTC 1162
Db 1162 ATCTGTTGATACAGAAAAACAAACACATAAAGGCTGGCTGCAAGTGAAGTCTTCTTC 1162
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Db	1574	ATCTGTTGATACAGAAAAACAAACACAAATAAAGGTGTGGCTGCCAAGTGACTTTCATTC	1633
Qy	1163	GGAGCCGPGACCACACTGTGGAGACCTAGCTCTCGAGGGGTGTGTTCTCCACAAAGTTTGATT	1222
Db	1634	GGAGCCGPGACCACACTGTGGAGACCTAGCTCTCGAGGGGTGTGTTCTCCACAAAGTTTGATT	1693
Qy	1223	TCGAACCTGCAGSAGTGTCCAGCGTGAATGAGSAGTGTCTGCTGACAACTGGGCTCCCTCT	1282
Db	1694	TCGAACCTGCAGSAGTGTCCAGCGTGAATGAGSAGTGTCTGCTGACAACTGGGCTCCCTCT	1753
Qy	1283	GTAATAATACAGCTCAAAGGTTCAAGCCAAAGTATAAAATCTTTTCACAAGTCATTCCAGG	1342
Db	1754	GTAATAATACAGCTCAAAGGTTCAAGCCAAAGTATAAAATCTTTTCACAAGTCATTCCAGG	1813
Qy	1343	AGTACACAGCAGGACGAAGACTCAGCAGTATTATTCAGCTCTCATGAGCCAGAGGAGTGA	1402
Db	1814	AGTACACAGCAGGACGAAGACTCAGCAGTATTATTCAGCTCTCATGAGCCAGAGGAGTGA	1873
Qy	1403	CCAAGGGGAATGCTTACTTTCGCAAGAAATGGTTTCCATTTTCGGACATTACATCCACTTATA	1462
Db	1874	CCAAGGGGAATGCTTACTTTCGCAAGAAATGGTTTCCATTTTCGGACATTACATCCACTTATA	1933
Qy	1463	GCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGGAAGCCACACAGGCGCTGTATTGAAGC	1522
Db	1934	GCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGGAAGCCACACAGGCGCTGTATTGAAGC	1993
Qy	1523	ACCTCGCAGCAGTGTATCAACACAGCGTGCCTTCTCGGACTTTTCCATCGCCAAAGAGCGCTC	1582
Db	1994	ACCTCGCAGCAGTGTATCAACACAGCGTGCCTTCTCGGACTTTTCCATCGCCAAAGAGCGCTC	2053
Qy	1583	TCTGGAGACAGSAGTAATCTTTGCAAAGTGTGAAAAACACCACTGAGCAAGAAATTCGAAAG	1642
Db	2054	TCTGGAGACAGSAGTAATCTTTGCAAAGTGTGAAAAACACCACTGAGCAAGAAATTCGAAAG	2113
Qy	1643	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTAGTACATCCA	1702
Db	2114	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTAGTACATCCA	2173
Qy	1703	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAAAGCTTATATATCAACT	1762
Db	2174	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAAAGCTTATATATCAACT	2233
Qy	1763	CAGGGAACATCCCCCGATTACTTATTGTACTTCTTTGAACATTTGGCCAAATTTGCAAGTG	1822
Db	2234	CAGGGAACATCCCCCGATTACTTATTGTACTTCTTTGAACATTTGGCCAAATTTGCAAGTG	2293
Qy	1823	CTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGCTTTCATGGGAAAAGCGTG	1882
Db	2294	CCCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGCTTTCATGGGAAAAGCGTG	2353
Qy	1883	CAGAGACACAGGTGGAATCCACATGGAGAGGCCCCAGAACCTACATTCCTCCAGCAGGG	1942
Db	2354	CAGAGACACAGGTGGAATCCACATGGAGAGGCCCCAGAACCTACATTCCTCCAGCAGGG	2413
Qy	1943	CTGTATCTTTGTCTTCACTGGAGCAGGAAATTCAGACTCTGGAGGTCACTCCGGG	2002
Db	2414	CTGTATCTTTGTCTTCACTGGAGCAGGAAATTCAGACTCTGGAGGTCACTCCGGG	2473
Qy	2003	ATTTTCAGCAAGTTGAATAAGCAAGATATACATATCTCTGGGAAAATATTCAGCTCTGCCA	2062
Db	2474	ATTTTCAGCAAGTTGAATAAGCAAGATATACATATCTCTGGGAAAATATTCAGCTCTGCCA	2533
Qy	2063	CAAGCCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTGGCTCGAAGCCTCAGTTTGGTGCC	2122
Db	2534	CAAGCCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTGGCTCGAAGCCTCAGTTTGGTGCC	2593
Qy	2123	TCAGCACCTGTAAGAACATTTATCTCTCATGGTGGAGCCAGCTCCCTCCACCATAGAAG	2182
Db	2594	TCAGCACCTGTAAGAACATTTATCTCTCATGGTGGAGCCAGCTCCCTCCACCATAGAAG	2653
Qy	2183	ATGAGAGGCACATCACATCTGTAAACAAACCTGAAAAACCTTGAGTATTTCATGACCTACAGA	2242
Db	2654	ATGAGAGGCACATCACATCTGTAAACAAACCTGAAAAACCTTGAGTATTTCATGACCTACAGA	2713

RESULT 25

US-09-841-739-12/11

; Sequence 12, Application US/09841739

; GENERAL INFORMATION:

APPLICANT: Berlin, John

; AFFILIANT: BELTILL, JOHN  
 ; TITLE OF INVENTION: NOVEL

FILE REFERENCE 07334-32900

FILE REFERENCE: 07334 323001  
CURRENT APPLICATION NUMBER: US/09/841.739

; CURRENT APPLICATION NUMBER: US/  
 : CURRENT FILING DATE: 2001-08-29

: CURRENT FILING DATE: 2001-08-29  
 : PRIOR APPLICATION NUMBER: US 09/697,089

; PRIOR APPLICATION NUMBER: US 09/  
 ; PRIOR FILING DATE: 2000-10-26

PRIOR FILING DATE: 2000-10-28  
PRIOR APPLICATION NUMBER: US 60/161,822

: PRIOR APPLICATION NUMBER: US  
 : PRIOR FILING DATE: 1999-10-27

; PRIOR FILING DATE: 1999-  
; NUMBER OF SEQ ID NOS: 16

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; NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-12

Query Match      85.7%; Score 2634; DB 32; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCCTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
DB 2882 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 2823
QY 323 TGTACCATACCCCATCTTTTCTGAACTTTATCCCTTGGTGAAGATATTGACATATT 382
DB 2822 TGTACCATACCCCATCTTTTCTGAACTTTATCCCTTGGTGAAGATATTGACATATT 2763
QY 383 TTAACCTGAAAGACGCTTTCAGAAACCTTCTCTGTGGAGGAGGACCAACACCATCAC 442
DB 2762 TTAACCTGAAAGACGCTTTCAGAAACCTTCTCTGTGGAGGAGGACCAACACCATCAC 2703
QY 443 GCGTGGAGCAGCTGACCCCTGAATGCCCTCTGCAGGCTCTTCAGAGCCCTGCATCAT 502
DB 2702 GCGTGGAGCAGCTGACCCCTGAATGCCCTCTGCAGGCTCTTCAGAGCCCTGCATCAT 2643
QY 503 AAGGGAATCTGGCAAGGCAAGTCCACCTCTGCTGCAGCGCATTTGCCATGCTCTGGGGCT 562
DB 2642 AAGGGAATCTGGCAAGGCAAGTCCACCTCTGCTGCAGCGCATTTGCCATGCTCTGGGGCT 2583
QY 563 CCGGAAAGTGAAGGCTCTGACAAAGTTCAAATTCGTCTTCTTCCCTCCGCTCAGCAGGG 622
DB 2582 CCGGAAAGTGAAGGCTCTGACAAAGTTCAAATTCGTCTTCTTCCCTCCGCTCAGCAGGG 2523
QY 623 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCACAATCA 682
DB 2522 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCACAATCA 2463
QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCGCAGAGGGTTCTTTCTCTTGG 742
DB 2462 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCGCAGAGGGTTCTTTCTCTTGG 2403
QY 743 ATGGCTACAAATGAATTCAGGCCCCAGAACTGCCAGAAATTCGAAGCCCTGTATAAGGAAA 802
DB 2402 ATGGCTACAAATGAATTCAGGCCCCAGAACTGCCAGAAATTCGAAGCCCTGTATAAGGAAA 2343
QY 803 ACCACCGCTTCAAGACATGGTCACTGTCACCACTACCACTGAGTCCCTGAGGCACATAC 862
DB 2342 ACCACCGCTTCAAGACATGGTCACTGTCACCACTACCACTGAGTCCCTGAGGCACATAC 2283
QY 863 GGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTC 922
DB 2282 GGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTC 2223
QY 923 TCATCCGAGAAGTGTGATCAAGAGGCTTGTCTGAAGGCTTGTGCTCCAAATTCAGAAAT 982
DB 2222 TCATCCGAGAAGTGTGATCAAGAGGCTTGTCTGAAGGCTTGTGCTCCAAATTCAGAAAT 2163
QY 983 CCAGGTGCTTGAGGATCTCATGAAGACCCCTCTCTTGTGGTCATCATCTGTGCAATCC 1042
DB 2162 CCAGGTGCTTGAGGATCTCATGAAGACCCCTCTCTTGTGGTCATCATCTGTGCAATCC 2103
QY 1043 AGATGGGTGAAAGTGTGATTCCTCACTCTCACACACAACACGCTGTTCACATACCTTCTATG 1102
DB 2102 AGATGGGTGAAAGTGTGATTCCTCACTCTCACACACAACACGCTGTTCACATACCTTCTATG 2043
QY 1103 ATCTGTTGATACAGAAAAACAAACACATATAAGGCTGTGGCTGCAAGTGACTTTCATTC 1162
DB 2042 ATCTGTTGATACAGAAAAACAAACACATATAAGGCTGTGGCTGCAAGTGACTTTCATTC 1983
QY 1163 GGAGCCTGGACACCTGTGGAGACCTAGCTCTCGAGGGGTGTCTTCCCAACAAAGTTGATT 1222
DB 1982 GGAGCCTGGACACCTGTGGAGACCTAGCTCTCGAGGGGTGTCTTCCCAACAAAGTTGATT 1923

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QY 1223 TCGAACTGCAGGATGTGTCCAGGTGAATGAGGATCTCTGCTGACAACTGGGCTCTCT 1282
DB 1922 TCGAACTGCAGGATGTGTCCAGGTGAATGAGGATCTCTGCTGACAACTGGGCTCTCT 1863
QY 1283 GTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAAATCTTTTCAAAAGTCAATCCAGG 1342
DB 1862 GTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAAATCTTTTCAAAAGTCAATCCAGG 1803
QY 1343 AGTACACACGAGGACGAAAGACTTCAGCAGTTTATTGACGTTCTCATGAGCCAGAGGAGTGA 1402
DB 1802 AGTACACACGAGGACGAAAGACTTCAGCAGTTTATTGACGTTCTCATGAGCCAGAGGAGTGA 1743
QY 1403 CCAAGGGGAATGGTTACTTTCGAGAAATGGTTTCCATTTTCGGACATTTACATCCACTTATA 1462
DB 1742 CCAAGGGGAATGGTTACTTTCGAGAAATGGTTTCCATTTTCGGACATTTACATCCACTTATA 1683
QY 1463 GCAGCCTGCTCGGTACACCTGTGGGTCACTGTGTGAAGCCACCAGGCTGTATGAAGC 1522
DB 1682 GCAGCCTGCTCGGTACACCTGTGGGTCACTGTGTGAAGCCACCAGGCTGTATGAAGC 1623
QY 1523 ACCTGCACAGCTGTATCAACACGCTGCTTCTCGGACTTTTCCATCGCAAGAGGCCCTC 1582
DB 1622 ACCTGCACAGCTGTATCAACACGCTGCTTCTCGGACTTTTCCATCGCAAGAGGCCCTC 1563
QY 1583 TCTGGAGACAGGAAATCTTTGCAAAAGTGTGAAAAACACCACCTGAGCAAGAAATTTCTGAAAG 1642
DB 1562 TCTGGAGACAGGAAATCTTTGCAAAAGTGTGAAAAACACCACCTGAGCAAGAAATTTCTGAAAG 1503
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTTATCAAGAGAGTACATCCA 1702
DB 1502 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTTATCAAGAGAGTACATCCA 1443
QY 1703 AATCAGCCCTGAGCCAAAGATTTGAGACTTTCTTCAAGSTAAAGCTTATATATCAACT 1762
DB 1442 AATCAGCCCTGAGCCAAAGATTTGAGACTTTCTTCAAGSTAAAGCTTATATATCAACT 1383
QY 1763 CAGGGAACATCCCGGATTAATTTGACTTCTTTGAACATTTGCCCCAATTTGTGCAAGTG 1822
DB 1382 CAGGGAACATCCCGGATTAATTTGACTTCTTTGAACATTTGCCCCAATTTGTGCAAGTG 1323
QY 1823 CTCTGACTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
DB 1322 CCCTGACTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1263
QY 1883 CAGAGACACAGTGGAAATCCACATGGAAGGCCCCAGAAACCTACATTTCCACAGCAGG 1942
DB 1262 CAGAGACACAGTGGAAATCCACATGGAAGGCCCCAGAAACCTACATTTCCACAGCAGG 1203
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGTGAGGTCAACACTCCGG 2002
DB 1202 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGTGAGGTCAACACTCCGG 1143
QY 2003 ATTTACAGAAAGTGAATAAGCAAGATATACATATCTGGGGAAAATATTTCAGCTCTGCCA 2062
DB 1142 ATTTACAGAAAGTGAATAAGCAAGATATACATATCTGGGGAAAATATTTCAGCTCTGCCA 1083
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGCTGCTGCTGCAAGCCTCAGTTTGGTCC 2122
DB 1082 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGCTGCTGCTGCAAGCCTCAGTTTGGTCC 1023
QY 2123 TCAGCACCTGTGAAGACATTTTCTCTCATGTGTGAAGCCAGTCCCTCCACCATAGAAG 2182
DB 1022 TCAGCACCTGTGAAGACATTTTCTCTCATGTGTGAAGCCAGTCCCTCCACCATAGAAG 963
QY 2183 ATGAGAGGCACATCACATCTGTAAACAAACCTGAAAACCTTGAGTATTTCATGACCTACAGA 2242
DB 962 ATGAGAGGCACATCACATCTGTAAACAAACCTGAAAACCTTGAGTATTTCATGACCTACAGA 903
QY 2243 ATCAACGCGCTGCGGGGTGTGCTGACTGACAGCTTGGGTGAGTGAAGACCTTACAAAGC 2302
DB 902 ATCAACGCGCTGCGGGGTGTGCTGACTGACAGCTTGGGTGAGTGAAGACCTTACAAAGC 843

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Db 3877 AAGGGTTACAGTCCCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGAACATATCCTCTA 3936  
Qy 241 TTTCAGGACTCAATGGACAAAGTCTTTTTCATCAGACATCAGAAGGACATTTGACAGAT 300  
Db 3937 TTTCAGGACTCAATGGACAAAGTCTTTTTCATCAGACATCAGAAGGACATTTGACAGAT 3996  
Qy 301 TTGGCTCAGGATTTAAAGGACATTTGACCATACCCCATCTTTTCTGAACATTTTATCCCTTT 360  
Db 3997 TTGGCTCAGGATTTAAAGGACATTTGACCATACCCCATCTTTTCTGAACATTTTATCCCTTT 4056  
Qy 361 GGTGAAGATATGACATATTTTAACTTGAAGACACCTTCCACAGAACCTGCTCTGTGG 420  
Db 4057 GGTGAAGATATGACATATTTTAACTTGAAGACACCTTCCACAGAACCTGCTCTGTGG 4116  
Qy 421 AGGAAGGACCAACACATCACCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGAGGCT 480  
Db 4117 AGGAAGGACCAACACATCACCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGAGGCT 4176  
Qy 481 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 540  
Db 4177 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 4236  
Qy 541 CGCATTTGCCATCTCTGGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAATTCGTC 600  
Db 4237 CGCATTTGCCATCTCTGGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAATTCGTC 4296  
Qy 601 TTCTTCTCCCTGCTCAGCAGGCCCCAGGGTGGACATTTTGAACCCCTCTGTGATCAACTC 660  
Db 4297 TTCTTCTCCCTGCTCAGCAGGCCCCAGGGTGGACATTTTGAACCCCTCTGTGATCAACTC 4356  
Qy 661 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGCGCCATGCTGCTGAAGCTGGG 720  
Db 4357 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGCGCCATGCTGCTGAAGCTGGG 4416  
Qy 721 CAGAGGGTCTTTTCTCTTCTGATGGCTACAAATGAATTCAGCCCGCAGAACTGCCAGAA 780  
Db 4417 CAGAGGGTCTTTTCTCTTCTGATGGCTACAAATGAATTCAGCCCGCAGAACTGCCAGAA 4476  
Qy 781 ATCGAAGCCCTGATTAAGGAAGAAACACCGCTTCAGAGACATGGTATGTCACCACTACC 840  
Db 4477 ATCGAAGCCCTGATTAAGGAAGAAACACCGCTTCAGAGACATGGTATGTCACCACTACC 4536  
Qy 841 ACTGAGTCTGAGGCACATACGGCAGATTTGGTGCCCTGACTGCTGAGGTGGGGATATG 900  
Db 4537 ACTGAGTCTGAGGCACATACGGCAGATTTGGTGCCCTGACTGCTGAGGTGGGGATATG 4596  
Qy 901 ACAGAAAGCAGCCCGCAGGCTCTATCCGAGAAAGTCTGATCAAGAGCTTCTGCTGAAGGC 960  
Db 4597 ACAGAAAGCAGCCCGCAGGCTCTATCCGAGAAAGTCTGATCAAGAGCTTCTGCTGAAGGC 4656  
Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTTT 1020  
Db 4657 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTTT 4716  
Qy 1021 GTGGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGAAGTTCCTCTCAGACACAAACA 1080  
Db 4717 GTGGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGAAGTTCCTCTCAGACACAAACA 4776  
Qy 1081 AGCTGTGTCATACCTCTATGATCTGTTGATACAGAAACAAACACAAACATAAAGT 1140  
Db 4777 AGCTGTGTCATACCTCTATGATCTGTTGATACAGAAACAAACACAAACATAAAGT 4836  
Qy 1141 GTGGTGCAGATGACTTCAATCCGAGCCTGGACCACTGTGGAGCTAGCTCTGAGGCT 1200  
Db 4837 GTGGTGCAGATGACTTCAATCCGAGCCTGGACCACTGTGGAGCTAGCTCTGAGGCT 4896  
Qy 1201 GTGTTCTCCACAAAGTTTGATTTGCAATTCAGAGTGTCTCCAGCGTGAATGAGGATGTC 1260  
Db 4897 GTGTTCTCCACAAAGTTTGATTTGCAATTCAGAGTGTCTCCAGCGTGAATGAGGATGTC 4956  
Qy 1261 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAGTTCAGGCCAAAGTATAA 1320  
Db 4957 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAGTTCAGGCCAAAGTATAA 5016

Qy 1321 TTCTTTTCAAGTCTATCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGAGC 1380  
Db 5017 TTCTTTTCAAGTCTATCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGAGC 5076  
Qy 1381 TCTCATGAGCCAGAGGAGGTGACCAAGGGAATGGTTACTTTCAGAAAAATGGTTTCCATT 1440  
Db 5077 TCTCATGAGCCAGAGGAGGTGACCAAGGGAATGGTTACTTTCAGAAAAATGGTTTCCATT 5136  
Qy 1441 TCGGACATTTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGTCTCTCTGGAA 1500  
Db 5137 TCGGACATTTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGTCTCTCTGGAA 5196  
Qy 1501 GCCACAGGCTGTTATGAAGCACCCTCGCAGCAGTGTATCAACAGGCTGCTCTCGGA 1560  
Db 5197 GCCACAGGCTGTTATGAAGCACCCTCGCAGCAGTGTATCAACAGGCTGCTCTCGGA 5256  
Qy 1561 CTTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
Db 5257 CTTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 5316  
Qy 1621 ACTGAGCAAGAAATTTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680  
Db 5317 ACTGAGCAAGAAATTTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 5376  
Qy 1681 TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTCAAGCTTTCTTTCAA 1740  
Db 5377 TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTTCTTTCAA 5436  
Qy 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTATTTGACTTTCTTTGAA 1800  
Db 5437 GGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTATTTGACTTTCTTTGAA 5496  
Qy 1801 CATTTGCCAAATTTGTCAAGTCTCTGGACTTCATTAACACTGGACTTTTATGGGGAGCT 1860  
Db 5497 CATTTGCCAAATTTGTCAAGTCTCTGGACTTCATTAACACTGGACTTTTATGGGGAGCT 5556  
Qy 1861 ATGGCTTCATGGAAGAGGCTCGAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
Db 5557 ATGGCTTCATGGAAGAGGCTCGAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 5616  
Qy 1921 GAAACTCATTTCCAGCAGGCTGTATCTTTTCTTCAACTGGAAGCAGGAATTCAGG 1980  
Db 5617 GAAACTCATTTCCAGCAGGCTGTATCTTTTCTTCAACTGGAAGCAGGAATTCAGG 5676  
Qy 1981 ACTCTGGAGGTCACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTG 2040  
Db 5677 ACTCTGGAGGTCACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTG 5736  
Qy 2041 GGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTG 2100  
Db 5737 GGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTG 5796  
Qy 2101 GCTGGAAGCCTCAGTTTGGTCTCAGCAGCCTGTAAGAACATTTATCTCTCATGTGGAA 2160  
Db 5797 GCTGGAAGCCTCAGTTTGGTCTCAGCAGCCTGTAAGAACATTTATTTCTCTCATGTGGAA 5856  
Qy 2161 GCCAGTCCCTCACCATAGAAGATGAGAGGCACATCATCTGTACAAACCTGAAAACC 2220  
Db 5857 GCCAGTCCCTCACCATAGAAGATGAGAGGCACATCATCTGTACAAACCTGAAAACC 5916  
Qy 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGT 2259  
Db 5917 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGT 5955

RESULT 29  
US-10-042-938-917  
; Sequence 917, Application US/10042938  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith  
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-136

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; CURRENT APPLICATION NUMBER: US/10/042,938
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 09/557,676
; PRIOR FILING DATE: 2000-APR-25
; NUMBER OF SEQ ID NOS: 986
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 917
; LENGTH: 6012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-938-917

Query Match          71.9%; Score 2208; DB 38; Length 6012;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2258; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTTATA 60
DB 3697 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTTATA 3756

QY 61 AAGCAATATCAGATGACCTATTTGTATGTAATGTTCTGAATCGCGAAGATGAATATC 120
DB 3757 AAGCAATATCAGATGACCTATTTGTATGTAATGTTCTGAATCGCGAAGATGAATATC 3816

QY 121 ATTTGCTGCGAAGAGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGA 180
DB 3817 ATTTGCTGCGAAGAGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGA 3876

QY 181 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTTAAATPCCCTTAAAGGAGTGGAACTATPC 240
DB 3877 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTTAAATPCCCTTAAAGGAGTGGAACTATPC 3936

QY 241 TTTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGGAG 300
DB 3937 TTTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGGAG 3996

QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 360
DB 3997 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 4056

QY 361 GGTCAAGATATGACATATTTTAACTTGAAGGACCTTCAGACACTGCTCTGCTGG 420
DB 4057 GGTGAAGATATGACATATTTTAACTTGAAGGACCTTCAGACACTGCTCTGCTGG 4116

QY 421 AGAAGGACCAACACATACCGGCTGGAGCAGCTGACCTGATGAGCCCTCTGCGAGCT 480
DB 4117 AGAAGGACCAACACATACCGGCTGGAGCAGCTGACCTGATGAGCCCTCTGCGAGCT 4176

QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTCG 540
DB 4177 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTCG 4236

QY 541 CGCAATGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAAATTCG 600
DB 4237 CGCAATGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAAATTCG 4296

QY 601 TTCTTCCTCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTC 660
DB 4297 TTCTTCCTCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTC 4356

QY 661 CTGATATACCTGGCAACATCAGGAAGCAGACATTTACATGCTGCTGGAAGCTCGG 720
DB 4357 CTGATATACCTGGCAACATCAGGAAGCAGACATTTACATGCTGCTGGAAGCTCGG 4416

QY 721 CAGAGGCTCTTTCTTCTTGTGGCTACAATGAATCAAGCCCAAGACTGCCAGAA 780
DB 4417 CAGAGGCTCTTTCTTCTTGTGGCTACAATGAATCAAGCCCAAGACTGCCAGAA 4476

QY 781 ATCGAAGCCCTGATTAAGGAAGAACCCCGCTTCAAGAACATGCTCATCAGCACTACC 840
DB 4477 ATCGAAGCCCTGATTAAGGAAGAACCCCGCTTCAAGAACATGCTCATCAGCACTACC 4536

QY 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATG 900
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DB 4537 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 4596
QY 901 ACAGAAACACAGCGCCAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTCTGAAGGC 960
DB 4597 ACAGAAACACAGCGCCAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTCTGAAGGC 4656
QY 961 TTGTTGCTCCAAATTCAGAAATCAGGTGCTTGGAGGAATCTCATGAAGACCCCTCTCTTT 1020
DB 4657 TTGTTGCTCCAAATTCAGAAATCAGGTGCTTGGAGGAATCTCATGAAGACCCCTCTCTTT 4716
QY 1021 GTGGTCTATCACTTGTGCAATCCAGATGGGTGAAAGTGAAGTGTCCACTCTCACACACAAACA 1080
DB 4717 GTGGTCTATCACTTGTGCAATCCAGATGGGTGAAAGTGAAGTGTCCACTCTCACACACAAACA 4776
QY 1081 ACCTGTCTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGGT 1140
DB 4777 ACCTGTCTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGGT 4836
QY 1141 GTGGCTCAAGTGTGACTTCAATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 1200
DB 4837 GTGGCTCAAGTGTGACTTCAATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 4896
QY 1201 GTGTTCTCCACAAAGTTTGAATTCGAACCTGCAGGATGTGCCAGCTGATGAGGATGTC 1260
DB 4897 GTGTTCTCCACAAAGTTTGAATTCGAACCTGCAGGATGTGCCAGCTGATGAGGATGTC 4956
QY 1261 CTGCTGTCAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTTCAAGCCAAAGTATATA 1320
DB 4957 CTGCTGTCAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTTCAAGCCAAAGTATATA 5016
QY 1321 TTCTTTTACAAGTCAATTCAGAGGAGTACACAGCAGGAGAACTCAGCAGTTTATTGACG 1380
DB 5017 TTCTTTTACAAGTCAATTCAGAGGAGTACACAGCAGGAGAACTCAGCAGTTTATTGACG 5076
QY 1381 TCTCATCAGCAGAGGAGTGAACAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 1440
DB 5077 TCTCATCAGCAGAGGAGTGAACAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 5136
QY 1441 TCGGACATACATCCACTTATAGCAGCTCTCCGGTACACCTGTGGTCTCATCTGTGAA 1500
DB 5137 TCGGACATACATCCACTTATAGCAGCTCTCCGGTACACCTGTGGTCTCATCTGTGAA 5196
QY 1501 GCCACCAAGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACAGGCTGCTCTCGGA 1560
DB 5197 GCCACCAAGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACAGGCTGCTCTCGGA 5256
QY 1561 CTTTCCAAGCAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC 1620
DB 5257 CTTTCCAAGCAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC 5316
QY 1621 ACTGAGCAGAAAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
DB 5317 ACTGAGCAGAAAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 5376
QY 1681 TTATATCTAGAGAGTACATCAAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 1740
DB 5377 TTATATCTAGAGAGTACATCAAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 5436
QY 1741 GGTAAAAATCTATATATCAACTCAGGGAACATCCCGGATTTATTTGACTTTCTTTGAA 1800
DB 5437 GGTAAAAATCTATATATCAACTCAGGGAACATCCCGGATTTATTTGACTTTCTTTGAA 5496
QY 1801 CATTTGCTCAATGTGCAAGTGTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT 1860
DB 5497 CATTTGCTCAATGTGCAAGTGTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT 5556
QY 1861 ATGGCTTATGGGAAAAAGGCTGCAGAAAGACACAGGTGGATTCACATGGAAGAGGCCCA 1920
DB 5557 ATGGCTTATGGGAAAAAGGCTGCAGAAAGACACAGGTGGATTCACATGGAAGAGGCCCA 5616
QY 1921 GAAACCTATCATTCGCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 1980
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Db 5617 GAAACCTACATCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 5676  
Qy 1981 ACTCTGGAGGTCACACTCCGGGATTTACAGAGTTTGAATAAGCAAGATATCACATATCTG 2040  
Db 5677 ACTCTGGAGGTCACACTCCGGGATTTACAGAGTTTGAATAAGCAAGATATCACATATCTG 5736  
Qy 2041 GGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 2100  
Db 5737 GGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 5796  
Qy 2101 GCTGGAAGCCTCAGTTTGTCTCAGCACCTGTAAAGACATTTATTTCTCTATGTGTGAA 2160  
Db 5797 GCTGGAAGCCTCAGTTTGTCTCAGCACCTGTAAAGACATTTATTTCTCTATGTGTGAA 5856  
Qy 2161 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCTGTAAACAACTGAAACCC 2220  
Db 5857 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCTGTAAACAACTGAAACCC 5916  
Qy 2221 TTGAGTATTCATGACCTACAGAAATCAAGGCTGCCGGGT 2259  
Db 5917 TTGAGTATTCATGACCTACAGAAATCAAGGCTGCCGGGT 5955

## RESULT 30

US-09-578-789-15  
; Sequence 15, Application us/09578789  
; GENERAL INFORMATION:  
; APPLICANT: John C. Reed  
; APPLICANT: Frederick Plo  
; APPLICANT: Adam Godzik  
; TITLE OF INVENTION: Novel Card Polypeptides  
; FILE REFERENCE: P-LJ 4141  
; CURRENT APPLICATION NUMBER: US/09/578,789  
; CURRENT FILING DATE: 2000-05-23  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 2343  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2340)  
US-09-578-789-15

Query Match 71.8%; Score 2207; DB 22; Length 2343;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATATA 61  
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Qy 62 AGCAATCACAGATGACCTATTTGTATGAATGTTCTGAATCGCGAAGATTAACATCA 121  
Db 89 AGCAATCACAGATGACCTATTTGTATGAATGTTCTGAATCGCGAAGATTAACATCA 148  
Qy 122 TTTGCTGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAATA 181  
Db 149 TTTGCTGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAATA 208  
Qy 182 AGGGTTTCAGAGTCCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTAT 241  
Db 209 AGGGTTTCAGAGTCCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTAT 268  
Qy 242 TTCAGAGTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGGAGATT 301  
Db 269 TTCAGAGTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGGAGATT 328  
Qy 302 TGGCTCAGAGTTAAAGACATGTACCATACCCCATCTTTCTGAACTTTTATCCCTTG 361  
Db 329 TGGCTCAGAGTTAAAGACATGTACCATACCCCATCTTTCTGAACTTTTATCCCTTG 388

Qy 362 GTGAAGATATTGACATATTTTTAACTTGAAGACACCTTTCACAGAACCTGCTCTGTGTA 421  
Db 389 GTGAAGATATTGACATATTTTTAACTTGAAGACACCTTTCACAGAACCTGCTCTGTGTA 448  
Qy 422 GGAAGGACCAACACCATCACCCGCTGGAGCAGCTGACCCCTGAATGCCCTCTCTGCAAGGTC 481  
Db 449 GGAAGGACCAACACCATCACCCGCTGGAGCAGCTGACCCCTGAATGCCCTCTCTGCAAGGTC 508  
Qy 482 TTCAGAGCCCTTGCATCATTTGAAGGGATCTGGCAAGGCAAGTCCACTCTGCTGCAGC 541  
Db 509 TTCAGAGCCCTTGCATCATTTGAAGGGATCTGGCAAGGCAAGTCCACTCTGCTGCAGC 568  
Qy 542 GCATTGCCATGCTCTGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAAATTCGTCT 601  
Db 569 GCATTGCCATGCTCTGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAAATTCGTCT 628  
Qy 602 TCTTCTCCGCTCAGCAGGCCCCAGGGTGGACTTTTTTGAACCCCTCTGTGTAACTTCC 661  
Db 629 TCTTCTCCGCTCAGCAGGCCCCAGGGTGGACTTTTTTGAACCCCTCTGTGTAACTTCC 688  
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Qy 782 TCGAAGCCCTGATAAAGGAAAAACCCGCTTCAAGAACATGCTCATGCTCACCATTACA 841  
Db 809 TCGAAGCCCTGATAAAGGAAAAACCCGCTTCAAGAACATGCTCATGCTCACCATTACA 868  
Qy 842 CTGAGTGGCTGAGCACAATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 901  
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Qy 902 CAGAAGACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGGAGCTTGTGAGGCT 961  
Db 929 CAGAAGACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGGAGCTTGTGAGGCT 988  
Qy 962 TGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAACTCATGAAGACCCCTCTCTTTG 1021  
Db 989 TGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAACTCATGAAGACCCCTCTCTTTG 1048  
Qy 1022 TGGTATCATCTGTGCAATCCAGATGGGTGAAGTGAGTTCCACTCTCACACACAAACA 1081  
Db 1049 TGGTATCATCTGTGCAATCCAGATGGGTGAAGTGAGTTCCACTCTCACACACAAACA 1108  
Qy 1082 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACAAATAAGGTG 1141  
Db 1109 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACAAATAAGGTG 1168  
Qy 1142 TGGCTGCAAGTGAATTCAGTTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGTG 1201  
Db 1169 TGGCTGCAAGTGAATTCAGTTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGTG 1228  
Qy 1202 TGTGCTCCCAAGTTTGTATTTTGAAGTGCAGAGTGTGTCAGCGTGAATGAGGATGCC 1261  
Db 1229 TGTGCTCCCAAGTTTGTATTTTGAAGTGCAGAGTGTGTCAGCGTGAATGAGGATGCC 1288  
Qy 1262 TGCTGACAACTGGGCTCCTCTGTAATATACAGCTCAAGGTTCAAGCCCAAGTATAAT 1321  
Db 1289 TGCTGACAACTGGGCTCCTCTGTAATATACAGCTCAAGGTTCAAGCCCAAGTATAAT 1348  
Qy 1322 TCTTTTCAAGTTCATTCAGGAGTACACAGCAGGAGAGACTCAGAGTTTATTGAGCT 1381  
Db 1349 TCTTTTCAAGTTCATTCAGGAGTACACAGCAGGAGAGACTCAGAGTTTATTGAGCT 1408  
Qy 1382 CTCATGAGCCAGAGGAGTACCAAGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 1441  
Db 1409 CTCATGAGCCAGAGGAGTACCAAGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 1468  
Qy 1442 CGGACATTACATCCACTTATAGCAGCTCTCCGGTACACCTGTGGGTCTATCTGTGGAAG 1501

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Db 1469 CGGACATTACATCCATATAGACGCTGCTCCGGTACACTGTTGGGTCACTGTGGAAG 1528
Qy 1502 CCACAGGGCTGTTATGAAGCACCCTCGACAGTGTATCAACAGCGTGCTTCTCGGAC 1561
Db 1529 CCACAGGGCTGTTATGAAGCACCCTCGACAGTGTATCAACAGCGTGCTTCTCGGAC 1588
Qy 1562 TTTCCATCGCCAGAGGCTCTCTGAGACAGAGGAATCTTTGCAAGTGTGAAACACCA 1621
Db 1589 TTTCCATCGCCAGAGGCTCTCTGAGACAGAGGAATCTTTGCAAGTGTGAAACACCA 1648
Qy 1622 CTGAGCAAGAAATCTGAAGCCATAAATCAATCAATCTCTTTGTAGAGTGTGGCATCAT 1681
Db 1649 CTGAGCAAGAAATCTGAAGCCATAAATCAATCAATCTCTTTGTAGAGTGTGGCATCAT 1708
Qy 1682 TATATCAAGAGATACATCCAAATCAGCCTGAGCCAGATTTGAAGCTTCTTTCAAG 1741
Db 1709 TATATCAAGAGATACATCCAAATCAGCCTGAGCCAGATTTGAAGCTTCTTTCAAG 1768
Qy 1742 GTAAAGCTTATATCAATCACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAAC 1801
Db 1769 GTAAAGCTTATATCAATCACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAAC 1828
Qy 1802 ATTTGCCCAATTTGCAAGTCTCTGAGCTTCATTAACCTGGAGCTTTTATGGGGAGCTA 1861
Db 1829 ATTTGCCCAATTTGCAAGTCTCTGAGCTTCATTAACCTGGAGCTTTTATGGGGAGCTA 1888
Qy 1862 TGGCTTCATGGGAAAGGCTGCAAGACACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921
Db 1889 TGGCTTCATGGGAAAGGCTGCAAGACACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1948
Qy 1922 AAACCTACATTCACAGGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 1981
Db 1949 AAACCTACATTCACAGGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 2008
Qy 1982 CTCTGGAGGTCACACTCCGGGATTTACAGCAAGTTGTAATAGCAAGATATCACATATCTGG 2041
Db 2009 CTCTGGAGGTCACACTCCGGGATTTACAGCAAGTTGTAATAGCAAGATATCACATATCTGG 2068
Qy 2042 GGAATATTCAGCTCTGCCACAGCTCAGGCTGCAATTAAGAGATGTCTGTCTGG 2101
Db 2069 GGAATATTCAGCTCTGCCACAGCTCAGGCTGCAATTAAGAGATGTCTGTCTGG 2128
Qy 2102 CTGGAAGCCTCAGTTTGTCTCAGACCTGTAGAACATTTATCTCATGTGTGAAG 2161
Db 2129 CTGGAAGCCTCAGTTTGTCTCAGACCTGTAGAACATTTATCTCATGTGTGAAG 2188
Qy 2162 CCAGTCCCTCACCATAGAGATGAGAGGACATCATCTGTAAACCTGAAACCT 2221
Db 2189 CCAGTCCCTCACCATAGAGATGAGAGGACATCATCTGTAAACCTGAAACCT 2248
Qy 2222 TGATATTCAGCTCAGAAATCAACGGCTGCGGGT 2259
Db 2249 TGATATTCAGCTCAGAAATCAACGGCTGCGGGT 2286
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RESULT 31
US-09-579-240-15
; SEQUENCE 15, Application US/09579240
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card-Domain Containing
; FILE REFERENCE: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/579,240
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2343
; TYPE: DNA
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; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CUS
; LOCATION: (..)(2340)
US-09-579-240-15
Query Match 71.8%; Score 2207; DB 22; Length 2343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TGAATTCATATAAGGACAATAGCGGCCCTTATTCAAGAAATGGGAATGACTCTTTATA 61
Db 29 TGAATTCATATAAGGACAATAGCGGCCCTTATTCAAGAAATGGGAATGACTCTTTATA 88
Qy 62 AGCAATTCACAGATGACCTATTTCTATGGAATGTTCTGAATCGGAGAGTAACATCA 121
Db 89 AGCAATTCACAGATGACCTATTTCTATGGAATGTTCTGAATCGGAGAGTAACATCA 148
Qy 122 TTTGCTTCGAGAGAGTGAGCAGAGTCTGCTAGAGGATCATTCACATGATTTTGA 181
Db 149 TTTGCTTCGAGAGAGTGAGCAGAGTCTGCTAGAGGATCATTCACATGATTTTGA 208
Qy 182 AGGTTTAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAATATCTCTAT 241
Db 209 AGGTTTAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAATATCTCTAT 268
Qy 242 TTCAGGCTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGAGACTTGGACGATT 301
Db 269 TTCAGGCTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGAGACTTGGACGATT 328
Qy 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTG 361
Db 329 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTG 388
Qy 362 GTGAAGCTATTGACATTTATTTTAACTTGAAGACACCTTTCACAGAACCTGTCTGTGA 421
Db 389 GTGAAGCTATTGACATTTATTTTAACTTGAAGACACCTTTCACAGAACCTGTCTGTGA 448
Qy 422 GGAAGCTCAGACACCTACCGGCTGAGCAGCTGACCTGATGAGCTCTCTCGAGCTC 481
Db 449 GGAAGCTCAGACACCTACCGGCTGAGCAGCTGACCTGATGAGCTCTCTCGAGCTC 508
Qy 482 TTCAGACCTCTGATCATTTGAAGGGAATCTGGCAAGGAACTCAGCTCTCTGTGAGC 541
Db 509 TTCAGACCTCTGATCATTTGAAGGGAATCTGGCAAGGAACTCAGCTCTCTGTGAGC 568
Qy 542 GCATTCATGCTCTGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTCT 601
Db 569 GCATTCATGCTCTGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTCT 628
Qy 602 TCTTCCTCCTGCTCAGCAGGCGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCC 661
Db 629 TCTTCCTCCTGCTCAGCAGGCGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCC 688
Qy 662 TGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAAGTGGGC 721
Db 689 TGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAAGTGGGC 748
Qy 722 AGAGGCTCTTTTCTCTTGTGAGTGGCTTACAAATGAATCAAGCCCGCAAGTCTGCCAGAAA 781
Db 749 AGAGGCTCTTTTCTCTTGTGAGTGGCTTACAAATGAATCAAGCCCGCAAGTCTGCCAGAAA 808
Qy 782 TCGAAGCTCTGATAAGGAAACACCGCTTCAAGAACATGGTCTGTCACCACTACCA 841
Db 809 TCGAAGCTCTGATAAGGAAACACCGCTTCAAGAACATGGTCTGTCACCACTACCA 868
Qy 842 CTGAGTCTCTGAGCAGATACCGCAGTTTGTGCTGCTGCTGAGTGGGGATATGA 901
Db 869 CTGAGTCTCTGAGCAGATACCGCAGTTTGTGCTGCTGCTGAGTGGGGATATGA 928
Qy 902 CAGAAGTACGCGCCAGGCTCTCATCGGAGAAAGTGTGATCAAGGAGCTTGTCTGAAGCT 961
Db 929 CAGAAGTACGCGCCAGGCTCTCATCGGAGAAAGTGTGATCAAGGAGCTTGTCTGAAGCT 988
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QY 962 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1021  
Db TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1048  
QY 1022 TGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGGAGTTCACCTCTCACACACAAACAA 1081  
Db TGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGGAGTTCACCTCTCACACACAAACAA 1108  
QY 1082 CGCTGTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACACATAAAGGTG 1141  
Db CGCTGTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACACATAAAGGTG 1168  
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QY 1202 TGTTCTCCCAAGTTGATTTTGGAACTGCAGGATGTGCCAGGTGAATGAGATGTC 1261  
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QY 1442 CGGACATTACATCCACTTATAGAGCCTGCTCCGGTACACCTGTGGGTATCTGTGGAAG 1501  
Db CGGACATTACATCCACTTATAGAGCCTGCTCCGGTACACCTGTGGGTATCTGTGGAAG 1528  
QY 1502 CCACCAAGGCTGTTATGAAGCCTCGCAGCAGTGTATCAACAGCGCTGCTTCGCGAC 1561  
Db CCACCAAGGCTGTTATGAAGCCTCGCAGCAGTGTATCAACAGCGCTGCTTCGCGAC 1588  
QY 1562 TTTCCATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1621  
Db TTTCCATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1648  
QY 1622 CTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGATCCATT 1681  
Db CTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGATCCATT 1708  
QY 1682 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAG 1741  
Db TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAG 1768  
QY 1742 GTAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTTGAAC 1801  
Db GTAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTTGAAC 1828  
QY 1802 ATTTGCCCAATTTGTCAAGTGTCTTGACCTTCATTTAACTGGACTTTTATTTGGGGAGCTA 1861  
Db ATTTGCCCAATTTGTCAAGTGTCTTGACCTTCATTTAACTGGACTTTTATTTGGGGAGCTA 1888  
QY 1862 TGGCTTCATGGAAAAGGCTGCAGAGACACACAGTGAATCCACATGGAAGAGCCCCAG 1921  
Db TGGCTTCATGGAAAAGGCTGCAGAGACACACAGTGAATCCACATGGAAGAGCCCCAG 1948  
QY 1922 AAAGCTACATTTCCAGCAGGCTGTATCTTTTGTCTTCAACTGGAAGCAGGAATTCAGGA 1981  
Db AAAGCTACATTTCCAGCAGGCTGTATCTTTTGTCTTCAACTGGAAGCAGGAATTCAGGA 2008  
QY 1982 CTCGGAGGTACACTCCGGATTTTCAGCAAGTTTGAATAAGCAGATATCACATATCTGG 2041  
Db CTCGGAGGTACACTCCGGATTTTCAGCAAGTTTGAATAAGCAGATATCACATATCTGG 2068

QY 2042 GGAATAATATTAGCTTGCACCAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTGG 2101  
Db GGAATAATATTAGCTTGCACCAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTGG 2128  
QY 2102 CTGGAAGCCTCAGTTTGGTCTCTCAGCACCTGTGAAGACATTTATTTCTCATGTTGGAAG 2161  
Db CTGGAAGCCTCAGTTTGGTCTCTCAGCACCTGTGAAGACATTTATTTCTCATGTTGGAAG 2188  
QY 2162 CCAGTCCCTTCACATAGAAGATGAGAGGCACATCAGATCTGTAACAAACCTGAAAACCT 2221  
Db CCAGTCCCTTCACATAGAAGATGAGAGGCACATCAGATCTGTAACAAACCTGAAAACCT 2248  
QY 2222 TGAGTATTTCATGACCTACAGAATCAACGGCTGCGGGT 2259  
Db TGAGTATTTCATGACCTACAGAATCAACGGCTGCGGGT 2286  
RESULT 32  
US-09-578-789-17  
; Sequence 17, Application US/09578789  
; GENERAL INFORMATION:  
; APPLICANT: John C. Reed  
; APPLICANT: Frederick Plo  
; APPLICANT: Adam Godzik  
; TITLE OF INVENTION: Novel Card Polypeptides  
; FILE REFERENCE: P-LJ 4141  
; CURRENT APPLICATION NUMBER: US/09/578,789  
; CURRENT FILING DATE: 2000-05-23  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 2415  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2412)  
US-09-578-789-17

Query Match 71.8%; Score 2205; DB 22; Length 2415;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTCTTTATAA 61  
Db 29 TGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTCTTTATAA 88  
QY 62 AGCAAAATCACAGATGACCTATTTGTATGGAATGTCTGAATCGCGAAGAAAGTAACATCA 121  
Db 89 AGCAAAATCACAGATGACCTATTTGTATGGAATGTCTGAATCGCGAAGAAAGTAACATCA 148  
QY 122 TTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAATA 181  
Db 149 TTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAATA 208  
QY 182 AGGTTTCAGAGTCTCTGTAACCTCTTTCTAAATCCCTTAAAGGAGTGAATCTCTAT 241  
Db 209 AGGTTTCAGAGTCTCTGTAACCTCTTTCTAAATCCCTTAAAGGAGTGAATCTCTAT 268  
QY 242 TTCAAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGAGATTTGACCAT 301  
Db 269 TTCAAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGAGATTTGACCAT 328  
QY 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCCCTG 361  
Db 329 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCCCTG 388  
QY 362 GTGAAGATATTGACATTTATTTTAACTTGAAGACCTTCACAGACCTGTCTCTGTGA 421  
Db 389 GTGAAGATATTGACATTTATTTTAACTTGAAGACCTTCACAGACCTGTCTCTGTGA 448  
QY 422 GGAAGGACCAACCACTACCGGCTGAGGAGCTGACCCCTGAATGGCTCTCTGAGGCTC 481



Db 449 GGAAGGCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCTCTCTGAGGCTC 508  
QY 482 TTCAGAGCCCTGATCATTTGAAGGGAAATCTGCRAAGCAAGTCCACTCTGCTGAGC 541  
Db 509 TTCAGAGCCCTGATCATTTGAAGGGAAATCTGCRAAGCAAGTCCACTCTGCTGAGC 568  
QY 542 GCATTGCCATGCTCTGGGCTCCGGAAGTGCRAAGGCTCTGCACCAAGTTCAAATTCGCT 601  
Db 569 GCATTGCCATGCTCTGGGCTCCGGAAGTGCRAAGGCTCTGCACCAAGTTCAAATTCGCT 628  
QY 602 TCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTGAACCCCTCTGTGATCAACTCC 661  
Db 629 TCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTGAACCCCTCTGTGATCAACTCC 688  
QY 662 TGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 721  
Db 689 TGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 748  
QY 722 AGAGGGTCTTCTTCTTCTGATGGCTACAAATGAATTCGAAGCCCAAGAACTGCCAGAAA 781  
Db 749 AGAGGGTCTTCTTCTTCTGATGGCTACAAATGAATTCGAAGCCCAAGAACTGCCAGAAA 808  
QY 782 TCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCAATGCTCAACCACTACCA 841  
Db 809 TCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCAATGCTCAACCACTACCA 868  
QY 842 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 901  
Db 869 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 928  
QY 902 CAGAAAGACGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 961  
Db 929 CAGAAAGACGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 988  
QY 962 TGTGTCTCCAAATTCAGAAATCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTG 1021  
Db 989 TGTGTCTCCAAATTCAGAAATCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTG 1048  
QY 1022 TGTGTATCACTTGTGCAATCCAGTGGTGAAGTGGTTCCTCACTCACACAAACAA 1081  
Db 1049 TGTGTATCACTTGTGCAATCCAGTGGTGAAGTGGTTCCTCACTCACACAAACAA 1108  
QY 1082 CGTGTTCATACCTTCTATGATCTGTTGATACAGAAAACAAACAAACATAAAGGTG 1141  
Db 1109 CGTGTTCATACCTTCTATGATCTGTTGATACAGAAAACAAACAAACATAAAGGTG 1168  
QY 1142 TGGCTGCAAGTGACTTCATTCGAGGCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTG 1201  
Db 1169 TGGCTGCAAGTGACTTCATTCGAGGCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTG 1228  
QY 1202 TGTCTCCCAAGTTTGATTTTTCGAAGTGCAGGATGTGTCCAGCGTGAATGAGGATGCC 1261  
Db 1229 TGTCTCCCAAGTTTGATTTTTCGAAGTGCAGGATGTGTCCAGCGTGAATGAGGATGCC 1288  
QY 1262 TGCTGACAACTGGGCTCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAAT 1321  
Db 1289 TGCTGACAACTGGGCTCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAAT 1348  
QY 1322 TCTTTTCAAGTCAATTCAGAGGATACAGCAGGACGAGACTCAGCAGTTTATTCAGCT 1381  
Db 1349 TCTTTTCAAGTCAATTCAGAGGATACAGCAGGACGAGACTCAGCAGTTTATTCAGCT 1408  
QY 1382 CTCATGAGCCAGAGGTCACCAAGGGAATGGTTACTTCAGAAAATGGTTCCATTT 1441  
Db 1409 CTCATGAGCCAGAGGTCACCAAGGGAATGGTTACTTCAGAAAATGGTTCCATTT 1468  
QY 1442 CGGACATTCACCTTATAGCAGCCCTGCTCCGGTACACCTGTGGGTTCATCTGTGGAAG 1501  
Db 1469 CGGACATTCACCTTATAGCAGCCCTGCTCCGGTACACCTGTGGGTTCATCTGTGGAAG 1528  
QY 1502 CCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACAGGCTGCCTTCTCGGAC 1561  
Db 1529 CCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACAGGCTGCCTTCTCGGAC 1588

QY 1562 TTTCATTCGCCAAGAGCGCTCTCTTGAGACAGGAATCTTTGCAAGTGTGAAAAACACCA 1621  
Db 1589 TTTCATTCGCCAAGAGCGCTCTCTTGAGACAGGAATCTTTGCAAGTGTGAAAAACACCA 1648  
QY 1622 CTGAACCAAGAAATTTCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681  
Db 1649 CTGAACCAAGAAATTTCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCATT 1708  
QY 1682 TATAACCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAG 1741  
Db 1709 TATAACCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAG 1768  
QY 1742 GTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTTGACTTCTTTGAAC 1801  
Db 1769 GTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTTGACTTCTTTGAAC 1828  
QY 1802 ATTTGTCCTGCAAGTCTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTA 1861  
Db 1829 ATTTGTCCTGCAAGTCTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTA 1888  
QY 1862 TGGCTTCATGGGAAAGGCTGCAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921  
Db 1889 TGGCTTCATGGGAAAGGCTGCAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1948  
QY 1922 AAACCTACATTCAGGAGGCTGTATCTTTGTCTTCACTGGAAGCAGGAATTCAGGA 1981  
Db 1949 AAACCTACATTCAGGAGGCTGTATCTTTGTCTTCACTGGAAGCAGGAATTCAGGA 2008  
QY 1982 CTCTGAGGTCACTCCGGGATTTTCAGCAAGTTCGAATGAAGCAAGATATCAGATATCTGG 2041  
Db 2009 CTCTGAGGTCACTCCGGGATTTTCAGCAAGTTCGAATGAAGCAAGATATCAGATATCTGG 2068  
QY 2042 GGAATATTCATGCTCTGCCAAGCTCAGGCTGCAATAAAGAGATGTGCTGGTGTGG 2101  
Db 2069 GGAATATTCATGCTCTGCCAAGCTCAGGCTGCAATAAAGAGATGTGCTGGTGTGG 2128  
QY 2102 CTGGAAACCTCAGTTTGTCTCAGCACCTGTAAAGAACATTTATCTCTCATGTGTGAAG 2161  
Db 2129 CTGGAAACCTCAGTTTGTCTCAGCACCTGTAAAGAACATTTATCTCTCATGTGTGAAG 2188  
QY 2162 CCAGTCTCCTCACCATAGAAGATGAGGACACATCATCTGTACAAACCTGAAACCT 2221  
Db 2189 CCAGTCTCCTCACCATAGAAGATGAGGACACATCATCTGTACAAACCTGAAACCT 2248  
QY 2222 TCAGTAATTCATGACCTACAGAAATCAACGCTGCCGG 2257  
Db 2249 TCAGTAATTCATGACCTACAGAAATCAACGCTGCCGG 2284

RESULT 33  
US-09-579-240-17  
; Sequence 17, Application US/09579240  
; GENERAL INFORMATION:  
; APPLICANT: JoIn C. Reed  
; APPLICANT: Frederick Pio  
; APPLICANT: Adam Godzik  
; TITLE OF INVENTION: Novel Card-Domain Containing  
; FILE REFERENCE: P-LJ 4211  
; CURRENT APPLICATION NUMBER: US/09/579,240  
; CURRENT FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 2415  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ..(2412)  
US-09-579-240-17



Query Match	71.8%;	Score 2205;	DB 22;	Length 2415;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2255;	Conservative	0;	Mismatches 1;	Indels 0; Gaps
Qy	2	TGAATTTTCATAAAGGACAATAGCGAGCCCTTATTTCAAAGATGGGAATGACTGTTATAA	61	
Db	29			
Qy	62	AGCAAAATCACAGATGACCTATTTTGTATGGAATGTCTTGAATCGCGAAGAAGTAAACATCA	121	
Db	89	AGCAAAATCACAGATGACCTATTTTGTATGGAATGTCTTGAATCGCGAAGAAGTAAACATCA	148	
Qy	122	TTTGCTGCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA AAA	181	
Db	149	TTTGCTGCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA AAA	208	
Qy	182	AGGGTTCAGAGTCCTCTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTAT	241	
Db	209	AGGGTTCAGAGTCCTCTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCCTCTAT	268	
Qy	242	TTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGACGATT	301	
Db	269	TTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGACGATT	328	
Qy	302	TGCGTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCCTG	361	
Db	329	TGCGTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCCTG	388	
Qy	362	GTGAAGATATGACATATATTTTAACTTGAAGACACCTTTCACAGAACCCTGCTCTGTGGA	421	
Db	389	GTGAAGATATGACATATATTTTAACTTGAAGACACCTTTCACAGAACCCTGCTCTGTGGA	448	
Qy	422	GGAAGGACCAACACCATCATCCGGTGGAGCAGCTGACCCCTGAAATGGCTCTCTGCAGGCTC	481	
Db	449	GGAAGGACCAACACCATCATCCGGTGGAGCAGCTGACCCCTGAAATGGCTCTCTGCAGGCTC	508	
Qy	482	TTCAGAGCCCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGC	541	
Db	509	TTCAGAGCCCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGC	568	
Qy	542	GCATTGCCATGCTCTGGGGCTCGGNAAGTCAAGGCTCTGACCAAGTTCAAATTCGTCT	601	
Db	569	GCATTGCCATGCTCTGGGGCTCGGNAAGTCAAGGCTCTGACCAAGTTCAAATTCGTCT	628	
Qy	602	TCATTCTCCGCTCTCACAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCC	661	
Db	629	TCATTCTCCGCTCTCACAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCC	688	
Qy	662	TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGGC	721	
Db	689	TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGGC	748	
Qy	722	AGAGGTTCTTTTCCCTTTTGATGGGTACATGAATTCAGGCCCGAGAACTGCCAGAAA	781	
Db	749	AGAGGTTCTTTTCCCTTTTGATGGGTACATGAATTCAGGCCCGAGAACTGCCAGAAA	808	
Qy	782	TCGAAGCCCTGTATAAAGGAAAACCCGGCTTCAAGAACTGGTCACTCGTCAACACTACCA	841	
Db	809	TCGAAGCCCTGTATAAAGGAAAACCCGGCTTCAAGAACTGGTCACTCGTCAACACTACCA	868	
Qy	842	CTGAGTGCCTGAGGCACATACGGCATTTTGGTGGCCCTGACTGCTGAGTGGGGGATATGA	901	
Db	869	CTGAGTGCCTGAGGCACATACGGCATTTTGGTGGCCCTGACTGCTGAGTGGGGGATATGA	928	
Qy	902	CAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTGCTCAAGGCT	961	
Db	929	CAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTGCTCAAGGCT	988	
Qy	962	TGTTGCTCCAAATTCAGAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG	1021	
Db	989	TGTTGCTCCAAATTCAGAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG	1048	
Qy	1022	TGTCATCACTTGTGCAATTCAGATGGGTGAAAGTGAAGTGCCTCTCACACAAAAACA	1081	

Db	1049	 TGGTCACTACCTTGTGCAATCCAGATTGGGTGAAGTGAAGTTCCACTCTCACACAACA	1108
Qy	1082	CGCTGTTTCACATACTCTTATGATCTGTTGCATACAGAAAAAACAACAACAATAAAGGTG	1141
Db	1109	CGCTGTTTCACATACTCTTATGATCTGTTGCATACAGAAAAAACAACAACAATAAAGGTG	1168
Qy	1142	TGCTGCCAAGTGACTTCATTTCGGAGCCTGGACCCTCTGGAGACCTAGCTCTGGAGGGTG	1201
Db	1169	TGCTGCCAAGTGACTTCATTTCGGAGCCTGGACCCTCTGGAGACCTAGCTCTGGAGGGTG	1228
Qy	1202	TGTTCTCCCACAAGTTTGATTTTCGAACCTCCAGCATGTGTCCAGCGTGAATCAGGATGTCC	1261
Db	1229	TGTTCTCCCACAAGTTTGATTTTCGAACCTCCAGCATGTGTCCAGCGTGAATCAGGATGTCC	1288
Qy	1262	TGCTGCACAACTGGGCTCCTCTGTAATATACAGCTCAAAGGTTCAAGGTTCAAGCCAAGTATAAT	1321
Db	1289	TGCTGCACAACTGGGCTCCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAGTATAAT	1348
Qy	1322	TCTTTCACAACTCATTCAGGAGTACACAGCAGGACGAGACTCAGCAGTTTATTGACGT	1381
Db	1349	TCTTTCACAACTCATTCAGGAGTACACAGCAGGACGAGACTCAGCAGTTTATTGACGT	1408
Qy	1382	CTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGTTTTCCATTT	1441
Db	1409	CTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGTTTTCCATTT	1468
Qy	1442	CGGACATATACATCCACTTATAGCAGCCTGCTCCGCTACACCTGTGGGTCATCTCTGGAG	1501
Db	1469	CGGACATATACATCCACTTATAGCAGCCTGCTCCGCTACACCTGTGGGTCATCTCTGGAG	1528
Qy	1502	CCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTCTCCGGAC	1561
Db	1529	CCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTCTCCGGAC	1588
Qy	1562	TTTCCATCGCCAAAGAGGCCTCTCTGGAGACAGGAATCTTGC AAAAGTGTGAAAAACACA	1621
Db	1589	TTTCCATCGCCAAAGAGGCCTCTCTGGAGACAGGAATCTTGC AAAAGTGTGAAAAACACA	1648
Qy	1622	CTGAGCAGAANAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATT	1681
Db	1649	CTGAGCAGAANAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATT	1708
Qy	1682	TATATCAAGAGGTACATCCAATCAGCCCTCAGGCCAAGAATTTCAAGCTTTCTTTCAAG	1741
Db	1709	TATATCAAGAGGTACATCCAATCAGCCCTCAGGCCAAGAATTTCAAGCTTTCTTTCAAG	1768
Qy	1742	GTA AAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAAC	1801
Db	1769	GTA AAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAAC	1828
Qy	1802	ATTTGCCAAATGTGCAAGTGCTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCTA	1861
Db	1829	ATTTGCCAAATGTGCAAGTGCTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCTA	1888
Qy	1862	TGCTTCATG G G A A A A G C T T C A G A A G A C A C A G S T G G A A T C C A C A T G G A A G C C C C A G	1921
Db	1889	TGCTTCATG G G A A A A G C T T C A G A A G A C A C A G S T G G A A T C C A C A T G G A A G C C C C A G	1948
Qy	1922	A A A C C T A C A T P C C C A G S G G T G R A T C T T T C T T C A A C T G G A A G C A G G A A T T C A G A	1981
Db	1949	A A A C C T A C A T P C C C A G S G G T G R A T C T T T C T T C A A C T G G A A G C A G G A A T T C A G A	2008
Qy	1982	C T C T G G A G G T C A C A C T C C G G G A T T T C A G A A G T T G A A T A A C A A G A T A T C A C A T C T G G	2041
Db	2009	C T C T G G A G G T C A C A C T C C G G G A T T T C A G A A G T T G A A T A A C A A G A T A T C A G A T T C T G G	2068
Qy	2042	G G A A A A T A T T C A G C T C T G C C A A A G C C T C A G S C T G C A A A T A A A G A G A T G C T G G T G G	2101
Db	2069	G G A A A A T A T T C A G C T C T G C C A A A G C C T C A G S C T G C A A A T A A A G A G A T G C T G G T G G	2128
Qy	2102	C T G G A A G C C T C A G T T T G T C C T C A G C A C C T G T A A G A A C A T T A T T C T C A T G T G G A A G	2161

Db 2129 CTGGAAGCCCTCAGTTGGTCCCTCAGCACCTGTGAAGAACATTTATCTCTCATGTGTGAAG 2188  
QY 2162 CCAGTCCCTCAGCATAGAGATGAGAGGACATCATCATCTGTAAACAAACCTGAAACCT 2221  
Db 2189 CCAGTCCCTCAGCATAGAGATGAGAGGACATCATCATCTGTAAACAAACCTGAAACCT 2248  
QY 2222 TGAGTATTCATGACCTCAGCAATCAAGGCTGCGCG 2257  
Db 2249 TGAGTATTCATGACCTCAGCAATCAAGGCTGCGCG 2284

## RESULT 34

US-09-577-408-3077  
; Sequence 3077, Application US/09577408  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Tillinghast, John  
; APPLICANT: Sinku, Ankura  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; FILE REFERENCE: Polypeptides  
; CURRENT APPLICATION NUMBER: US/09/577,408  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 8502  
; SOFTWARE: PL\_GCT\_genes version 1.0  
; SEQ ID NO 3077  
; LENGTH: 3018  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (682)...(2040)  
; OTHER INFORMATION: similar to g13688110 in the genepept database release 115,  
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
US-09-577-408-3077

Query Match 71.8%; Score 2205; DB 22; Length 3018;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAATTTCAATAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTGTATATA 61  
Db 236 TGAATTTCAATAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTGTATATA 295  
QY 62 AGCAATACAGATGACCTATTTGTATGGAATGTTCTGAATCGGAAGAGTAAACATCA 121  
Db 296 AGCAATACAGATGACCTATTTGTATGGAATGTTCTGAATCGGAAGAGTAAACATCA 355  
QY 122 TTGCTCGGAGAGGTGGAGAGATGCTGCTAGAGGGATCATTCACATGATTTGAAAA 181  
Db 356 TTGCTCGGAGAGGTGGAGAGATGCTGCTAGAGGGATCATTCACATGATTTGAAAA 415  
QY 182 AGGTTTCAGAGTCTCTTAACCTCTTTCTTAAATCCCTTAAGAGAGTGAACATATCCCTCAT 241  
Db 416 AGGTTTCAGAGTCTCTTAACCTCTTTCTTAAATCCCTTAAGAGAGTGAACATATCCCTCAT 475  
QY 242 TTCAGGACTTGAATGGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTGGACGATT 301  
Db 476 TTCAGGACTTGAATGGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTGGACGATT 535  
QY 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCATCTTTTCTGAATTTATCCCTTG 361  
Db 536 TGGCTCAGGATTTAAAGGACTTGTACCATACCCATCTTTTCTGAATTTATCCCTTG 595  
QY 362 GTGAGATATGACATTTATTTAACTTGAAGACCTTTCACAGAACCTGCTGTGGA 421  
Db 596 GTGAGATATGACATTTATTTAACTTGAAGACCTTTCACAGAACCTGCTGTGGA 655  
QY 422 GGAAGGACCAACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 481  
Db 656 GGAAGGACCAACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 715

QY 482 TTCAAGTCCCTCAGATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACATCTCTGCTGAGC 541  
Db 716 TTCAAGTCCCTCAGATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACATCTCTGCTGAGC 775  
QY 542 GCATTC CATATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCT 601  
Db 776 GCATTC CATATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCT 835  
QY 602 TCTTTC TCCGCTCTCAGCAGGGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCC 661  
Db 836 TCTTTC TCCGCTCTCAGCAGGGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCC 895  
QY 662 TGGATATACCTGTCACAAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGTGGCG 721  
Db 896 TGGATATACCTGTCACAAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGTGGCG 955  
QY 722 AGAGGCTCTCTTTCCTTGTATGGCTACAAATGAATCAAGCCCAAGTCCGCAAGTCCGCA 781  
Db 956 AGAGGCTCTCTTTCCTTGTATGGCTACAAATGAATCAAGCCCAAGTCCGCAAGTCCGCA 1015  
QY 782 TCGAAGTCCCTGATTAAGGAAACACCGCTTCAAGAACATGGTCACTGCTCACCACATCA 841  
Db 1016 TCGAAGTCCCTGATTAAGGAAACACCGCTTCAAGAACATGGTCACTGCTCACCACATCA 1075  
QY 842 CTGAGT TCCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 901  
Db 1076 CTGAGT TCCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 1135  
QY 902 CAGAAG VCAGCGCCAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTCTGAAGGCT 961  
Db 1136 CAGAAG VCAGCGCCAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTCTGAAGGCT 1195  
QY 962 TGTGTC TCCAAATTCAGAAATCCAGGTGCTTGAAGGATCTCATGAAGACCCCTCTCTTTG 1021  
Db 1196 TGTGTC TCCAAATTCAGAAATCCAGGTGCTTGAAGGATCTCATGAAGACCCCTCTCTTTG 1255  
QY 1022 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1081  
Db 1256 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1315  
QY 1082 CGCTGT TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1375  
Db 1316 CGCTGT TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1435  
QY 1142 TGGCTGT TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1501  
Db 1376 TGGCTGT TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1561  
QY 1202 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1615  
Db 1436 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1675  
QY 1262 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1735  
Db 1496 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1795  
QY 1322 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1855  
Db 1556 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1915  
QY 1382 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1441  
Db 1616 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1675  
QY 1442 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1735  
Db 1676 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1795  
QY 1502 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1855  
Db 1736 TGTGTC TCACTTGTGCAATCCAGATGGTGAAGTGTGTTCCACTCTTCACACACAAACAA 1915

QY 1562 TTTCCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1621  
Db 1796 TTTCCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1855  
QY 1622 CTGAGCAAGAAATCTGAAAGCCATAAATCAATCTCTTTGTAGAGTGTGGCATCCATT 1681  
Db 1856 CTGAGCAAGAAATCTGAAAGCCATAAATCAATCTCTTTGTAGAGTGTGGCATCCATT 1915  
QY 1682 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCAAGAAATTTGAAGCTTTCTTTCAAG 1741  
Db 1916 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCAAGAAATTTGAAGCTTTCTTTCAAG 1975  
QY 1742 GTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTTGAAC 1801  
Db 1976 GTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTTGAAC 2035  
QY 1802 ATTTGCCCAATTTGCAAGTCTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCTA 1861  
Db 2036 ATTTGCCCAATTTGCAAGTCTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCTA 2095  
QY 1862 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAAATCCACATGGAAGAGGCCCCAG 1921  
Db 2096 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAAATCCACATGGAAGAGGCCCCAG 2155  
QY 1922 AAACCTACATTTCCACAGAGGCTGTATCTTTGCTTCAACTGGAAGCAGGAATTCAGGA 1981  
Db 2156 AAACCTACATTTCCACAGAGGCTGTATCTTTGCTTCAACTGGAAGCAGGAATTCAGGA 2215  
QY 1982 CTCTGGAGGTACACTCCGGGATTCAGCAAGTTTCAAGCAAGATATCATATCTGG 2041  
Db 2216 CTCTGGAGGTACACTCCGGGATTCAGCAAGTTTCAAGCAAGATATCATATCTGG 2275  
QY 2042 GAAAAATATTGAGCTCTGCCACAAGCCTCAGCTGCACAAATAAGAGATGTGCTGTGTGG 2101  
Db 2276 GAAAAATATTGAGCTCTGCCACAAGCCTCAGCTGCACAAATAAGAGATGTGCTGTGTGG 2335  
QY 2102 CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGACATTTATTTCTCATGTGTGAAG 2161  
Db 2336 CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGACATTTATTTCTCATGTGTGAAG 2395  
QY 2162 CCAGTCCCTCACCATAGAAGATGAGGCACATCAGATCTGTACAAACCTGAAAACT 2221  
Db 2396 CCAGTCCCTCACCATAGAAGATGAGGCACATCAGATCTGTACAAACCTGAAAACT 2455  
QY 2222 TGAGTATTATGACCTACAGAAATCAACGGCTGCCGG 2257  
Db 2456 TGAGTATTATGACCTACAGAAATCAACGGCTGCCGG 2491

RESULT 35  
PCT-US01-07143-22  
; Sequence 22, Application PC/TUS0107143  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM p.l.c.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50016  
; CURRENT APPLICATION NUMBER: PCT/US01/07143  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/187,107  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: 60/236,874  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/188,916  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/237,846  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 2215  
; TYPE: DNA  
; ORGANISM: Homo sapiens

PCT-US01-07143-22  
Query Match 67.1%; Score 2062; DB 1; Length 2215;  
Best Local Similarity 99.9%; Pred No. 0;  
Matches 2212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 43 ATGGAATGACTGTTTATAAAGCAAAATCAGATGACCTATTTGTATGGAATCTTCTGAAT 102  
Db 1 ATGGAATGACTGTTTATAAAGCAAAATCAGATGACCTATTTGTATGGAATCTTCTGAAT 60  
QY 103 CGCGAAGAAAGTAAACATCATTTGCTGCGAAGAGTGGAGCAGAGATGCTCTAGAGGATC 162  
Db 61 CGCGAAGAAAGTAAACATCATTTGCTGCGAAGAGTGGAGCAGAGATGCTCTAGAGGATC 120  
QY 163 ATTCACATGATTTTCAAAAAGGTTTCAGAGTCTCTGTAACCTCTTTCTTTAAATCCCTTAAG 222  
Db 121 ATTCACATGATTTTCAAAAAGGTTTCAGAGTCTCTGTAACCTCTTTCTTTAAATCCCTTAAG 180  
QY 223 GAGTGGAACTATCCCTCTATTTTCAGGACTTGAATGAGCAAAAGTCTTTTTCATCAGACATCA 282  
Db 181 GAGTGGAACTATCCCTCTATTTTCAGGACTTGAATGAGCAAAAGTCTTTTTCATCAGACATCA 240  
QY 283 GAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTGTACATACCCCATCTTTT 342  
Db 241 GAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTGTACATACCCCATCTTTT 300  
QY 343 CTGAACTTTTATCCCTCTGTTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCCTTC 402  
Db 301 CTGAACTTTTATCCCTCTGTTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCCTTC 360  
QY 403 ACAGAACTCTCTGTGGAGGAAGCAACACCATCATCCCGCTGGAGCAGCTGACCCTG 462  
Db 361 ACAGAACTCTCTGTGGAGGAAGCAACACCATCATCCCGCTGGAGCAGCTGACCCTG 420  
QY 463 AATGCCCTCTCGCAGGCTCTTCAGAGCCCTGCATCATTTGAAGGGAATCTGGCAAGGC 522  
Db 421 AATGCCCTCTCGCAGGCTCTTCAGAGCCCTGCATCATTTGAAGGGAATCTGGCAAGGC 480  
QY 523 AAGTCCACTCTGCTCAGCGCATTTGCCATGTCTGGGGCTCGGAAAGTGAAGGCTCTG 582  
Db 481 AAGTCCACTCTGCTCAGCGGAATTTGCCATGTCTGGGGCTCGGAAAGTGAAGGCTCTG 540  
QY 583 ACCAAGTTCAAATTCGTCTTCTTCTCCGTCTCAGCAGGGGCCAGGGTGGACTTTTGA 642  
Db 541 ACCAAGTTCAAATTCGTCTTCTTCTCCGTCTCAGCAGGGGCCAGGGTGGACTTTTGA 600  
QY 643 ACCCTCTGTGATCAACTCTCTGGATATACCTGGCAAAATCAGGAAGCAGACATTCATGGCC 702  
Db 601 ACCCTCTGTGATCAACTCTCTGGATATACCTGGCAAAATCAGGAAGCAGACATTCATGGCC 660  
QY 703 ATGCTGCTGAAGCTCGCGCAGAGGTTTCTTTTCTTCTTGTATGGCTACAAATGAATCAAG 762  
Db 661 ATGCTGCTGAAGCTCGCGCAGAGGTTTCTTTTCTTCTTGTATGGCTACAAATGAATCAAG 720  
QY 763 CCCAGAACTGCCAGAAATCGAAGCCCTGTATTAAGGAAAAACCCCGCTTCAAGAACATG 822  
Db 721 CCCAGAACTGCCAGAAATCGAAGCCCTGTATTAAGGAAAAACCCCGCTTCAAGAACATG 780  
QY 823 GTCATCGTCAACACTTACCACACTGAGTGCCTTGAGGCACATACGGCAGTTTGGTCCCTGACT 882  
Db 781 GTCATCGTCAACACTTACCACACTGAGTGCCTTGAGGCACATACGGCAGTTTGGTCCCTGACT 840  
QY 883 GCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTGTCTGATC 942  
Db 841 GCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTGTCTGATC 900  
QY 943 AAGGAGCTTGTGAAAGGCTTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGGAATCTC 1002  
Db 901 AAGGAGCTTGTGAAAGGCTTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGGAATCTC 960  
QY 1003 ATGAAGACCCCTCTCTTTGTGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAATTC 1062  
Db 961 ATGAAGACCCCTCTCTTTGTGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAATTC 1020

QY 1063 CACTCTCACACAAACAGCGTGTCCATACCTTCTATGATGTTGATACAGAAAAC 1122  
Db 1021 CACTCTCACACAAACAGCGTGTCCATACCTTCTATGATGTTGATACAGAAAAC 1080  
QY 1123 AAACACAAACATAAAGGTGTGGTGCAGAGTCTTATTCGGAGCCTGGACCACTGTGGA 1182  
Db 1081 AAACACAAACATAAAGGTGTGGTGCAGAGTCTTATTCGGAGCCTGGACCACTGTGGA 1140  
QY 1183 GACTAGCTCTGGAGGTGTGTCTCCCAAGTGTGATTTCGAACATGCAGGATGTGTC 1242  
Db 1141 GACTAGCTCTGGAGGTGTGTCTCCCAAGTGTGATTTCGAACATGCAGGATGTGTC 1200  
QY 1243 AGCGTGAATCAGATGTCCTGTCGACAGTGGCTCTCTGTAATATACAGCTCAAGG 1302  
Db 1201 AGCGTGAATCAGATGTCCTGTCGACAGTGGCTCTCTGTAATATACAGCTCAAGG 1260  
QY 1303 TTCAAGCCAAAGTATTAATTTCTTTCACAACTCAATTCAGAGGTACACAGCAGGACGA 1362  
Db 1261 TTCAAGCCAAAGTATTAATTTCTTTCACAACTCAATTCAGAGGTACACAGCAGGACGA 1320  
QY 1363 CTCAGCAGTTTATGAGCTCTCATGAGCCAGAGAGGTGACCAAGGGGAATGTTACTTG 1422  
Db 1321 CTCAGCAGTTTATGAGCTCTCATGAGCCAGAGAGGTGACCAAGGGGAATGTTACTTG 1380  
QY 1423 CAGAAATGTTTCCATTTTCGGACATATACATCCACTTATAGCAGCCTGCTCCCGGTACAC 1482  
Db 1381 CAGAAATGTTTCCATTTTCGGACATATACATCCACTTATAGCAGCCTGCTCCCGGTACAC 1440  
QY 1483 TGTGGGTGATCTGTGGAAGCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAA 1542  
Db 1441 TGTGGGTGATCTGTGGAAGCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAA 1500  
QY 1543 CAGGCTGCTCTCTCGACATTTCCATCGCCCAAGAGCCTCTCGGACAGGATCTTTG 1602  
Db 1501 CAGGCTGCTCTCTCGACATTTCCATCGCCCAAGAGCCTCTCTCGGACAGGATCTTTG 1560  
QY 1603 CAAAGTGTGAAGAACACCACTGACGAGAAATTCGAAAGCCATTAACATCTCTTT 1662  
Db 1561 CAAAGTGTGAAGAACACCACTGACGAGAAATTCGAAAGCCATTAACATCTCTTT 1620  
QY 1663 GTAGAGTGGCATCCATTTATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAA 1722  
Db 1621 GTAGAGTGGCATCCATTTATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAA 1680  
QY 1723 TTTGAAGCTTCTTCAAGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTA 1782  
Db 1681 TTTGAAGCTTCTTCAAGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTA 1740  
QY 1783 TTATTTGACTTCTTTGAACATTTGCCAATTTGCGAAGTCTCTGGACTTTCATTAACATG 1842  
Db 1741 TTATTTGACTTCTTTGAACATTTGCCAATTTGCGAAGTCTCTGGACTTTCATTAACATG 1800  
QY 1843 GACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCAAGACACAGGTGGAATC 1902  
Db 1801 GACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCAAGACACAGGTGGAATC 1860  
QY 1903 CACATGAAGAGCCCGCAGAAACCTACATCCAGAGGCTGTATCTTTGTTCTCAAC 1962  
Db 1861 CACATGAAGAGCCCGCAGAAACCTACATCCAGAGGCTGTATCTTTGTTCTCAAC 1920  
QY 1963 TGAAGCAGAAATTCAGGACTCTGGAGTCACTCCGGAATTCAGCAAGTTGAATAAG 2022  
Db 1921 TGAAGCAGAAATTCAGGACTCTGGAGTCACTCCGGAATTCAGCAAGTTGAATAAG 1980  
QY 2023 CAGATATACATATCTGGGGAATAATTCAGCTCTGCGCAAGCCTCAGGCTGCAATA 2082  
Db 1981 CAGATATACATATCTGGGGAATAATTCAGCTCTGCGCAAGCCTCAGGCTGCAATA 2040  
QY 2083 AAGAGATGCTGCTGGTGGAGCCTCAGTTTGGTCTCAGCAGCCTCTAAGAACAT 2142  
Db 2041 AAGAGATGCTGCTGGTGGAGCCTCAGTTTGGTCTCAGCAGCCTCTAAGAACAT 2100

QY 2143 TATTCTTTTCATGTTGGAAGCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCT 2202  
Db 2101 TATTCTTTTCATGTTGGAAGCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCT 2160  
QY 2203 GTAACACACCTGAAAACCTTGGATGATTCATGACCTACAGAAATCAACGGCTGCCGG 2257  
Db 2161 GTAACACACCTGAAAACCTTGGATGATTCATGACCTACAGAAATCAACGGCTGCCGG 2215

RESULT 36  
US-10-221-097-22  
; Sequence 22, Application US/10221097  
; GENERAL INFORMATION:  
; APPLICANT: Agriwell, Pankaj  
; APPLICANT: Birdock, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Xiang, Zhaoxing  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50016  
; CURRENT APPLICATION NUMBER: US/10/221,097  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: PCT/US01/07143  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/187,107  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: 60/236,874  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/188,916  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/237,846  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 22  
; LENGTH: 2215  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-221-097-22

Query Match 57.1%; Score 2062; DB 42; Length 2215;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 43 ATGGGAAAGACTGTATATAAGCAAAATCACAGATGACCTATTGTTGATGAAATGTTCTGAAT 102  
Db 1 ATGGGAAAGACTGTATATAAGCAAAATCACAGATGACCTATTGTTGATGAAATGTTCTGAAT 60  
QY 103 CGGGAAGAGTAACAACATCATTTGCTGCGAAGAGGTGGAGGAGGATGCTGTAGAGGATC 162  
Db 61 CGGGAAGAGTAACAACATCATTTGCTGCGAAGAGGTGGAGGAGGATGCTGTAGAGGATC 120  
QY 163 ATTCACAAGATTTGAAAAAGGTTTCAGAGTCTCTGTAACCTTTCTTAAATCCCTTAAG 222  
Db 121 ATTCACAAGATTTGAAAAAGGTTTCAGAGTCTCTGTAACCTTTCTTAAATCCCTTAAG 180  
QY 223 GAGTGGAGCTATCTCTATTTTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCA 282  
Db 181 GAGTGGAGCTATCTCTATTTTCAGGACTTGAATGGACAAAAGTCTTTTTCATCAGACATCA 240  
QY 283 GAAGGAGCTTGAGCAATTTGCTCAGGATTTAAGAGCTTGACATACCCCATCTTTT 342  
Db 241 GAAGGAGCTTGAGCAATTTGCTCAGGATTTAAGAGCTTGACATACCCCATCTTTT 300  
QY 343 CTGAACCTTTATCCCTTGTGGAAGATATTGACATTTATTTTAACTTGAAGACACCTTC 402  
Db 301 CTGAACCTTTATCCCTTGTGGAAGATATTGACATTTATTTTAACTTGAAGACACCTTC 360  
QY 403 ACAGAACCTGCTCTGTGGAGGAGGACCAACACCATCACCCTGAGGAGCAGTGAACCTG 462  
Db 361 ACAGAACCTGCTCTGTGGAGGAGGACCAACACCATCACCCTGAGGAGCAGTGAACCTG 420  
QY 463 AATGGCTCTGCGAGGCTCTTCAGAGCCCTGATCATTTGAAGGGGAATCTGCAAAAGGC 522

[illegible]

Db	1501	CACGGCTGCTCTCGGAGCTTTCCATCGCCAGAGAGCCCTCTCTGGAGACAGAGAAATCTTTG	1560
Qy	1603	CAAAAGTGTGAAAACACCACTGAGCAGAAGAAATTTGAAAGCCATAAATCAATTCCTTT	1662
Db	1561	CAAAAGTGTGAAAACACCACTGAGCAGAAGAAATTTGAAAGCCATAAATCAATTCCTTT	1620
Qy	1663	GTAGAGTGTGGCATCCATTTATATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAA	1722
Db	1621	GTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAA	1680
Qy	1723	TTTCAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAC	1782
Db	1681	TTTCAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAC	1740
Qy	1783	TATTTGACTTCTTTTGAACATTTGCCAATTTGTGCAAGTGCTCTGGACTTCATTTAAACTG	1842
Db	1741	TATTTGACTTCTTTTGAACATTTGCCAATTTGTGCAAGTGCTCTGGACTTCATTTAAACTG	1800
Qy	1843	GACTTTTATGGGGAGCTATGGCTTTCATCGGAAAAGGCTGCAAGAGACACAGGTGGGAATC	1902
Db	1801	GACTTTTATGGGGAGCTATGGCTTTCATCGGAAAAGGCTGCAAGAGACACAGGTGGGAATC	1860
Qy	1903	CACATGGAAGAGGCCCCAGAAACCTTACATTTCCCAGCGGCTGTATCTTTGTTCTTCAAC	1962
Db	1861	CACATGGAAGAGGCCCCAGAAACCTTACATTTCCCAGCGGCTGTATCTTTGTTCTTCAAC	1920
Qy	1963	TGGAAGCAGAGAAATTCAGGACTCTGGAGTCCACATCCCGGATTTTCAGCAAGTTGAATAAG	2022
Db	1921	TGGAAGCAGAGAAATTCAGGACTCTGGAGTCCACATCCCGGATTTTCAGCAAGTTGAATAAG	1980
Qy	2023	CAAGATATCACATATCTCGGGGAAAATTTACGCTCTGCCACAAGCCTCAGGCTGCAAAATA	2082
Db	1981	CAAGATATCAGATATCTGGGGGAAAATTTACGCTCTGCCACAAGCCTCAGGCTGCAAAATA	2040
Qy	2083	AAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCCCTCAGCACCTGTGAAGAACATT	2142
Db	2041	AAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCCCTCAGCACCTGTGAAGAACATT	2100
Qy	2143	TATTTCTCATGTTGGAAGCCAGTCCCTCACCATAGAGATGAGAGGCACATCACATCT	2202
Db	2101	TATTTCTCTATGTTGGAAGCCAGTCCCTCACCATAGAGATGAGAGGCACATCACATCT	2160
Qy	2203	GTAACAAACCTGAAAACCTTTGAGTATTTCTATGACCTACAGAAATCAACGGCTCCGG	2257
Db	2161	GTAACAAACCTGAAAACCTTTGAGTATTTCTATGACCTACAGAAATCAACGGCTCCGG	2215

RESULT 37  
US-09-578-789-73  
: Sequence 73, Application US/09578789

```

, GENERAL INFORMATION:
, APPLICANT: John C. Reed
, APPLICANT: Frederick Pio
, APPLICANT: Adam Godzik
, TITLE OF INVENTION: Novel Card Polypeptides
, FILE REFERENCE: P-LJ 4141
, CURRENT APPLICATION NUMBER: US/09/578,789
, CURRENT FILING DATE: 2000-05-23
, NUMBER OF SEQ ID NOS: 75
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO. 73
, LENGTH: 6900
, TYPE: DNA
, ORGANISM: Homo Sapien
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (1)...(6900)
, OTHER INFORMATION: n = A,T,C or G
US-09-578-789-73

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Query Match	63.3%;	Score 1946;	DB 22;	Length 6900;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1996:	Conservative	0;	Mismatches	1;
	Indels	0;		

QY 263 GTCCTTTTCATCAGACATCAGAGGAGCTTGGCTCAGGATTTGGCTCAGGATTTAAAGGACT 322  
Db GTCCTTTTCATCAGACATCAGAGGAGCTTGGCTCAGGATTTGGCTCAGGATTTAAAGGACT 2738  
QY 323 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGTGTGAAGATATTGACATTAATTT 382  
Db TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGTGTGAAGATATTGACATTAATTT 2798  
QY 383 TTAACCTTGAAGAGCACCTTTCACAGAACTGTCTGTGTGGAGGAAGGACCAACACCATCACC 442  
Db TTAACCTTGAAGAGCACCTTTCACAGAACTGTCTGTGTGGAGGAAGGACCAACACCATCACC 2858  
QY 443 GCGTGGAGCAGCTGACCTCTGAATGGCTCTCTGACAGGCTCTTCAGAGCCCTGCAATATG 502  
Db GCGTGGAGCAGCTGACCTCTGAATGGCTCTCTGACAGGCTCTTCAGAGCCCTGCAATATG 2918  
QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGTGACGCGCATTTGCCATGCTCTGGGCT 562  
Db AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGTGACGCGCATTTGCCATGCTCTGGGCT 2978  
QY 563 CCGGAAAGTGCAGGCTCTGACGAAGTTCRAATTCGTCTTCTTCTCTCGTCTCAGCAGGG 622  
Db CCGGAAAGTGCAGGCTCTGACGAAGTTCRAATTCGTCTTCTTCTCTCGTCTCAGCAGGG 3038  
QY 623 CCGAGGCTGACCTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGGCACAATCA 682  
Db CCGAGGCTGACCTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGGCACAATCA 3098  
QY 683 GGAAGCAGACATCATGGCCATGCTGTGAAGCTGCGGCGAGAGGGTTCTTTTCTCTCTTG 742  
Db GGAAGCAGACATCATGGCCATGCTGTGAAGCTGCGGCGAGAGGGTTCTTTTCTCTCTTG 3158  
QY 743 ATGGCTACAATGAATTCAGAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 802  
Db ATGGCTACAATGAATTCAGAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 3218  
QY 803 ACCACCGCTTCAGAAACATGCTCATCTGCTACCACTACCTGAGTGGCTGAGGCACATAC 862  
Db ACCACCGCTTCAGAAACATGCTCATCTGCTACCACTACCTGAGTGGCTGAGGCACATAC 3278  
QY 863 GGCAGTTTGTGGCTGACTGCTGAGTGGGGATATGACAGAAGACAGCGCCAGGCTC 922  
Db GGCAGTTTGTGGCTGACTGCTGAGTGGGGATATGACAGAAGACAGCGCCAGGCTC 3338  
QY 923 TCATCCGAGAGTCTGATCAAGGAGCTTGTGAAGGCTTGTGCTCCAAATTCAGAAAT 982  
Db TCATCCGAGAGTCTGATCAAGGAGCTTGTGAAGGCTTGTGCTCCAAATTCAGAAAT 3398  
QY 983 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTTGGTCACTACCTTGTCATCC 1042  
Db CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTTGGTCACTACCTTGTCATCC 3458  
QY 1043 AGATGGGTGAAGTGGTTCCTACTCTCAGACAAACAGCGTGTCCATACCTTCTATG 1102  
Db AGATGGGTGAAGTGGTTCCTACTCTCAGACAAACAGCGTGTCCATACCTTCTATG 3518  
QY 1103 ATCTGTTGATACAGAAAACAAACACAAATGAAGTGTGGCTGCAAGTCAATTC 1162  
Db ATCTGTTGATACAGAAAACAAACACAAATGAAGTGTGGCTGCAAGTCAATTC 3578  
QY 1163 GGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGCTGTCTCCCAAGATTTGATT 1222  
Db GGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGCTGTCTCCCAAGATTTGATT 3638  
QY 1223 TCGAACTGCAGGATGTCTCAGGCTGAATGAGGATGTCTGCTGACAACTGGGCTCTCT 1282  
Db TCGAACTGCAGGATGTCTCAGGCTGAATGAGGATGTCTGCTGACAACTGGGCTCTCT 3698  
QY 1283 GTAATATACAGCTCAAGGTTCAAGCAAGTATAAATCTTTTCAACAAGTCAATTCAGG 1342  
Db GTAATATACAGCTCAAGGTTCAAGCAAGTATAAATCTTTTCAACAAGTCAATTCAGG 3758

QY 1343 ATRACACAGAGGAGAGACTCAGCAGTTTATTTGACGCTCTCATCAGCCAGAGAGGTGA 1402  
Db ATRACACAGAGGAGAGACTCAGCAGTTTATTTGACGCTCTCATCAGCCAGAGAGGTGA 3818  
QY 1403 CCAAGCGAATGGTTACTTGCAGAAAATGGTTTCCATTTCCGACATTTACATCCACTTATA 1462  
Db CCAAGCGAATGGTTACTTGCAGAAAATGGTTTCCATTTCCGACATTTACATCCACTTATA 3878  
QY 1463 GCAGCCGCTCCGGTACACCTGTGGGTCTATCTGTGAAGCCACAGGCTGTGTATGAAG 1522  
Db GCAGCCGCTCCGGTACACCTGTGGGTCTATCTGTGAAGCCACAGGCTGTGTATGAAG 3938  
QY 1523 ACCTCGAGAGTGTATCAACACGCTTCTCTCGGACTTTCCATCGCCAAAGAGGCTC 1582  
Db ACCTCGAGAGTGTATCAACACGCTTCTCTCGGACTTTCCATCGCCAAAGAGGCTC 3998  
QY 1583 TCTGGAACAGGAATCTTTCAGAAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAG 1642  
Db TCTGGAACAGGAATCTTTCAGAAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAG 4058  
QY 1643 GCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702  
Db GCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 4118  
QY 1703 AATCAGCCTGAGGCCAAGATTTGAAGCTTCTTTCAAGGTAAAGCTTATATCAACT 1762  
Db AATCAGCCTGAGGCCAAGATTTGAAGCTTCTTTCAAGGTAAAGCTTATATCAACT 4178  
QY 1763 CAGGGAACATCCCGATTTACTTTTGTGACTTCTTTGAACATTTGCCAAATTTGCAAGTG 1822  
Db CAGGGAACATCCCGATTTACTTTTGTGACTTCTTTGAACATTTGCCAAATTTGCAAGTG 4238  
QY 1823 CTCTGGAATTCATTAATGACTTTTATGGGGAGCTATGGCTTCTATGGGAAAAGCTG 1882  
Db CTCTGGAATTCATTAATGACTTTTATGGGGAGCTATGGCTTCTATGGGAAAAGCTG 4298  
QY 1883 CAGAAGAACAGGTGGAATCCACATGGAAGAGGCGCCAGAAACCTACATTTCCAGCAGGG 1942  
Db CAGAAGAACAGGTGGAATCCACATGGAAGAGGCGCCAGAAACCTACATTTCCAGCAGGG 4358  
QY 1943 CTGTATCTTTGTTCTTCAACTTGAAGCAGGAATTCAGGACTCTGGAGTCACTCCGCGG 2002  
Db CTGTATCTTTGTTCTTCAACTTGAAGCAGGAATTCAGGACTCTGGAGTCACTCCGCGG 4418  
QY 2003 ATTTCAAGCAAGTGAATGAATATACATATCTGGGAAAATATTCAGCTCTGCCA 2062  
Db ATTTCAAGCAAGTGAATGAATATACATATCTGGGAAAATATTCAGCTCTGCCA 4478  
QY 2063 CAAGCCTCAGGCTCAATTAAGAGATGTCTGCTGGTGGCTGGAAGCTCAGTTTGTGTC 2122  
Db CAAGCCTCAGGCTCAATTAAGAGATGTCTGCTGGTGGCTGGAAGCTCAGTTTGTGTC 4538  
QY 2123 TCAGCACCCTGAAGAACATTTATTTCTCTCATGTTGGAAGCCAGTCCCTCACCATAGAG 2182  
Db TCAGCACCCTGAAGAACATTTATTTCTCATGTTGGAAGCCAGTCCCTCACCATAGAG 4598  
QY 2183 ATGAGAGGACATCAGATCTGTAAACAACTGAAACCTTGAGTATTTCATGACCTACAGA 2242  
Db ATGAGAGGACATCAGATCTGTAAACAACTGAAACCTTGAGTATTTCATGACCTACAGA 4658  
QY 2243 ATCAACGGTTCGCGGGT 2259  
Db ATCAACGGTTCGCGGGT 4675

RESULT 38  
US-09-579-240-73  
; Sequence 73, Application US/09579240  
; GENERAL INFORMATION:  
; APPLICANT: John S. Reed  
; APPLICANT: Fredrick Plo  
; APPLICANT: Adam Godzik  
; TITLE OF INVENTION: Novel Card-Domain Containing

;  
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
; FILE REFERENCE: P-LJ 4211  
; CURRENT APPLICATION NUMBER: US/09/579,240  
; CURRENT FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 6900  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(6900)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-579-240-73

Query Match		63.3%	Score 1946;	DB 22;	Length 6900;
Best Local Similarity		99.9%	Pred. No. 0;		
Matches 1996;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	263	GTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT	322		
DB	2679	GTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT	2738		
QY	323	TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATTTGACATTTATTT	382		
DB	2739	TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATTTGACATTTATTT	2798		
QY	383	TTAATTGAAAGACCTTTCACAGAACCTGTCTCTGTGGAGGAAGGACCAACCATCACCC	442		
DB	2799	TTAATTGAAAGACCTTTCACAGAACCTGTCTCTGTGGAGGAAGGACCAACCATCACCC	2858		
QY	443	GCCTGGAGCAGCTCACCTCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTTGCATCATTTG	502		
DB	2859	GCCTGGAGCAGCTCACCTCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTTGCATCATTTG	2918		
QY	503	AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGCTCTGGGGCT	562		
DB	2919	AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGCTCTGGGGCT	2978		
QY	563	CCGGAAGTGCAGGCTCTGACCAAGTTCAAATTCGTCCTCCCTCCCTCAGCAGGG	622		
DB	2979	CCGGAAGTGCAGGCTCTGACCAAGTTCAAATTCGTCCTCCCTCCCTCAGCAGGG	3038		
QY	623	CCCAGGTGGACTTTTGAACCCCTCTGTGATCAACTCTTGGATATACCTTGGCACAATCA	682		
DB	3039	CCCAGGTGGACTTTTGAACCCCTCTGTGATCAACTCTTGGATATACCTTGGCACAATCA	3098		
QY	683	GGAAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGCAGAGGGTTCTTTTCCCTTTTG	742		
DB	3099	GGAAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGCAGAGGGTTCTTTTCCCTTTTG	3158		
QY	743	ATGCTACATGAATTCAGCCCCAGAACTGCCCAGAAATCGAAGCCCTGATAAAGGAAA	802		
DB	3159	ATGCTACATGAATTCAGCCCCAGAACTGCCCAGAAATCGAAGCCCTGATAAAGGAAA	3218		
QY	803	ACCACCGCTTCAAGAACATGTCATCTGCACCACTACCCTGAGTGGCTGAGGCACATAC	862		
DB	3219	ACCACCGCTTCAAGAACATGTCATCTGCACCACTACCCTGAGTGGCTGAGGCACATAC	3278		
QY	863	GGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGGATATGACAGAGACAGCGCCCGAGGCTC	922		
DB	3279	GGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGGATATGACAGAGACAGCGCCCGAGGCTC	3338		
QY	923	TCATCCGAGAAGTCTGATCAAGGAGCTTGTGTAAGGCTTTGTCTCCAAATTCAGAAAT	982		
DB	3339	TCATCCGAGAAGTCTGATCAAGGAGCTTGTGTAAGGCTTTGTCTCCAAATTCAGAAAT	3398		
QY	983	CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTTGGGTGATCATCTGTGCAATCC	1042		
DB	3399	CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTTGGGTGATCATCTGTGCAATCC	3458		
QY	1043	AGATGGGTGAAAGTGAGTTCACACTCTCACACAAACACGCTCTTCCATACCTTCTATG	1102		

DB	3459	AGATGGGTGAAAGTGAGTTCACACTCTCACACAAACAAACGCTGTTCATACCTTCTATG	3518		
QY	1103	ATCTGTTGATACAGAAAAACAAACACAAACATAAAGTGTGGCTGCAAGTCACTTCAATTC	1162		
DB	3519	ATCTGTTGATACAGAAAAACAAACACAAACATAAAGTGTGGCTGCAAGTCACTTCAATTC	3578		
QY	1163	GGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTCTTCCACACAAGTTTGATT	1222		
DB	3579	GGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTCTTCCACACAAGTTTGATT	3638		
QY	1223	TCGAACCTGCAGGATGTGTCCAGCCTGAATGAGGATGTCTCTGACAACTGGGCTCTCTCT	1282		
DB	3639	TCGAACCTGCAGGATGTGTCCAGCCTGAATGAGGATGTCTCTGACAACTGGGCTCTCTCT	3698		
QY	1283	GTAATAATACAGCTCAAAGGTTCAAGCCAAAGTATAAATCTTTTCACAAGTCATTCCAGG	1342		
DB	3699	GTAATAATACAGCTCAAAGGTTCAAGCCAAAGTATAAATCTTTTCACAAGTCATTCCAGG	3758		
QY	1343	AGTACACAGCAGGACGAGACTCAGCAGTTTATTTGACCTCTCATGAGCCAGAGAGGTGA	1402		
DB	3759	AGTACACAGCAGGACGAGACTCAGCAGTTTATTTGACCTCTCATGAGCCAGAGAGGTGA	3818		
QY	1403	CCAAGGGGAATGTACTTGCAGAAAAATGGTTTCCATTTTCGGACATTTACATCCACTTATA	1462		
DB	3819	CCAAGGGGAATGTACTTGCAGAAAAATGGTTTCCATTTTCGGACATTTACATCCACTTATA	3878		
QY	1463	GCAGCCTGCTCCGTCACACCTGTGGTGCATCTGTGGAGCCACACAGGCTCTTATGAAGC	1522		
DB	3879	GCAGCCTGCTCCGTCACACCTGTGGTGCATCTGTGGAGCCACACAGGCTCTTATGAAGC	3938		
QY	1523	ACCTCGCAGCAGTGTATCAACACGCTTCTCGGACTTTTCCATGCCAAGAGGCTC	1582		
DB	3939	ACCTCGCAGCAGTGTATCAACACGCTTCTCGGACTTTTCCATGCCAAGAGGCTC	3998		
QY	1583	TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACACACTGAGCAAGAAATTCGAAAG	1642		
DB	3999	TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACACACTGAGCAAGAAATTCGAAAG	4058		
QY	1643	CCATAAACATCAATCTTCTGTAGAGTGGCATCCATTTATATCAAGAGAGTACATCCA	1702		
DB	4059	CCATAAACATCAATCTTCTGTAGAGTGGCATCCATTTATATCAAGAGAGTACATCCA	4118		
QY	1703	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTTCAAGGTAAAAGCTTATATATCAACT	1762		
DB	4119	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTTCAAGGTAAAAGCTTATATATCAACT	4178		
QY	1763	CAGGAAACATCCCGATTACTTATTTGACTTCTTTTGAACATTTGCCAAATTTGTGCAAGTG	1822		
DB	4179	CAGGAAACATCCCGATTACTTATTTGACTTCTTTTGAACATTTGCCAAATTTGTGCAAGTG	4238		
QY	1823	CTCTGGACTTCATTTAAACTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG	1882		
DB	4239	CTCTGGACTTCATTTAAACTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG	4298		
QY	1883	CAGAAGACACAGGTGGAAATCCACATGGAAGAGGCCCAAGAACTTACATTTCCACAGCAGG	1942		
DB	4299	CAGAAGACACAGGTGGAAATCCACATGGAAGAGGCCCAAGAACTTACATTTCCACAGCAGG	4358		
QY	1943	CTGTATCTTTTCTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGG	2002		
DB	4359	CTGTATCTTTTCTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGG	4418		
QY	2003	ATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTCTGGGAAAAATATTCAGCTCTTGCCA	2062		
DB	4419	ATTTTCAGCAAGTTGAATAAGCAAGATATCATATCTCTGGGAAAAATATTCAGCTCTTGCCA	4478		
QY	2063	CAAGCCTCAGCTGCAAAATAAGAGATGTCTGTGTGGCTGGAAGCCCTCAGTTTGGTCC	2122		
DB	4479	CAAGCCTCAGCTGCAAAATAAGAGATGTCTGTGTGGCTGGAAGCCCTCAGTTTGGTCC	4538		
QY	2123	TCAGCACCTGTGAAGAACATTTTATCTCTCATGGTGGAGAGCCAGTCCCTCACCATAGAAG	2182		



Db 4539 TCAGCACCTGTAAGAACATTTATTCTCTCATGCTGGAAGCCAGTCCCTCACCATAGAAG 4598  
Qy 2183 ATGAGAGGCACATCACATCTGTACAAACCTGAAACCTTTGAGTATTTCATGACCTACAGA 2242  
Db 4599 ATGAGAGGCACATCACATCTGTACAAACCTGAAACCTTTGAGTATTTCATGACCTACAGA 4658  
Qy 2243 ATCAACGGCTGCCGGT 2259  
Db 4659 ATCAACGGCTGCCGGT 4675  
RESULT 39  
US-09-686-347-73  
; Sequence 73, Application US/09686347  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Plo, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Lee, Sug Hyung  
; APPLICANT: Stehlik, Christian  
; TITLE OF INVENTION: Novel Card-Domain Containing  
; FILE REFERENCE: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
; CURRENT APPLICATION NUMBER: US/09/686,347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/579,240  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 6900  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(6900)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-686-347-73  
Query Match 63.3%; Score 1946; DB 27; Length 6900;  
Best Local Similarity 99.9%; Pred No. 0;  
Matches 1996; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322  
Db 2679 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 2738  
Qy 323 TGTACCATACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATATGACATTTATTT 382  
Db 2739 TGTACCATACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATATGACATTTATTT 2798  
Qy 383 TTAACCTGAAAGACCTTTCACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACCC 442  
Db 2799 TTAACCTGAAAGACCTTTCACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACCC 2858  
Qy 443 GCGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 502  
Db 2859 GCGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 2918  
Qy 503 AAGGGGAATCTGGCAAAGGCAAGTCCACCTCTGCTGCAGGCGCATTTGCCATGCTCTGGGGCT 562  
Db 2919 AAGGGGAATCTGGCAAAGGCAAGTCCACCTCTGCTGCAGGCGCATTTGCCATGCTCTGGGGCT 2978  
Qy 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTTCTTCTCCCTCTCAGCAGG 622  
Db 2979 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTTCTTCTCCCTCTCAGCAGG 3038  
Qy 623 CCAGGGTGGACTTTTGAACCCCTGTGATCACTCTGATCACTCTGATACCTGGCAACAATCA 682  
Db 3039 CCAGGGTGGACTTTTGAACCCCTGTGATCACTCTGATCACTCTGATACCTGGCAACAATCA 3098  
Qy 683 GGNAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGCGAGAGGGTTCTTTCTCTCTTG 742

Db 3099 GGAAG:AGACATTCATGGCCATGCTGCTGAAGCTGCGGAGAGGGTTCTTTTCTCTCTTG 3158  
Qy 743 ATGGC:ACAAATGAATTCAGAGCCCAAGAACTGCCCCAGAAATCGAAGCCCTGTATGAAGGAA 802  
Db 3159 ATGGC:ACAAATGAATTCAGAGCCCAAGAACTGCCCCAGAAATCGAAGCCCTGTATGAAGGAA 3218  
Qy 803 ACCAC:GCTTCAAGAACATGGTTCATGTCACCACTACCACTAGTGCCTGAGGACATAC 862  
Db 3219 ACCAC:GCTTCAAGAACATGGTTCATGTCACCACTACCACTAGTGCCTGAGGACATAC 3278  
Qy 863 GGCAG:TTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGGCCCGGAGCTC 922  
Db 3279 GGCAG:TTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGGCCCGGAGCTC 3338  
Qy 923 TCATCC:GAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCTTGTGTCTCCAAATTCAGAAAT 982  
Db 3339 TCATCC:GAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCTTGTGTCTCCAAATTCAGAAAT 3398  
Qy 983 CCAGGT:GCTTGAAGAAATCTCATGAAGACCCCTCTCTTTGTGTGTCATCACTTGTGCAATCC 1042  
Db 3399 CCAGGT:GCTTGAAGAAATCTCATGAAGACCCCTCTCTTTGTGTGTCATCACTTGTGCAATCC 3458  
Qy 1043 AGATGG:GTGAAAGTGTGCTCCACTCTCACACACAAACAAACGCTGTGTCCATACCTTCTATG 1102  
Db 3459 AGATGG:GTGAAAGTGTGCTCCACTCTCACACACAAACAAACGCTGTGTGTCCATACCTTCTATG 3518  
Qy 1103 ATCTGT:IGATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGTGACTTCATTC 1162  
Db 3519 ATCTGT:IGATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGTGACTTCATTC 3578  
Qy 1163 GGAGCC:GGACCACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTTGTAT 1222  
Db 3579 GGAGCC:GGACCACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTTGTAT 3638  
Qy 1223 TGGAC:TCAGGATGTGTCAGGCTGAATGAGGATGCTCTGCTGACAACTGGCTCCTCT 1282  
Db 3639 TGGAC:TCAGGATGTGTCAGGCTGAATGAGGATGCTCTGCTGACAACTGGCTCCTCT 3698  
Qy 1343 AGTAC:AGCAGACGAAAGACTCAGAGTTTATGAGTCTCATGAGCCAGAGGAGGTGA 1402  
Db 3759 AGTAC:AGCAGACGAAAGACTCAGAGTTTATGAGTCTCATGAGCCAGAGGAGGTGA 3818  
Qy 1403 CCAAGG:GAATGGTTACTTGCAGAAATGGTTTCCATTTCCGACATTTACATCCACTATA 1462  
Db 3819 CCAAGG:GAATGGTTACTTGCAGAAATGGTTTCCATTTCCGACATTTACATCCACTATA 3878  
Qy 1463 GCAGCC:GCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCCACAGGGCTGTATGAAGC 1522  
Db 3879 GCAGCC:GCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCCACAGGGCTGTATGAAGC 3938  
Qy 1523 AGCTGC:AGCAGTGTATCAACACAGGCTGCTTCTCGGACTTTCCATTCGCAAGAGGCTC 1582  
Db 3939 AGCTGC:AGCAGTGTATCAACACAGGCTGCTTCTCGGACTTTCCATTCGCAAGAGGCTC 3998  
Qy 1583 TCTGGAG:ACAGAAATCTTTTGAAGTGTGAAACAAACCACTGAGCAAGAAATTCCTCAAG 1642  
Db 3999 TCTGGAG:ACAGAAATCTTTTGAAGTGTGAAACAAACCACTGAGCAAGAAATTCCTCAAG 4058  
Qy 1643 CCATTA:CATCAATCTTTGTAGAGTGGGATCCATTTATATCAAGAGATACATCCA 1702  
Db 4059 CCATTA:CATCAATCTTTGTAGAGTGGGATCCATTTATATCAAGAGATACATCCA 4118  
Qy 1703 AATCAG:CTGAGCCAGAAATTTGAGCTTCTTCAAGGTAAAGCTTATATCAACT 1762  
Db 4119 AATCAG:CTGAGCCAGAAATTTGAGCTTCTTCAAGGTAAAGCTTATATCAACT 4178  
Qy 1763 CAGGGA:ATCCCCGATTTACTTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1822



Db 4179 CAGGGAACATCCCCGATTAATTTGACTCTTTTGAACATTTGCCCCAATTTGTGCAAGT 4238  
Qy 1823 CTCGTGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG 1882  
Db 4239 CTCGTGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG 4298  
Qy 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATCCACAGGG 1942  
Db 4299 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATCCACAGGG 4358  
Qy 1943 CTGTATCTTTTCTTCACTGGAAGCAGGAATTCAGAGCTCTGGAGTTCACACTCCGG 2002  
Db 4359 CTGTATCTTTTCTTCACTGGAAGCAGGAATTCAGAGCTCTGGAGTTCACACTCCGG 4418  
Qy 2003 ATTTTCAGCAAGTTGAATGAAGCAAGATATCACATATCTGGGAAATATTCAGCTCTGCCA 2062  
Db 4419 ATTTTCAGCAAGTTGAATGAAGCAAGATATCACATATCTGGGAAATATTCAGCTCTGCCA 4478  
Qy 2063 CAAGCCTCAGGCTGCAAAATAAAGAGATGCTGTGGTGGGAAAGCCTCAGTTTGGTCC 2122  
Db 4479 CAAGCCTCAGGCTGCAAAATAAAGAGATGCTGTGGTGGGAAAGCCTCAGTTTGGTCC 4538  
Qy 2123 TCAGCACCCTGAAGCAATTTATCTCTCATGCTGGTGAAGCCAGTCCCTCACCATTAGAG 2182  
Db 4539 TCAGCACCCTGAAGCAATTTATCTCTCATGCTGGTGAAGCCAGTCCCTCACCATTAGAG 4598  
Qy 2183 ATGAGAGGCATCATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTTACAGA 2242  
Db 4599 ATGAGAGGCATCATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTTACAGA 4658  
Qy 2243 ATCAACGGCTGCGGGT 2259  
Db 4659 ATCAACGGCTGCGGGT 4675

## RESULT 40

US-09-557-676-906  
; Sequence 906, Application US/09557676  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith  
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-136  
; CURRENT APPLICATION NUMBER: US/09/557,676  
; CURRENT FILING DATE: 2000-04-25  
; NUMBER OF SEQ. ID NOS: 986  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 906  
; LENGTH: 4098  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-676-906

Query Match 63.3%; Score 1945; DB 22; Length 4098;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 263 GTCCTTTTCATCAGACATCAGAAGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 322  
Db 275 GTCCTTTTCATCAGACATCAGAAGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 334  
Qy 323 TGTACCATACCCATCTTTTCTGAACTTTTATCCCTTTGGTGAAGATATTGACATATT 382  
Db 335 TGTACCATACCCATCTTTTCTGAACTTTTATCCCTTTGGTGAAGATATTGACATATT 394  
Qy 383 TTAACCTGAAAGCAACCTTCAGAACCTGTCCTGTGGAGGAAGCAACCAACCATCACC 442  
Db 395 TTAACCTGAAAGCAACCTTCAGAACCTGTCCTGTGGAGGAAGCAACCAACCATCACC 454  
Qy 443 CGGTGGACAGCTGACCTGATGGCTCTCTGCAGGCTCTTCAGAGCCCTTCATCAT 502  
Db 455 CGGTGGACAGCTGACCTGATGGCTCTCTGCAGGCTCTTCAGAGCCCTTCATCAT 514  
Qy 503 AAGGGGAATCTGGGAAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGCT 562

Db 515 AAGGGGAATCTGGCAAGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGCT 574  
Qy 563 CCGGAAGCTGAAGGCTCTGACCAAGTTCAAAATTCGTTCTTCTCCGTCGTCACAGG 622  
Db 575 CCGGAAGCTGAAGGCTCTGACCAAGTTCAAAATTCGTTCTTCTCCGTCGTCACAGG 634  
Qy 623 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCAACAATCA 682  
Db 635 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCAACAATCA 694  
Qy 683 GGAAGCAGACATTCATGCGCATGCTGCTGAAGCTCGGGCAGAGGTTCTTTTCTCTCTG 742  
Db 695 GGAAGCAGACATTCATGCGCATGCTGCTGAAGCTCGGGCAGAGGTTCTTTTCTCTCTG 754  
Qy 743 ATGGCTACAAATTCAGAGCCCAAGACTGCCAGAAATCGAAGCCCTGATAAAGGAA 802  
Db 755 ATGGCTACAAATTCAGAGCCCAAGACTGCCAGAAATCGAAGCCCTGATAAAGGAA 814  
Qy 803 ACCACCGCTTCAAGAACATGGTCACTGCTCACCACCTACCACCTGAGTGCCTGAGGCACATAC 862  
Db 815 ACCACCGCTTCAAGAACATGGTCACTGCTCACCACCTACCACCTGAGTGCCTGAGGCACATAC 874  
Qy 863 GGCAGTTTGGTCCCTGACTGCTGAGTGGGGATATGACAGAAGACAGCGCCAGGCTC 922  
Db 875 GGCAGTTTGGTCCCTGACTGCTGAGTGGGGATATGACAGAAGACAGCGCCAGGCTC 934  
Qy 923 TCATCCGAGAGTGTGATCAAGAGACTTGTGTAAGGCTTGTGCTCCAAATTCAGAAAT 982  
Db 935 TCATCCGAGAGTGTGATCAAGAGACTTGTGTAAGGCTTGTGCTCCAAATTCAGAAAT 994  
Qy 983 CCAGTGTCTGAGGAATCTCATGAAGAGCCCTCTCTTGTGTGTCATCACTTGTGCAATCC 1042  
Db 995 CCAGTGTCTGAGGAATCTCATGAAGAGCCCTCTCTTGTGTGTCATCACTTGTGCAATCC 1054  
Qy 1043 AGATGGGTGAAAGTGAAGTTCACACTCTCACACACAAACACGCTGTTCATATCTTCTATG 1102  
Db 1055 AGATGGGTGAAAGTGAAGTTCACACTCTCACACACAAACACGCTGTTCATATCTTCTATG 1114  
Qy 1103 ATCTCTTATACAGAAACAAACAAACATAAAGGTGTGGCTGCAAGTGAATTCATTC 1162  
Db 1115 ATCTCTTATACAGAAACAAACAAACATAAAGGTGTGGCTGCAAGTGAATTCATTC 1174  
Qy 1163 GGAGCTTGACCACTGTGGAGACTTAGTCTCGAGGCTGTGTTCTCCCAACAGTTGATT 1222  
Db 1175 GGAGCTTGACCACTGTGGAGACTTAGTCTCGAGGCTGTGTTCTCCCAACAGTTGATT 1234  
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Db 1235 TCGAACTGCAGGATGTCTCCAGCGTGAATGAGGATGTCTGCTGACAACTGGGCTCCTCT 1294  
Qy 1283 GTAATATACAGCTCAAGGTTCAAGCCAAAGATATAATTTCTTTCACAGTCAATTCACAG 1342  
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Db 1475 GCAGCTGCTCGGTGACACTGTGGGTGATCTGTGGAAGCCACAGGCTGTGTTATGAAGC 1534  
Qy 1523 ACCTGCAGCAGTGTATCAACAGCGCTGCTTCTCGGACTTTTCCATTCGCAAGAGGCTC 1582  
Db 1535 ACCTGCAGCAGTGTATCAACAGCGCTGCTTCTCGGACTTTTCCATTCGCAAGAGGCTC 1594  
Qy 1583 TCTGAGACAGGAATCTTTTGAAGTGTGAAGAACCACTGAGCAAGAAATTTCTGAAG 1642

Db 1595 TCCTGGAGACAGGAATCTTTTCAAGGTGTGAAAAACACCACTGAGCAAGAAATTTCTGAAAG 1654  
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Db 1655 CCATAAACATCAATCTCTTTGTAGAGTGTGGCATCTCATTTATATCAAGAGGTACATCCA 1714  
QY 1703 AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762  
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Db 2255 ATCAAGCGTGCCTGGG 2270

## RESULT 41

US-09-557-676-912  
; Sequence 912, Application US/09557676  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith  
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-136  
; CURRENT APPLICATION NUMBER: US/09/557,676  
; CURRENT FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 986  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 912  
; LENGTH: 4098  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-676-912

Query Match 63.3%; Score 1945; DB 22; Length 4098;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 263 GTCTTTTTCATCAGATCAGAGAGACTTGGACAGATTTGGCTCAGGATTTAAAGGACT 322  
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QY 503 AAGGGGAATCTGCAAGGCAAGTCCACCTCTGCTGAGCGCATTTGTCATCTCTGGGCT 562  
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QY 563 CCGGAAAGTGCAGAGCTCTGACCAAGTTCAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 622  
Db 575 CCGGAAAGTGCAGAGCTCTGACCAAGTTCAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 634  
QY 623 CCGAGGATGAGCTTTTGAACCTCTGTGATCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 682  
Db 635 CCGAGGATGAGCTTTTGAACCTCTGTGATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 694  
QY 683 GGAAGCAGATTCATGAGCTGCTGCTGAACTGGGCGAGAGGTTCTTTCTCTCTCTCTCTCTCT 742  
Db 695 GGAAGCAGATTCATGAGCTGCTGCTGAACTGGGCGAGAGGTTCTTTCTCTCTCTCTCTCTCT 754  
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Db 1535 ACCTCGACAGTGTATCAACAGCGTGCCTTCTCGGACTTTCCATCGCAAGAGCCCTC 1594  
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QY 1643 CCATTAACATCAATCTCTTTGTAGAGTGTGGCATCTTATATCAAGAGAGTACATCCA 1702  
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QY 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGGCCCCAGAAACCTACATTCCCAGCAGGG 1942  
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QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 2122  
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QY 2243 ATCAACGGGTGCCGGG 2258  
Db 2255 ATCAACGGGTGCCGGG 2270

RESULT 42

US-10-042-938-906  
; Sequence 906, Application us/10042938  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith  
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-136  
; CURRENT APPLICATION NUMBER: US/10/042,938  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: 09/557,676  
; PRIOR FILING DATE: 2000-APR-25  
; NUMBER OF SEQ ID NOS: 986  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 906

; LENGTH: 4098  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-042-938-906  
Query Match 63.3%; Score 1945; DB 38; Length 4098;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 263 GTCCTTTTTCATCAGACATCAGAGGAGACTTGGACCAATTTGGCTCAGGATTTTAAAGGACT 322  
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QY 323 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTTATTT 382  
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QY 383 TTTAACTTGAAGACACCTTTCACAGAACCTTCTCTGTGGAGGAAGGACCACACCATCAC 442  
Db 395 TTTAACTTGAAGACACCTTTCACAGAACCTTCTCTGTGGAGGAAGGACCACACCATCAC 454  
QY 443 GCGTGGAGCAGCTGACCCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTTGCATCATTTG 502  
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QY 503 AAGGGGAATCTGGCAAAGGCAAGTCCACCTCTGCTGCAGGCAATTTGCCATGCTCTGGGGCT 562  
Db 515 AAGGGGAATCTGGCAAAGGCAAGTCCACCTCTGCTGCAGGCAATTTGCCATGCTCTGGGGCT 574  
QY 563 CCGGAAAGTGCAGGCTCTGACCAAGTTCAAAATTCCTTCTTCCCTCCGTTCTCAGCAGGG 622  
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QY 623 CCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTTGGCACAATCA 682  
Db 635 CCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTTGGCACAATCA 694  
QY 683 GGAAGCAGACATTCATGTGGCATCTGCTGAAGCTGCGGAGAGGTTCTTTCTCTCTCTTG 742  
Db 695 GGAAGCAGACATTCATGTGGCATCTGCTGNAAGCTGCGGAGAGGGTTCTTTCTCTCTTG 754  
QY 743 ATGGCTACAATGAATTCAGGCCCAAGAACTGCCCAGAAATCGAAGCCCTGTATAAAGAAA 802  
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QY 863 GGCAGTTTGGTGCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 922  
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Db 1175 GGAGCCTGGAACCACTGTGGAGACCTAGTCTCTGGAGGTTGTCTCTCCACAAAGTTTGAAT 1234

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Db 1235 TCGAACTCAGAGTGTCTCAGCGTGAATGAGGATGCTCTCTGACAACTGGGCTCTCT 1294
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Db 1295 GTAATATACAGCTCAAAAGTTCAAGCCAAAGATATAAATCTTTCACAAGTCATTCCAGG 1354
QY 1343 AGTACACAGCAGGAGGAAGACTCAGCAGTTTATTGACGCTCTCATGAGCGAGAGGAGTGA 1402
Db 1355 AGTACACAGCAGGAGGAAGACTCAGCAGTTTATTGACGCTCTCATGAGCGAGAGGAGTGA 1414
QY 1403 CCAAGGGAATGGTTTACTTTGAGAAAATGGTTTCCATTTCGGACATATACATCCACTTATA 1462
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QY 1703 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTTCAAGGTAAAGCTTATATATCAACT 1762
Db 1715 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTTCAAGGTAAAGCTTATATATCAACT 1774
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Db 1895 CAGAGACACAGGTGGATCCACATGGAGAGGCCGCCAAGAACCTACATTCACAGCAGG 1954
QY 1943 CTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGTCACTCCGG 2002
Db 1955 CTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGTCACTCCGG 2014
QY 2003 ATTTCAAGCAAGTTGAATGAAGCAAGATATACATATCTGGGGAAATATTCAGCTCTGCCA 2062
Db 2015 ATTTCAAGCAAGTTGAATGAAGCAAGATATACATATCTGGGGAAATATTCAGCTCTGCCA 2074
QY 2063 CAAGCCTCAGGCTGCAATAAAGAGATGTGCTGGTGGTGGAGGCTCAGTTTGGTCC 2122
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QY 2243 ATCAAGGCTCGCGGG 2258
Db 2255 ATCAAGGCTCGCGGG 2270
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RESULT 43
US-10-042-938-912
; SEQUENCE 912, Application US/10042938
; GENERAL INFORMATION:
; APPLICANT: R. Ison, Keith
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-136
; CURRENT APPLICATION NUMBER: US/10/042,938
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 09/557,676
; PRIOR FILING DATE: 2000-APR-25
; NUMBER OF SEQ ID NOS: 986
; SOFTWARE: FASTA/SEQ for Windows Version 3.0
; SEQ ID NO 912
; LENGTH: 4098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-938-912

Query Match 63.3%; Score 1945; DB 38; Length 4098;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 263 GTCCTTTTCATCAGACATCAGAAGAGACTTGGAGGATTTGGCTCAGGATTTAAAGGACT 322
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Db 1115 ATCTGTTGATACAGAAAAACAACAAACATAAAGGTGTGGCTGCAAGTGACTTCATTG 1174  
QY 1163 GGAGCCTGGACCACTGTGGAGACCTAGCTCTCGGAGGGTGTGTTCTCCCAACAAGTTTGATT 1222  
Db 1175 GGAGCCTGGACCACTGTGGAGACCTAGCTCTCGGAGGGTGTGTTCTCCCAACAAGTTTGATT 1234  
QY 1223 TCGAACTGCAGGATGTGTCAGCGTCAATGAGGATGCTCTGCTGACAACTGGGCTCCTCT 1282  
Db 1235 TCGAACTGCAGGATGTGTCAGCGTCAATGAGGATGCTCTGCTGACAACTGGGCTCCTCT 1294  
QY 1283 GTAATATATACAGTCAAGGTTCAAGCCAAAGTATAAATTCCTTTCACAAAGTCATTCCAGG 1342  
Db 1295 GTAATATATACAGTCAAGGTTCAAGCCAAAGTATAAATTCCTTTCACAAAGTCATTCCAGG 1354  
QY 1343 AGTACACAGCAGGACGAAGACTCAGCAGTTTATGACGTCCTATGAGCCAGAGGAGGTGA 1402  
Db 1355 AGTACACAGCAGGACGAAGACTCAGCAGTTTATGACGTCCTATGAGCCAGAGGAGGTGA 1414  
QY 1403 CCAAGGGGAATGTTACTTTCGAGAAATGTTTCCATTTCCGACATTACACCTTATA 1462  
Db 1415 CCAAGGGGAATGTTACTTTCGAGAAATGTTTCCATTTCCGACATTACACCTTATA 1474  
QY 1463 GCAGCCTGCTCGGTACACCTGTGGTCTCATCTGTGGAAGCCACGAGGCTGTATGAAGC 1522  
Db 1475 GCAGCCTGCTCGGTACACCTGTGGTCTCATCTGTGGAAGCCACGAGGCTGTATGAAGC 1534  
QY 1523 ACCTCCAGAGTGTATCAACAGCGGTGCTCTCTCGGACTTTCATTCGCAAGAGCGCTC 1582  
Db 1535 ACCTCCAGAGTGTATCAACAGCGGTGCTCTCTCGGACTTTCATTCGCAAGAGCGCTC 1594  
QY 1583 TCTGGAGACAGGAATCTTTGCAAGTGTGAAACACCACTGAGCAAGAAATTCCTGAAAG 1642  
Db 1595 TCTGGAGACAGGAATCTTTGCAAGTGTGAAACACCACTGAGCAAGAAATTCCTGAAAG 1654  
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGACTACATCCA 1702  
Db 1655 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGACTACATCCA 1714  
QY 1703 AATCAGCCCTGAGCCAAAGATTTGAAGCTTTCTTCAAGGTAAAGCTTTATATCAACT 1762  
Db 1715 AATCAGCCCTGAGCCAAAGATTTGAAGCTTTCTTCAAGGTAAAGCTTTATATCAACT 1774  
QY 1763 CAGGGAACATCCCGATTACTTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1822  
Db 1775 CAGGGAACATCCCGATTACTTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1834  
QY 1823 CTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882  
Db 1835 CTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1894  
QY 1883 CAGAAGACACAGTGGAAATCCACATGGAAGAGGCCCCAGAAACCTTACATTTCCAGCAGG 1942  
Db 1895 CAGAAGACACAGTGGAAATCCACATGGAAGAGGCCCCAGAAACCTTACATTTCCAGCAGG 1954  
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGG 2002  
Db 1955 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGG 2014  
QY 2003 ATTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 2062  
Db 2015 ATTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 2074  
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTGCTGGAAGCCTCAGTTGGTCC 2122  
Db 2075 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTGCTGGAAGCCTCAGTTGGTCC 2134

QY 2123 TCAGCACCTGTGAACACATTTATTTCTCTCATGGTGAAGCCAGTCCCTCACCATAGAAG 2182  
Db 2135 TCAGCACCTGTGAACACATTTATTTCTCTCATGGTGAAGCCAGTCCCTCACCATAGAAG 2194  
QY 2183 ATGAGAGGCACATCACATCTGTAAACAAACCTGAAACCTTTGAGTATTTCATGACCTACAGA 2242  
Db 2195 ATGAGAGGCACATCACATCTGTAAACAAACCTGAAACCTTTGAGTATTTCATGACCTACAGA 2254  
QY 2243 ATCAACGGCTGCGGG 2258  
Db 2255 ATCAACGGCTGCGGG 2270

RESULT 44  
US-10-029-386-25135/c  
; Sequence 25135, Application US/10029386  
; GENERAL INFORMATION:  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES  
; FILE REFERENCE: AEWICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 25135  
; LENGTH: 2002  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL121653.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.36  
; OTHER INFORMATION: EST\_HUMAN HIT: AV656315.1, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: Q9JIB6, EVALUE 2.00e-40  
; OTHER INFORMATION: NT HIT: g115296399, EVALUE 0.00e+00  
US-10-029-386-25135

Query Match 60.0%; Score 1844; DB 38; Length 2002;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1994; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTTGGCTCAGGATTTAAAGSACT 322  
Db 2000 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTTGGCTCAGGATTTAAAGSACT 1941  
QY 323 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTATTT 382  
Db 1940 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTATTT 1881  
QY 383 TTAACCTGAAAGCACCCTTCACAGAACCCTGCTGTGGAGGAAGGACCACCATCACC 442  
Db 1880 TTAACCTGAAAGCACCCTTCACAGAACCCTGCTGTGGAGGAAGGACCACCATCACC 1821  
QY 443 GGTGAGCAGCTGACCCCTGAATGGCTCCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 502  
Db 1820 GGTGAGCAGCTGACCCCTGAATGGCTCCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 1761  
QY 503 AAGGGGAATCTGGCAAAGGCAAGTCCACATCTCTGTCAGGCGCATTTGCCATGCTCTGGGGCT 562  
Db 1760 AAGGGGAATCTGGCAAAGGCAAGTCCACATCTCTGTCAGGCGAATTTGCCATGCTCTGGGGCT 1701  
QY 563 CCGGAAAGTGCAGGCTCTGACCAAAGTTCAAATTCGCTTCCTCCGCTCAGCAGG 632  
Db 1700 CCGGAAAGTGCAGGCTCTGACCAAAGTTCAAATTCGCTTCCTCCGCTCAGCAGG 1641  
QY 623 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 682  
Db 1640 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 1581  
QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGAGAGGGTTCTTTCTCTCTTG 742

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Db 1580 GGAACGACATTCATGCCATGCTGTAAGCTGGCGAGAGGTTCTTTTCTCTCTG 1521  
QY 743 ATGGCTACAATGAATTAAGCCCGCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAA 802  
Db 1520 ATGGCTACAATGAATTAAGCCCGCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAA 1461  
QY 803 ACCACCGCTTCAAGAACATGTCTATCGTCAACCTACCTAGCTGAGGACACATAC 862  
Db 1460 ACCACCGCTTCAAGAACATGTCTATCGTCAACCTACCTAGCTGAGGACACATAC 1401  
QY 863 GGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCCGCCAGGCTC 922  
Db 1400 GGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCCGCCAGGCTC 1341  
QY 923 TCATCCGGAAGTGTGATCAAGAGCTTGCTGAAGGCTTGTGCTCCAAATTCAGAAAT 982  
Db 1340 TCATCCGGAAGTGTGATCAAGAGCTTGCTGAAGGCTTGTGCTCCAAATTCAGAAAT 1281  
QY 983 CCAGGTGCTTCAGGAATCTCATGAAGACCCCTCTCTTGTGTCATCATCTTGTGCAATCC 1042  
Db 1280 CCAGGTGCTTCAGGAATCTCATGAAGACCCCTCTCTTGTGTCATCATCTTGTGCAATCC 1221  
QY 1043 AGATGGGTAAAGTGTTCACCTCTCACACAAACAAACGCTGTTCGATACCTTCTATG 1102  
Db 1220 AGATGGGTAAAGTGTTCACCTCTCACACAAACAAACGCTGTTCGATACCTTCTATG 1161  
QY 1103 ATCTGTTGATACAGAAACAAACACAAACATAAAGGTGTGGCTGCAAGTCACTTCATTC 1162  
Db 1160 ATCTGTTGATACAGAAACAAACACAAACATAAAGGTGTGGCTGCAAGTCACTTCATTC 1101  
QY 1163 GGAGCTGGACCTGTGGAGACCTAGCTGTGGAGGTGTGTTCTCCCAACAAGTTTGATT 1222  
Db 1100 GGAGCTGGACCTGTGGAGACCTAGCTGTGGAGGTGTGTTCTCCCAACAAGTTTGATT 1041  
QY 1223 TCGAACTGACGAGTGTCTGACGCTGAATGAGGTGTCTCTGACAACTGGGCTCTCTCT 1282  
Db 1040 TCGAACTGACGAGTGTCTGACGCTGAATGAGGTGTCTCTGACAACTGGGCTCTCTCT 981  
QY 1283 GTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATCTTTCACAAAGTCATTCCAGG 1342  
Db 980 GTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATCTTTCACAAAGTCATTCCAGG 921  
QY 1343 AGTACACAGCAGGACGAGACTCAGCAGTTTATTGACGTCTCATGAGCAGAGGAGTGA 1402  
Db 920 AGTACACAGCAGGACGAGACTCAGCAGTTTATTGACGTCTCATGAGCAGAGGAGTGA 861  
QY 1403 CCAAGGGGAATGGTTACTTGCAGAAATGGTTTCCATTTCGGACATTACATCCACTATA 1462  
Db 860 CCAAGGGGAATGGTTACTTGCAGAAATGGTTTCCATTTCGGACATTACATCCACTATA 801  
QY 1463 GCAGCTGCTCCGTACACCTGTGGGTCACTGTGGAGCCACAGGGCTGTTATGAAGC 1522  
Db 800 GCAGCTGCTCCGTACACCTGTGGGTCACTGTGGAGCCACAGGGCTGTTATGAAGC 741  
QY 1523 ACCTCGACGAGTGTATCAACACGGCTGCTTCTCGGACTTTCATCGCCAAAGAGGCTC 1582  
Db 740 ACCTCGACGAGTGTATCAACACGGCTGCTTCTCGGACTTTCATCGCCAAAGAGGCTC 681  
QY 1583 TCTGGAGACGAGTCTTTTGCAAGTGTGAAAAACACCACTGACGAAGAAATCTGAAAG 1642  
Db 680 TCTGGAGACGAGTCTTTTGCAAGTGTGAAAAACACCACTGACGAAGAAATCTGAAAG 621  
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702  
Db 620 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 561  
QY 1703 AATCAGCCCTCAGCAGAAATTTGAAGCTTTCCTTCAAGGTAAAGGCTTATATCAACT 1762  
Db 560 AATCAGCCCTCAGCAGAAATTTGAAGCTTTCCTTCAAGGTAAAGGCTTATATCAACT 501  
QY 1763 CAGGAACATCCCGGATTTACTTATTGACTCTTTTGAACATTTGCCCAATTTGTCAAGTG 1822  
|||||

Db 500 CAGGGAACATCCCCGATTAATTTGACTTCTTTGAACATTTGCCCAATTTGTCAAGTG 441  
QY 1823 CTCGGACTTCATTAATTAAGCTTTTATATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882  
Db 440 CCCTGGACTTCATTAATTAAGCTTTTATATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 381  
QY 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCACGACAGG 1942  
Db 380 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCACGACAGG 321  
QY 1943 CTGTATTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTTGAGGTCACTCCCGG 2002  
Db 320 CTGTATTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTTGAGGTCACTCCCGG 261  
QY 2003 ATTTCAACAAGTTCAATTAAGCAATATACATATCTGGGAAAATATTCAGCTCTGCCA 2062  
Db 260 ATTTCAACAAGTTCAATTAAGCAATATACATATCTGGGAAAATATTCAGCTCTGCCA 201  
QY 2063 CAAGCCACAGCTCAATTAAGAGATGTCTGCTGGTGGAGCTCAGTTTGTGTC 2122  
Db 200 CAAGCCACAGCTCAATTAAGAGATGTCTGCTGGTGGAGCTCAGTTTGTGTC 141  
QY 2123 TCAGCACTGTGAAGCAATTTATTTCTCTCATGTTGGAGCCAGTCCCTCACCATAGAAG 2182  
Db 140 TCAGCACTGTGAAGCAATTTATTTCTCTCATGTTGGAGCCAGTCCCTCACCATAGAAG 81  
QY 2183 ATGAGAGACATCACATCTGTAAACAACTGAAACCTTGAGTATTTCATGACCTACAGA 2242  
Db 80 ATGAGAGACATCACATCTGTAAACAACTGAAACCTTGAGTATTTCATGACCTACAGA 21  
QY 2243 ATCAACGCTGCGCGGT 2259  
Db 20 ATCAACGCTGCGCGGT 4  
RESULT 45  
US-10-029-386-228 :0/c  
: Sequence 22860, Application us/10029386  
: GENERAL INFORMATION:  
: APPLICANT: Penil, Sharon G.  
: APPLICANT: Raik, David R.  
: APPLICANT: Haizel, David K.  
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
: FILE REFERENCE: AROMICA-X-2  
: CURRENT APPLICATION NUMBER: US/10/029,386  
: NUMBER OF SEQ. NOS: 34288  
: SOFTWARE: Aromicax Sequence Listing Engine vers. 1.1  
: SEQ. ID NO 22860  
: LENGTH: 1376  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: OTHER INFORMATION: MAP TO AL121653.2  
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1  
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
: OTHER INFORMATION: SWISSPROT HIT: Q9JIB6, EVALUE 2.00e-40  
: OTHER INFORMATION: NT HIT: g115296399, EVALUE 0.00e+00  
: OTHER INFORMATION: EST\_HUMAN HIT: AV656315.1, EVALUE 0.00e+00  
US-10-029-386-22860  
Query Match 59.3% Score 1823; DB 38; Length 1976;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1973; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCCTTTTATCAGACATCAGAAGGAGACTTGGAGCTTGGCTCAGGATTTAAAGGACT 322  
Db 1976 GTCCTTTTATCAGACATCAGAAGGAGACTTGGAGCTTGGCTCAGGATTTAAAGGACT 1917  
QY 323 TGTACCATCCCATCTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTTATTT 382  
Db 1916 TGTACCATCCCATCTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTTATTT 1857  
|||||

QY 383 TTAACCTTGAAGACACCTTACAGAACCTGTCTCTGGAGGAAGACCAACACCATCAC 442  
DB 1856 TTAACCTTGAAGACACCTTACAGAACCTGTCTCTGGAGGAAGACCAACACCATCAC 1797  
QY 443 GCGTGGAGAGTGTACCGTGAATGCGCTCTGAGGCTCTTTCAGAGCCCTGCATCATG 502  
DB 1796 GCGTGGAGAGTGTACCGTGAATGCGCTCTGAGGCTCTTTCAGAGCCCTGCATCATG 1737  
QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGGCAATGGCCATGCTCTGGGCT 562  
DB 1736 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGGCAATGGCCATGCTCTGGGCT 1677  
QY 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTCTCTCCGCTCTCAGCAGG 622  
DB 1676 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTCTCTCCGCTCTCAGCAGG 1617  
QY 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCAACAATCA 682  
DB 1616 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCAACAATCA 1557  
QY 683 GGAAGCAGACATTCATGCGCATGCTGCAAGCTGCGCAGAGGCTCTTTTCCCTCTG 742  
DB 1556 GGAAGCAGACATTCATGCGCATGCTGCAAGCTGCGCAGAGGCTCTTTTCCCTCTG 1497  
QY 743 ATGGCTACAATGAATTCAGGCCCGCAGAACTGCCAGAAATCGAAGCCCTGTATAAGGAAA 802  
DB 1496 ATGGCTACAATGAATTCAGGCCCGCAGAACTGCCAGAAATCGAAGCCCTGTATAAGGAAA 1437  
QY 803 ACCACCGCTTCAAGAACATGTCATGTCACCACTACCACTGAGTGCCTGAGGCAACATAC 862  
DB 1436 ACCACCGCTTCAAGAACATGTCATGTCACCACTACCACTGAGTGCCTGAGGCAACATAC 1377  
QY 863 GCGAGTTGGTCCCTGACTGTGAGTGGGGATATGACAAAGACAGCGCCAGGCTC 922  
DB 1376 GCGAGTTGGTCCCTGACTGTGAGTGGGGATATGACAAAGACAGCGCCAGGCTC 1317  
QY 923 TCATCCGAGAGTGTGATCAAGAGGCTGTCTGAAAGGCTGTGTCTCCAAATTCAGAAAT 982  
DB 1316 TCATCCGAGAGTGTGATCAAGAGGCTGTCTGAAAGGCTGTGTCTCCAAATTCAGAAAT 1257  
QY 983 CCAGTGTCTGAGGAATCTCATGAAGACCCCTCTCTTTGGTGTATCATCTGTGCAATCC 1042  
DB 1256 CCAGTGTCTGAGGAATCTCATGAAGACCCCTCTCTTTGGTGTATCATCTGTGCAATCC 1197  
QY 1043 AGATGGGTGAAGTGAAGTCCACTCTCACACAACACGCTGTCCATACCTTCTATG 1102  
DB 1196 AGATGGGTGAAGTGAAGTCCACTCTCACACAACACGCTGTCCATACCTTCTATG 1137  
QY 1103 ATCTGTGTATACAGAAAAACAAACAAATATAAGGCTGTGCTGCAAGTGAATTCATTC 1162  
DB 1136 ATCTGTGTATACAGAAAAACAAACAAATATAAGGCTGTGCTGCAAGTGAATTCATTC 1077  
QY 1163 GGAGCCTGGACACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTTGAAT 1222  
DB 1076 GGAGCCTGGACACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTTGAAT 1017  
QY 1223 TCGAACTGAGATGTCTCCAGCGTGAATGAGGATGTCTGTGACAACTGGGCTCCTCT 1282  
DB 1016 TCGAACTGAGATGTCTCCAGCGTGAATGAGGATGTCTGTGACAACTGGGCTCCTCT 957  
QY 1283 GTAATATACACTCAAGGTTCAAGCCAAAGTATAAATCTTTCACAGTCAATTCACAGG 1342  
DB 956 GTAATATACACTCAAGGTTCAAGCCAAAGTATAAATCTTTCACAGTCAATTCACAGG 897  
QY 1343 AGTACACAGCAGGACGAACTCAGCAGTTTATGACGCTCTCATGAGCAGAGGAGTGA 1402  
DB 896 AGTACACAGCAGGACGAACTCAGCAGTTTATGACGCTCTCATGAGCAGAGGAGTGA 837  
QY 1403 CCAAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATTTCCGACATTCATCCACTTATA 1462  
DB 836 CCAAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATTTCCGACATTCATCCACTTATA 777

QY 1463 GCAGCCTGCTCGGTACACCTGTGGGTCTATCTGTGAAGCCACCGAGGCTGTATGAAGC 1522  
DB 776 GCAGCCTGCTCGGTACACCTGTGGGTCTATCTGTGAAGCCACCGAGGCTGTATGAAGC 717  
QY 1523 ACCTCGCAGCAGTGTATCAACACGCGTGCCTTCTCGGACTTTCCATCGCAAGAGCCCTC 1582  
DB 716 ACCTCGCAGCAGTGTATCAACACGCGTGCCTTCTCGGACTTTCCATCGCAAGAGCCCTC 657  
QY 1583 TCTGTGAGCAGCAATCTTTTGCAAGTGTGAAAAACACCACTGAGCAAGAAATTCGAAAG 1642  
DB 656 TCTGTGAGCAGCAATCTTTTGCAAGTGTGAAAAACACCACTGAGCAAGAAATTCGAAAG 597  
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGCAATCCATTTATATCAAGAGATACATCCA 1702  
DB 596 CCATAAACATCAATTCCTTTGTAGAGTGTGCAATCCATTTATATCAAGAGATACATCCA 537  
QY 1703 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAAGGTAAAAGCTTTATATCAACT 1762  
DB 536 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAAGGTAAAAGCTTTATATCAACT 477  
QY 1763 CAGGGAACATCCCGATTAATTTTGAAGTCTTTTGAACATTTGCCCAATTTGCAAGTG 1822  
DB 476 CAGGGAACATCCCGATTAATTTTGAAGTCTTTTGAACATTTGCCCAATTTGCAAGTG 417  
QY 1823 CTCTGAGCTTCAATAAAGTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882  
DB 416 CCCTGGACTTCAATAAAGTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 357  
QY 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGCAGGG 1942  
DB 356 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGCAGGG 297  
QY 1943 CTGTATCTTTGCTTCAACTGGAAGCAGAAATTCAGGACTCTGGAGGTCAACCTCCGGG 2002  
DB 296 CTGTATCTTTGCTTCAACTGGAAGCAGAAATTCAGGACTCTGGAGGTCAACCTCCGGG 237  
QY 2003 ATTTCCAGCAAGTTGAATGAAGCAAGATATCACATATCTGGGAAAAATATTTCAGCTCTGCCA 2062  
DB 236 ATTTCCAGCAAGTTGAATGAAGCAAGATATCACATATCTGGGAAAAATATTTCAGCTCTGCCA 177  
QY 2063 CAAGCCTCAGGCTGCAATTAAGAGATGTGCTGTGGCTGGAAGCCTCAGTTTGGTCC 2122  
DB 176 CAAGCCTCAGGCTGCAATTAAGAGATGTGCTGTGGCTGGAAGCCTCAGTTTGGTCC 117  
QY 2123 TCAGCAGCTGTGAAGCAATTTATCTCTCATGCTGGAAGCCAGTCCCTTCACCATAGAG 2182  
DB 116 TCAGCAGCTGTGAAGCAATTTATCTCTCATGCTGGAAGCCAGTCCCTTCACCATAGAG 57  
QY 2183 ATGAGAGGCACATCATCTGTAAACAAACCTGAAACCTTTGAGTATTTCATGACCTA 2238  
DB 56 ATGAGAGGCACATCATCTGTAAACAAACCTGAAACCTTTGAGTATTTCATGACCTA 1

## RESULT 46

PCT-US00-35017A-416  
; Sequence 416, Application PC/TUS0035017A  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/35017A  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 416  
; LENGTH: 2950  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US00-35017A-416



[illegible]



; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: pt\_ct\_genes Version 1.0
; SEQ ID NO 7095
; LENGTH: 3152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (20)...(1903)
; OTHER INFORMATION: similar to gi5932010 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-471-275-7095

Query Match 58.0%; Score 1781; DB 18; Length 3152;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1881; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1190 CTCGTGAGGGTGTCTCCACAAAGTTTGATTTGAACTGCAAGATGTCAGGATGTCACGGGTGA 1249
DB 45 CTCGTGAGGGTGTGTCTCCACAAAGTTTGATTTGAACTGCAAGATGTCAGGATGTCACGGGTGA 104
QY 1250 ATGAGGATGTCGTGTCGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTTCAAGC 1309
DB 105 ATGAGGATGTCGTGTCGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTTCAAGC 164
QY 1310 CAAAGTATAAATTTCTTCAAGTCAATCCAGGAGTACACAGCAGCAGGAGTCAAGCA 1369
DB 165 CAAAGTATAAATTTCTTCAAGTCAATCCAGGAGTACACAGCAGCAGGAGTCAAGCA 224
QY 1370 GTTTATTGACGCTCATGACCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAA 1429
DB 225 GTTTATTGACGCTCATGACCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAA 284
QY 1430 TGGTTTCCATTTCCGACATTTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGT 1489
DB 285 TGGTTTCCATTTCCGACATTTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGT 344
QY 1490 CATCTGTGAAGCCACCCAGGGGTGTTATGAAGCACTTCGACAGTGTATCAACAGGGCT 1549
DB 345 CATCTGTGAAGCCACCCAGGGGTGTTATGAAGCACTTCGACAGTGTATCAACAGGGCT 404
QY 1550 GCCTTCTCGGACTTTCCATTCGCAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTG 1609
DB 405 GCCTTCTCGGACTTTCCATTCGCAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTG 464
QY 1610 TGAAGAACACCACTGAGCAAGAAATTTCTGAAAGCCATAACATCAATTCCTTTGTAGAGT 1669
DB 465 TGAAGAACACCACTGAGCAAGAAATTTCTGAAAGCCATAACATCAATTCCTTTGTAGAGT 524
QY 1670 GTGGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAG 1729

DB 525 GTGGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAG 584
QY 1730 CTTTCTTTCAAGGTAAAGCTTATATCAACTCAGGGAAACATCCCGGATTACTTATTTG 1789
DB 585 CTTTCTTTCAAGGTAAAGCTTATATCAACTCAGGGAAACATCCCGGATTACTTATTTG 644
QY 1790 ACTTCTTTGAACATTTGCCCAATTTGCAAGTCTCTGGACTTTCATTAACACTGGACTTTT 1849
DB 645 ACTTCTTTGAACATTTGCCCAATTTGCAAGTCTCTGGACTTTCATTAACACTGGACTTTT 704
QY 1850 ATGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAACACAGGTGGAATCCACATGG 1909
DB 705 ATGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAACACAGGTGGAATCCACATGG 764
QY 1910 AAGAGCCCCAGAAAACCTACATTTCCAGAGGGCTCTATCTTTGTTCTTCAACTGGAAGC 1969
DB 765 AAGAGCCCCAGAAAACCTACATTTCCAGAGGGCTCTATCTTTGTTCTTCAACTGGAAGC 824
QY 1970 AGGAATTCAGGACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATA 2029
DB 825 AGGAATTCAGGACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATA 884
QY 2030 TCACATATCTGGGGAAAATATTTCAGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAGAGAT 2089
DB 885 TCAGATATCTGGGGAAAATATTTCAGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAGAGAT 944
QY 2090 GTGCTGGTGTGGCTGGAAGCCTCAGTTTGGTCTCAGCACCCTGTAAAGAACATTTATTTCTC 2149
DB 945 GTGCTGGTGTGGCTGGAAGCCTCAGTTTGGTCTCAGCACCCTGTAAAGAACATTTATTTCTC 1004
QY 2150 TCATGTGTGAAGCCAGCTCCCTCACCATAGAAGATCAGAGGCACATCACAATCTGTAACAA 2209
DB 1005 TCATGTGTGAAGCCAGCTCCCTCACCATAGAAGATCAGAGGCACATCACAATCTGTAACAA 1064
QY 2210 ACCTGAAAACCTTTGAGTATTCATGACCTACAGAAATCAAGGGCTGCGGGGTGGTCTGACTG 2269
DB 1065 ACCTGAAAACCTTTGAGTATTCATGACCTACAGAAATCAAGGGCTGCGGGGTGGTCTGACTG 1124
QY 2270 ACAGCTTGGGTAACTTTGAAGAACCTTTACAAAGCTCAATAATGGATACATAAAGATCAATG 2329
DB 1125 ACAGCTTGGGTAACTTTGAAGAACCTTTACAAAGCTCAATAATGGATACATAAAGATCAATG 1184
QY 2330 AAGAAGTCTATATAAAGTCTGAAAGGCTGAAAGGCTGAAAGGCTGAAAGGCTGAAAGGCTGAAAG 2389
DB 1185 AAGAAGTCTATATAAAGTCTGAAAGGCTGAAAGGCTGAAAGGCTGAAAGGCTGAAAGGCTGAAAG 1244
QY 2390 ATTTGACCCACTTGTCTGACATTTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAA 2449
DB 1245 ATTTGACCCACTTGTCTGACATTTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAA 1304
QY 2450 GTGAACCCCTGTGACCTTGAAGAAATTTCAATTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2509
DB 1305 GTGAACCCCTGTGACCTTGAAGAAATTTCAATTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1364
QY 2510 TGAAGAAATCCTAGCTCAGAAATTTTCAACATTTTGGTCAAACTGAGCATTCTTGATTTATCAG 2569
DB 1365 TGAAGAAATCCTAGCTCAGAAATTTTCAACATTTTGGTCAAACTGAGCATTCTTGATTTATCAG 1424
QY 2570 AAAATTACCTGGAAGAAAGATGGAATGAAAGTCTTTCATGAACATGATCGACAGGATGAAGC 2629
DB 1425 AAAATTACCTGGAAGAAAGATGGAATGAAAGTCTTTCATGAACATGATCGACAGGATGAAGC 1484
QY 2630 TGCTGAAGACGCTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGGAGGCTGA 2689
DB 1485 TGCTGAAGACGCTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGGAGGCTGA 1544
QY 2690 GCAGCCTGTTGAAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACT 2749
DB 1545 GCAGCCTGTTGAAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACT 1604
QY 2750 GGAGACTCACAGATACAGAGATTAGAAATTTTAGGTGCATTTTTTTGGAAAGAACCCCTCTGA 2809

Db 1605 GGAGACTCACAGATACAGAGATTAGAATTTTAGTGCATTTTGGAAAGAACCTCTGA 1664  
Qy 2810 AAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGATGGATGGCTTGCT 2869  
Db 1665 AAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGATGGATGGCTTGCT 1724  
Qy 2870 TCATGGGTGATTAGAGAACTTAAAGCAATAGTGTGTTTGGACTTTAGTACTAAAGAA 2929  
Db 1725 TCATGGGTGATTAGAGAACTTAAAGCAATAGTGTGTTTGGACTTTAGTACTAAAGAA 1784  
Qy 2930 TTCTACCTGATCCAGCATTAGTCCAGAACTTAGCAGTCTTATCCAGTTAACTTTTC 2989  
Db 1785 TTCTACCTGATCCAGCATTAGTCCAGAACTTAGCAGTCTTATCCAGTTAACTTTTC 1844  
Qy 2990 TGCAGAGAGCTAGGCTTGGTGGGCGCAATTTGATGATGATGATCTCAGTGTATTACAG 3049  
Db 1845 TGCAGAGAGCTAGGCTTGGTGGGCGCAATTTGATGATGATGATGATCTCAGTGTATTACAG 1904  
Qy 3050 GTGCTTTTAACTAGTAACTGCT 3072  
Db 1905 GTGCTTTTAACTAGTAACTGCT 1927

RESULT 48  
PCT-US02-09921-429/c  
; Sequence 429, Application PC/TUS0209921.

; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DAFFO, Abel  
; APPLICANT: JONES, Anissa L.  
; APPLICANT: TRAN, Alanna-Phung B.  
; APPLICANT: DAHL, Christopher R.  
; APPLICANT: GIETZEN, Darryl  
; APPLICANT: CHINN, Joyce  
; APPLICANT: DUFOUR, Gerard E.  
; APPLICANT: HULLMAN, Jennifer L.  
; APPLICANT: XU, Jimmy Y.  
; APPLICANT: TUASON, Olivia  
; APPLICANT: YAP, Pierre E.  
; APPLICANT: AMSEH, Stefan R.  
; APPLICANT: DAUGHERTY, Sean C.  
; APPLICANT: DAM, Tam C.  
; APPLICANT: LIU, Tommy F.  
; APPLICANT: NGUYEN, Duy-Viet An  
; APPLICANT: KLEEFELD, Yael  
; APPLICANT: GERSTIN JR., Edward H.  
; APPLICANT: PERALTA, Careyna H.  
; APPLICANT: DAVID, Marie H.  
; APPLICANT: LEWIS, Samantha A.  
; APPLICANT: CHEN, Alice J.  
; APPLICANT: PANZER, Scott R.  
; APPLICANT: HARRIS, Bernard  
; APPLICANT: FLORES, Vincent  
; APPLICANT: MARWAHA, Rakesh  
; APPLICANT: LO, Audrey  
; APPLICANT: LAN, Ruth Y.  
; APPLICANT: URASHKA, Michael  
; TITLE OF INVENTION: SECRETORY MOLECULES  
; FILE REFERENCE: PT-1232 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/09921  
; PRIOR FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;  
; 60/291,849; 60/299,428; 60/300,001; 60/299,776  
; PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17;  
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20  
; NUMBER OF SEQ ID NOS: 1146  
; SOFTWARE: PERL Program  
; SEQ ID NO 429  
; LENGTH: 4626  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No: LG:332701.3:2001JUN22  
; NAME/KEY: us:ure  
; LOCATION: 114, 199, 224, 231, 237-238, 255, 258-259  
; OTHER INFORMATION: a, t, c, g, or other  
PCT-US02-09921-429  
Query Match 41.2%; Score 1267; DB 1; Length 4626;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1755 TATCA/ CTCAGGGAACATCCCGGATTACTTATTTGACHTCTTTGACATTTTGGACATTTTGGCCAAATG 1814  
Db 4626 TATCA/ CTCAGGGAACATCCCGGATTACTTATTTGACHTCTTTGACATTTTGGACATTTTGGCCAAATG 4567  
Qy 1815 TGCAG/ TGCTCTGGACTTCATTTAACTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGA 1874  
Db 4566 TGCAG/ TGCTCTGGACTTCATTTAACTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGA 4507  
Qy 1875 AAGGC/ TGCAGAGACAGAGTGGAAATCCACATGGAAGAGCCGCCAGAAACCTACATTC 1934  
Db 4506 AAGGC/ TGCAGAGACAGAGTGGAAATCCACATGGAAGAGCCGCCAGAAACCTACATTC 4447  
Qy 1935 CAGCAG/ 3GCTGTATCTTTTGTCTTCACTGGAAGCAGGAATTCAGGACTCTGGAGGTCCAC 1994  
Db 4446 CAGCAG/ 3GCTGTATCTTTTGTCTTCACTGGAAGCAGGAATTCAGGACTCTGGAGGTCCAC 4387  
Qy 1995 ACTCCG/ 3GATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTGGGGAATAATTTTCAG 2054  
Db 4386 ACTCCG/ 3GATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTGGGGAATAATTTTCAG 4327  
Qy 2055 CTCGTC/ ACAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTGGCTGGAAGCTCCAG 2114  
Db 4326 CTCGTC/ ACAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTGGCTGGAAGCTCCAG 4267  
Qy 2115 TTTGGT/ CTCAGCAGCTGTAGAACATTTATCTCTCAGTGGAGCAGCTCCCTCCAC 2174  
Db 4266 TTTGGT/ CTCAGCAGCTGTAGAACATTTATCTCTCAGTGGAGCAGCTCCCTCCAC 4207  
Qy 2175 CATAGA/ GATGAGAGGCACATCATCTGTAAACAACCTGAAACCTTGAGTATTTCATGA 2234  
Db 4206 CATAGA/ GATGAGAGGCACATCATCTGTAAACAACCTGAAACCTTGAGTATTTCATGA 4147  
Qy 2235 CCTACA/ AATCAACGGCTGCGGGTGGTCTGACTGACAGCTTTGGTAACTTTGAAGAACT 2294  
Db 4146 CCTACA/ AATCAACGGCTGCGGGTGGTCTGACTGACAGCTTTGGTAACTTTGAAGAACT 4087  
Qy 2295 TACAAA/ CTCATAATGGATAACATAAAGATGAATGAAGAAGATGCTATATAAACTAGCTGA 2354  
Db 4086 TACAAA/ CTCATAATGGATAACATAAAGATGAATGAAGAAGATGCTATATAAACTAGCTGA 4027  
Qy 2355 AGGCCT/ AAAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCCACTTTGCTGACATTGG 2414  
Db 4026 AGGCCT/ AAAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCCACTTTGCTGACATTGG 3967  
Qy 2415 AGAGGG/ ATGGATTACATAGTCAAGTCTCTCAAGTGAACCTCTGTGACCTTGAAGAAAT 2474  
Db 3966 AGAGGG/ ATGGATTACATAGTCAAGTCTCTCAAGTGAACCTCTGTGACCTTGAAGAAAT 3907  
Qy 2475 TCAATT/ GTCTCTCTGCTGCTGTCTGCAAAATGCAGTGAATAATCCTAGCTCAGATCTTCA 2534  
Db 3906 TCAATT/ GTCTCTCTGCTGCTGTCTGCAAAATGCAGTGAATAATCCTAGCTCAGATCTTCA 3847  
Qy 2535 CAATTT/ GTCAAACTGACATCTTGTATTTATCATGAAAATTTACCTGGAAAAGATGGAAA 2594  
Db 3846 CAATTT/ GTCAAACTGACATCTTGTATTTATCAGAAAATTTACCTGGAAAAGATGGAAA 3787  
Qy 2595 TGAAGCT/ TTTCATGAAGTGTGACAGAGGATGAAGTGTGATAGAACAGCTCACCGCACTGAT 2654  
Db 3786 TGAAGCT/ TTTCATGAAGTGTGACAGAGGATGAAGTGTGATAGAACAGCTCACCGCACTGAT 3727  
Qy 2655 GCTGCC/ TGGGGCTGTGACGTGCAAGGCAGCTGAGAGCCTGTGTAACATTTTGGAGGA 2714  
Db 3726 GCTGCC/ TGGGGCTGTGACGTGCAAGGCAGCTGAGAGCCTGTGTAACATTTTGGAGGA 3667

QY	2715	GGTCCACAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAG	2774
Db	3666	GGTCCACAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAG	3607
QY	2775	AATTTTAGTGCATTTTGGGAAAGAACCCCTCTGAAAACTTCACAGAGTTGAATTTGGC	2834
Db	3606	AATTTTAGTGCATTTTGGGAAAGAACCCCTCTGAAAACTTCACAGAGTTGAATTTGGC	3547
QY	2835	GGAAATCGTGTGAGCAGTGATGGATGGCTTGCCCTCATGGTGTTATTGAGAACTCTAA	2894
Db	3546	GGAAATCGTGTGAGCAGTGATGGATGGCTTGCCCTCATGGTGTTATTGAGAACTCTAA	3487
QY	2895	GCAATTAGTGTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAG	2954
Db	3486	GCAATTAGTGTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAG	3427
QY	2955	AAAACTTAGCAGAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCTAGGCGTTGTGGGTG	3014
Db	3426	AAAACTTAGCAGAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCTAGGCGTTGTGGGTG	3367
QY	3015	GCAATTTGATGATGATCTCAGTGTGTTATACAGGTGCTTTTAACTAGTAACTGCT	3072
Db	3366	GCAATTTGATGATGATCTCAGTGTGTTATACAGGTGCTTTTAACTAGTAACTGCT	3309

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RESULT 49
US-09-864-921-179
; Sequence 179, Application US/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(891)
US-09-864-921-179

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		Query Match	27.3%	Score 840;	DB 33;	Length 891;	
		Best Local Similarity	99.9%;	Pred. No. 0;			
		Matches 890;	Conservative	0;	Mismatches	1;	Gaps
							0;
QY	481	CTTCAGAGCCCTGCATCATTTGAAGGGGAAATCTGGCAAAAGCGAAGTCCACACTCTGTGCGAG	540				
Dd	1	CTTCAGAGCCCTGCATCATTTGAAGGGGAAATCTGGCAAAAGCGAAGTCCACACTCTGTGCGAG	60				
QY	541	CGCAATGCCATGCTCTCGGGGCTCCGGAAAAGTGCAAGGCTCTGACCAAGTTCAAATTCTGTC	600				
Dd	61	CGCAATGCCATGCTCTCGGGGCTCCGGAAAAGTGCAAGGCTCTGACCAAGTTCAAATTCTGTC	120				

Qy	601	TTCTTCC	TCCGTC	CTCAGC	AGGCC	CCAGG	TGGAC	TTT	TTGAA	ACCCT	CTGT	GATCA	CACTC	660				
Db	121	TTCTTCC	TCCGTC	CTCAGC	AGGCC	CCAGG	TGGAC	TTT	TTGAA	ACCCT	CTGT	GATCA	CACTC	180				
Qy	661	CTG	GATATAC	CTG	GCACAAT	CAG	GAAGC	A	GACAT	TTCA	TG	CCCATC	GCTG	CTGAAGCTGCGG	720			
Db	181	CTG	GATATAC	CTG	GCACAAT	CAG	GAAGC	A	GACAT	TTCA	TG	CCCATC	GCTG	CTGAAGCTGCGG	240			
Qy	721	CAG	AGGGT	TTCT	TTT	TCTT	CTTG	TG	GGCT	ACA	TGA	ATTTCA	AG	CCCCAGAACTG	CCCGAGAA	780		
Db	241	CAG	AGGGT	TTCT	TTT	TCTT	CTTG	TG	GGCT	ACA	TGA	ATTTCA	AG	CCCCAGAACTG	CCCGAGAA	300		
Qy	781	ATC	GAAGCC	CTG	ATAA	AGG	AAAC	ACC	CGCTT	C	A	GAACAT	CGT	CGT	CACAC	TACC	840	
Db	301	ATC	GAAGCC	CTG	ATAA	AGG	AAAC	ACC	CGCTT	C	A	GAACAT	CGT	CGT	CACAC	TACC	360	
Qy	841	ACT	GAGT	GCCT	GAGG	CACAT	AC	GGCAG	TTG	TG	CGCC	TGAC	TG	CG	AGSTG	GGGGATATG	900	
Db	361	ACT	GAGT	GCCT	GAGG	CACAT	AC	GGCAG	TTG	TG	CGCC	TGAC	TG	CG	AGSTG	GGGGATATG	420	
Qy	901	AC	AGAAG	CAC	AGC	CC	CAGG	CTC	T	CAT	C	C	GAG	AAGT	GCTG	TATCA	AGGAGC	960
Db	421	AC	AGAAG	CAC	AGC	CC	CAGG	CTC	T	CAT	C	C	GAG	AAGT	GCTG	TATCA	AGGAGC	480
Qy	961	TTG	TG	TG	CTC	AAAT	T	C	AGAA	T	CC	AGG	T	G	CTT	GAG	AAT	1020
Db	481	TTG	TG	TG	CTC	AAAT	T	C	AGAA	T	CC	AGG	T	G	CTT	GAG	AAT	540
Qy	1021	GT	GGT	CAT	CAC	TTG	T	CCA	AT	C	CAG	AT	G	GGT	GAA	AGT	GAGT	1080
Db	541	GT	GGT	CAT	CAC	TTG	T	CCA	AT	C	CAG	AT	G	GGT	GAA	AGT	GAGT	600
Qy	1081	AC	G	TG	T	T	CCAT	AC	CTT	C	TAT	GAT	CT	G	T	T	GAT	1140
Db	601	AC	G	TG	T	T	CCAT	AC										

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RESULT 50
US-09-686-347-98
; Sequence 98, Application US/09686347
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: Novel Card-Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4271
; CURRENT APPLICATION NUMBER: US/09/686,347
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98

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; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277) ... (1353)
US-09-686-347-98

Query Match      26.5%; Score 815; DB 27; Length 1395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2258 GTGGTCTGACTGACAGCTTGGGTAACTTGAAGAAGCTTACAAAGCTCATATGGNTAACA 2317
DB 539 GTGGTCTGACTGACAGCTTGGGTAACTTGAAGAAGCTTACAAAGCTCATATGGNTAACA 598
QY 2318 TAAAGATGAATGAAGAAGCTTATATAAAGCTAGCTGAAGGCTGAAAAACCTGAAGAAGA 2377
DB 599 TAAAGATGAATGAAGAAGCTTATATAAAGCTAGCTGAAGGCTGAAAAACCTGAAGAAGA 658
QY 2378 TGTGTTTATTTCAATTGACCCACTTGTCTGACATTTGGAGAGGAATGGATTACATAGTCA 2437
DB 659 TGTGTTTATTTCAATTGACCCACTTGTCTGACATTTGGAGAGGAATGGATTACATAGTCA 718
QY 2438 AGTCTCTGTCAGTGAAGCCCTGTGACCTTGAAGAAATTCAAATTTAGTCTCTGCTGCTTGT 2497
DB 719 AGTCTCTGTCAGTGAAGCCCTGTGACCTTGAAGAAATTCAAATTTAGTCTCTGCTGCTTGT 778
QY 2498 CTGCAAAATGCAAGTGAAGAAATTCCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTC 2557
DB 779 CTGCAAAATGCAAGTGAAGAAATTCCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTC 838
QY 2558 TTGATTTTATCAGAAATTTACCTGGAAAGATGGAATGGAAGCTTTCATGAAGCTGATCG 2617
DB 839 TTGATTTTATCAGAAATTTACCTGGAAAGATGGAATGGAAGCTTTCATGAAGCTGATCG 898
QY 2618 ACAGATGAAGCTGCTAGACAGCTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACGTGC 2677
DB 899 ACAGATGAAGCTGCTAGACAGCTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACGTGC 958
QY 2678 AAGCGAGCTGAGCAGCTGTTGAAACATTTGGAGAGGTCCTCCACAACTCGTCAAGCTTG 2737
DB 959 AAGCGAGCTGAGCAGCTGTTGAAACATTTGGAGAGGTCCTCCACAACTCGTCAAGCTTG 1018
QY 2738 GGTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAGGTGCATTTTGGAA 2797
DB 1019 GGTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAGGTGCATTTTGGAA 1078
QY 2798 AGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGATG 2857
DB 1079 AGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGATG 1138
QY 2858 GATGGCTTGCCTTCATGGTGTATTGAGAACTTAAAGCAATTTAGTGTGTTTGTGACTTTA 2917
DB 1139 GATGGCTTGCCTTCATGGTGTATTGAGAACTTAAAGCAATTTAGTGTGTTTGTGACTTTA 1198
QY 2918 GTACTTAAGAATTTCTACCTCATCCAGCATTTAGTCAGAAACTTAGCCAACTGTATCCA 2977
DB 1199 GTACTTAAGAATTTCTACCTCATCCAGCATTTAGTCAGAAACTTAGCCAACTGTATCCA 1258
QY 2978 AGTTAACTTTCTGCAAGAAGCTAGGCTGTTGGGTGGCAATTTGATGATGATCATCTCA 3037
DB 1259 AGTTAACTTTCTGCAAGAAGCTAGGCTGTTGGGTGGCAATTTGATGATGATCATCTCA 1318
QY 3038 GTGTATTACAGGTGCTTTTAACTAGTAAGTCT 3072
DB 1319 GTGTATTACAGGTGCTTTTAACTAGTAAGTCT 1353
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Search completed: January 31, 2003, 04:07:38  
Job time : 6602 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 23:02:25 ; search time 469 seconds  
(without alignments)  
7985.160 Million cell updates/sec

Title: US-09-697-089-3  
Perfect score: 3072  
Sequence: 1 atgaatttcataaaggacaa.....cttttaactagtaactgct 3072

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2500250 seqs, 609544256 residues

Word size : 12

Total number of hits satisfying chosen parameters: 207489

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
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7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2919	95.0	1 PCT-US02-21946A-1	Sequence 1, Appli
2	2919	95.0	1 PCT-US02-21946A-14	Sequence 14, Appli
3	2919	95.0	6 US-10-276-781-111	Sequence 111, Appl
4	242	7.9	6 US-10-203-138A-4307	Sequence 4307, Ap
5	220	7.2	6 US-10-203-138A-9429	Sequence 9429, Ap
6	20	0.7	6 US-09-949-004-6715	Sequence 6715, Ap
7	20	0.7	5 US-09-949-004-6933	Sequence 693, App
8	19	0.6	5 US-09-531-113-38966	Sequence 38966, A
9	19	0.6	6 US-10-240-425-462	Sequence 462, App
10	19	0.6	5 US-09-724-676A-16013	Sequence 16013, A
11	19	0.6	5 US-09-724-676A-16013	Sequence 16013, A
12	19	0.6	1 PCT-US02-32727-122	Sequence 122, App
13	19	0.6	6 US-10-057-488-122	Sequence 122, App
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c 102	17	0.6	244	5	US-09-531-113-33819	Sequence 33819, A	c 175	17	0.6	2291	6	US-10-320-351-17	Sequence 17, Appl
c 103	17	0.6	244	5	US-09-531-113-36575	Sequence 36575, A	c 176	17	0.6	2291	6	US-10-320-351-17	Sequence 17, Appl
c 104	17	0.6	245	5	US-09-531-113-35612	Sequence 35612, A	c 177	17	0.6	2471	6	US-10-120-801-9	Sequence 9, Appl
c 105	17	0.6	246	5	US-09-531-113-15493	Sequence 15493, A	c 178	17	0.6	2471	6	US-10-297-880-8	Sequence 8, Appl
c 106	17	0.6	246	5	US-09-531-113-15493	Sequence 15493, A	c 179	17	0.6	2491	1	PCT-US02-32851-87	Sequence 87, Appl
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c 108	17	0.6	246	5	US-09-531-113-35320	Sequence 35320, A	c 181	17	0.6	2553	7	US-60-417-155-4	Sequence 4, Appl
c 109	17	0.6	248	5	US-09-531-113-34131	Sequence 34131, A	c 182	17	0.6	2604	5	US-09-950-084-582	Sequence 582, App
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c 118	17	0.6	259	5	US-09-531-113-28418	Sequence 28418, A	c 191	17	0.6	4000	1	PCT-US02-39126-44	Sequence 44, Appl
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c 156	17	0.6	1013	6	US-10-276-774-646	Sequence 646, App	c 229	17	0.6	11976	6	US-10-311-455-568	Sequence 568, App
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c 265	17	0.6	475970	5	US-09-950-084-7438	Sequence 7438, Ap	c 338	16	0.5	129	6	US-10-327-713-820	Sequence 820, App
c 266	17	0.6	611259	5	US-09-948-124-8	Sequence 8, Appli	c 339	16	0.5	138	6	US-10-205-562-7	Sequence 7, Appli
c 267	17	0.6	646370	5	US-09-948-124-108	Sequence 108, App	c 340	16	0.5	138	6	US-10-205-562-10	Sequence 10, Appl
c 268	17	0.6	646370	5	US-09-948-124-108	Sequence 108, App	c 341	16	0.5	141	6	US-10-203-138A-8655	Sequence 8655, Ap
c 269	16	0.5	19	6	US-10-310-188-55122	Sequence 55122, A	c 342	16	0.5	147	6	US-10-266-131-738	Sequence 738, App
c 270	16	0.5	25	7	US-60-417-190-18146	Sequence 18146, A	c 343	16	0.5	183	6	US-09-534-850-14142	Sequence 14142, A
c 271	16	0.5	25	7	US-60-417-190-18147	Sequence 18147, A	c 344	16	0.5	202	5	US-09-513-999C-12540	Sequence 12540, A
c 272	16	0.5	25	7	US-60-417-190-18148	Sequence 18148, A	c 345	16	0.5	208	5	US-09-534-850-14163	Sequence 14163, A
c 273	16	0.5	25	7	US-60-417-190-18149	Sequence 18149, A	c 346	16	0.5	216	5	US-09-534-850-14161	Sequence 14161, A
c 274	16	0.5	25	7	US-60-417-190-18150	Sequence 18150, A	c 347	16	0.5	217	5	US-09-534-850-20474	Sequence 20474, A
c 275	16	0.5	25	7	US-60-417-190-76888	Sequence 76888, A	c 348	16	0.5	217	5	US-09-534-850-20511	Sequence 20511, A
c 276	16	0.5	25	7	US-60-417-190-76889	Sequence 76889, A	c 349	16	0.5	219	5	US-09-534-850-14108	Sequence 14108, A
c 277	16	0.5	25	7	US-60-417-190-76890	Sequence 76890, A	c 350	16	0.5	220	6	US-10-203-138A-8358	Sequence 8358, Ap
c 278	16	0.5	25	7	US-60-417-190-76891	Sequence 76891, A	c 351	16	0.5	232	5	US-09-534-850-14113	Sequence 14113, A
c 279	16	0.5	25	7	US-60-417-190-109583	Sequence 109583, A	c 352	16	0.5	236	5	US-09-534-850-14167	Sequence 14167, A
c 280	16	0.5	25	7	US-60-417-190-109584	Sequence 109584, A	c 353	16	0.5	236	5	US-09-531-113-13805	Sequence 13805, A
c 281	16	0.5	25	7	US-60-417-190-109585	Sequence 109585, A	c 354	16	0.5	236	5	US-09-531-113-34374	Sequence 34374, A
c 282	16	0.5	25	7	US-60-417-190-109586	Sequence 109586, A	c 355	16	0.5	239	5	US-09-534-850-14148	Sequence 14148, A
c 283	16	0.5	25	7	US-60-417-190-109587	Sequence 109587, A	c 356	16	0.5	239	5	US-09-531-113-38807	Sequence 38807, A
c 284	16	0.5	25	7	US-60-417-190-109588	Sequence 109588, A	c 357	16	0.5	242	5	US-09-531-113-35841	Sequence 35841, A
c 285	16	0.5	25	7	US-60-427-808-6042	Sequence 6042, Ap	c 358	16	0.5	243	5	US-09-531-113-31143	Sequence 31143, A
c 286	16	0.5	25	7	US-60-427-808-27819	Sequence 27819, A	c 359	16	0.5	244	5	US-09-534-850-14118	Sequence 14118, A
c 287	16	0.5	25	7	US-60-427-808-30853	Sequence 30853, A	c 360	16	0.5	244	5	US-09-534-850-14127	Sequence 14127, A
c 288	16	0.5	25	7	US-60-427-808-96867	Sequence 96867, A	c 361	16	0.5	245	5	US-09-534-850-20473	Sequence 20473, A
c 289	16	0.5	25	7	US-60-427-808-128295	Sequence 128295, A	c 362	16	0.5	247	5	US-09-513-999C-34995	Sequence 34995, A
c 290	16	0.5	25	7	US-60-427-808-157246	Sequence 157246, A	c 363	16	0.5	247	5	US-09-531-113-37893	Sequence 37893, A
c 291	16	0.5	25	7	US-60-427-808-156677	Sequence 156677, A	c 364	16	0.5	250	5	US-09-534-850-14166	Sequence 14166, A
c 292	16	0.5	25	7	US-60-427-808-226607	Sequence 226607, A	c 365	16	0.5	250	5	US-09-531-113-13336	Sequence 13336, A
c 293	16	0.5	25	7	US-60-427-808-261911	Sequence 261911, A	c 366	16	0.5	251	5	US-09-531-113-21411	Sequence 21411, A
c 294	16	0.5	25	7	US-60-427-808-323347	Sequence 323347, A	c 367	16	0.5	251	5	US-09-531-113-36520	Sequence 36520, A
c 295	16	0.5	25	7	US-60-427-808-406973	Sequence 406973, A	c 368	16	0.5	251	5	US-09-531-113-40669	Sequence 40669, A
c 296	16	0.5	25	7	US-60-427-808-609848	Sequence 609848, A	c 369	16	0.5	252	5	US-09-534-850-13505	Sequence 13505, A
c 297	16	0.5	25	7	US-60-427-808-638248	Sequence 638248, A	c 370	16	0.5	252	5	US-09-531-113-35954	Sequence 35954, A
c 298	16	0.5	25	7	US-60-427-808-638519	Sequence 638519, A	c 371	16	0.5	252	6	US-10-203-138A-7707	Sequence 7707, Ap
c 299	16	0.5	25	7	US-60-427-808-687341	Sequence 687341, A	c 372	16	0.5	254	5	US-09-531-113-1061	Sequence 1061, Ap
c 300	16	0.5	25	7	US-60-427-808-898894	Sequence 898894, A	c 373	16	0.5	254	5	US-09-531-113-19121	Sequence 19121, A
c 301	16	0.5	25	7	US-60-427-808-939179	Sequence 939179, A	c 374	16	0.5	255	5	US-09-531-113-24210	Sequence 24210, A
c 302	16	0.5	25	7	US-60-427-808-943215	Sequence 943215, A	c 375	16	0.5	255	5	US-09-747-358A-263	Sequence 263, App
c 303	16	0.5	25	7	US-60-427-808-982255	Sequence 982255, A	c 376	16	0.5	256	5	US-09-531-113-22670	Sequence 22670, A
c 304	16	0.5	25	7	US-60-427-836-7102	Sequence 7102, Ap	c 377	16	0.5	256	5	US-09-531-113-26109	Sequence 26109, A
c 305	16	0.5	25	7	US-60-427-836-66322	Sequence 66322, A	c 378	16	0.5	258	5	US-09-531-113-14851	Sequence 14851, A
c 306	16	0.5	25	7	US-60-427-836-100573	Sequence 100573, A	c 379	16	0.5	260	5	US-09-513-999C-3556	Sequence 3556, Ap
c 307	16	0.5	25	7	US-60-427-836-115604	Sequence 115604, A	c 380	16	0.5	260	5	US-09-534-850-14153	Sequence 14153, A
c 308	16	0.5	25	7	US-60-427-836-135906	Sequence 125906, A	c 381	16	0.5	261	5	US-09-531-113-303	Sequence 303, App
c 309	16	0.5	25	7	US-60-427-836-143583	Sequence 143583, A	c 382	16	0.5	261	5	US-09-531-113-44808	Sequence 44808, A
c 310	16	0.5	25	7	US-60-427-836-189920	Sequence 189920, A	c 383	16	0.5	262	5	US-09-531-113-24588	Sequence 24588, A
c 311	16	0.5	25	7	US-60-427-836-194689	Sequence 194689, A	c 384	16	0.5	263	5	US-09-531-113-20441	Sequence 20441, A
c 312	16	0.5	25	7	US-60-427-836-229530	Sequence 229530, A	c 385	16	0.5	265	5	US-09-534-850-14124	Sequence 14124, A
c 313	16	0.5	25	7	US-60-427-836-255656	Sequence 255656, A	c 386	16	0.5	267	5	US-09-531-113-668	Sequence 668, App
c 314	16	0.5	25	7	US-60-427-836-268477	Sequence 268477, A	c 387	16	0.5	267	5	US-09-531-113-43592	Sequence 43592, A
c 315	16	0.5	25	7	US-60-427-836-347632	Sequence 347632, A	c 388	16	0.5	269	5	US-09-534-850-14119	Sequence 14119, A
c 316	16	0.5	25	7	US-60-427-836-377335	Sequence 377335, A	c 389	16	0.5	269	5	US-09-531-113-15951	Sequence 15951, A
c 317	16	0.5	25	7	US-60-427-836-403963	Sequence 403963, A	c 390	16	0.5	270	5	US-09-531-113-46774	Sequence 46774, A
c 318	16	0.5	25	7	US-60-427-836-403963	Sequence 403963, A	c 391	16	0.5	271	5	US-09-534-850-14112	Sequence 14112, A

392	16	0.5	271	6	US-09-531-113-23604	Sequence 6861, App	465	16	0.5	543	5	US-09-134-000C-394	Sequence 394, App
393	16	0.5	274	5	US-09-531-113-23604	Sequence 23604, A	466	16	0.5	543	5	US-09-134-000C-394	Sequence 394, App
394	16	0.5	278	6	US-10-335-066-1954	Sequence 1954, App	467	16	0.5	552	6	US-09-531-113-6221	Sequence 6221, App
395	16	0.5	282	6	US-10-335-066-1954	Sequence 1954, App	468	16	0.5	552	6	US-09-531-113-6221	Sequence 6221, App
396	16	0.5	287	5	US-09-531-113-45594	Sequence 45594, A	469	16	0.5	563	5	US-10-240-425-708	Sequence 708, App
397	16	0.5	290	5	US-09-531-113-45594	Sequence 45594, A	470	16	0.5	563	5	US-09-531-113-4122	Sequence 4122, App
398	16	0.5	302	6	US-10-071-510-11	Sequence 11, Appl	471	16	0.5	573	4	US-08-906-156A-67	Sequence 67, Appl
399	16	0.5	306	5	US-09-513-999C-27209	Sequence 27209, App	472	16	0.5	573	4	US-08-906-156A-67	Sequence 67, Appl
400	16	0.5	321	5	US-09-134-000C-3172	Sequence 3172, App	473	16	0.5	574	6	US-10-266-131-2355	Sequence 2355, App
401	16	0.5	321	5	US-09-134-000C-3172	Sequence 3172, App	474	16	0.5	578	1	PCT-US02-31467-58	Sequence 58, Appl
402	16	0.5	321	5	US-09-134-000C-3172	Sequence 3172, App	475	16	0.5	585	5	US-09-531-113-29196	Sequence 19, Appl
403	16	0.5	322	6	US-09-134-000C-3172	Sequence 3172, App	476	16	0.5	590	4	US-08-906-156A-19	Sequence 19, Appl
404	16	0.5	322	6	US-10-209-582-54	Sequence 54, Appl	477	16	0.5	590	4	US-08-906-156A-19	Sequence 19, Appl
405	16	0.5	331	6	US-10-071-510-6	Sequence 6, Appl	478	16	0.5	597	6	US-10-203-138A-10251	Sequence 10251, A
406	16	0.5	335	6	US-10-329-624-4258	Sequence 4258, App	479	16	0.5	600	6	US-09-531-113-12530	Sequence 12530, A
407	16	0.5	356	6	US-10-329-624-4258	Sequence 4258, App	480	16	0.5	601	5	US-09-949-002-3848	Sequence 3848, App
408	16	0.5	363	6	US-09-534-850-14158	Sequence 14158, App	481	16	0.5	601	5	US-09-949-002-8561	Sequence 8561, App
409	16	0.5	367	6	US-10-329-624-4109	Sequence 4109, App	482	16	0.5	601	5	US-09-949-004-848	Sequence 848, App
410	16	0.5	383	6	US-10-276-774-1210	Sequence 1210, App	483	16	0.5	601	5	US-09-949-004-1605	Sequence 1605, App
411	16	0.5	394	5	US-09-513-999C-34127	Sequence 34127, A	484	16	0.5	601	5	US-09-949-004-1650	Sequence 1650, App
412	16	0.5	397	5	US-09-724-676-30388	Sequence 30388, A	485	16	0.5	601	5	US-09-949-004-1729	Sequence 1729, App
413	16	0.5	397	5	US-09-724-676-30388	Sequence 30388, A	486	16	0.5	601	5	US-09-949-004-1851	Sequence 1851, App
414	16	0.5	403	6	US-10-276-781-857	Sequence 857, App	487	16	0.5	601	5	US-09-949-004-1896	Sequence 1896, App
415	16	0.5	411	5	US-09-513-999C-31900	Sequence 31900, A	488	16	0.5	601	5	US-09-949-004-3182	Sequence 3182, App
416	16	0.5	411	5	US-09-134-000C-3142	Sequence 3142, App	489	16	0.5	601	5	US-09-949-004-5506	Sequence 5506, App
417	16	0.5	415	6	US-09-134-000C-3142	Sequence 3142, App	490	16	0.5	604	6	US-10-203-138A-5427	Sequence 5427, App
418	16	0.5	415	6	US-10-203-138A-3207	Sequence 3207, App	491	16	0.5	607	5	US-09-531-113-12530	Sequence 12530, A
419	16	0.5	416	7	US-09-422-176-2757	Sequence 2757, App	492	16	0.5	626	5	US-09-724-676A-17161	Sequence 17161, A
420	16	0.5	417	5	US-09-513-999C-1951	Sequence 1951, App	493	16	0.5	626	5	US-09-724-676A-17161	Sequence 17161, A
421	16	0.5	422	5	US-09-724-676A-30391	Sequence 30391, A	494	16	0.5	631	5	US-09-531-113-7814	Sequence 7814, App
422	16	0.5	422	5	US-09-724-676A-30391	Sequence 30391, A	495	16	0.5	634	5	US-09-724-676-30385	Sequence 30385, A
423	16	0.5	425	6	US-10-218-140-619	Sequence 12134, A	496	16	0.5	694	5	US-09-724-676A-30385	Sequence 30385, A
424	16	0.5	425	6	US-10-218-140-619	Sequence 12134, A	497	16	0.5	694	5	US-10-203-138A-7222	Sequence 7222, App
425	16	0.5	437	6	US-10-152-319A-486	Sequence 486, App	498	16	0.5	695	6	US-10-218-140-2453	Sequence 2453, App
426	16	0.5	437	6	US-10-152-319A-486	Sequence 486, App	499	16	0.5	728	6	US-10-230-437-115	Sequence 115, App
427	16	0.5	439	6	US-09-949-002-6987	Sequence 6987, App	500	16	0.5	728	6	US-10-230-437-115	Sequence 115, App
428	16	0.5	439	6	US-10-264-237-49	Sequence 49, Appl	501	16	0.5	728	6	US-10-219-076-115	Sequence 115, App
429	16	0.5	441	5	US-09-724-676-30386	Sequence 30386, A	502	16	0.5	728	6	US-10-219-076-115	Sequence 115, App
430	16	0.5	441	5	US-09-724-676-30386	Sequence 30386, A	503	16	0.5	728	6	US-10-219-076-115	Sequence 115, App
431	16	0.5	443	6	US-10-240-425-868	Sequence 868, App	504	16	0.5	770	6	PCT-US02-28859-13	Sequence 13, Appl
432	16	0.5	445	6	US-10-203-138A-2206	Sequence 2206, App	505	16	0.5	770	6	PCT-US02-28859-13	Sequence 13, Appl
433	16	0.5	446	6	US-10-071-510-7	Sequence 7, Appl	506	16	0.5	799	1	PCT-US02-18666-5	Sequence 5, Appl
434	16	0.5	447	6	US-10-092-411A-1190	Sequence 1190, App	507	16	0.5	803	6	US-10-194-163-684	Sequence 684, App
435	16	0.5	449	5	US-09-534-850-22738	Sequence 22738, App	508	16	0.5	825	5	US-09-950-084-2672	Sequence 2672, App
436	16	0.5	456	5	US-09-531-113-9224	Sequence 9224, App	509	16	0.5	837	5	US-09-134-000C-319	Sequence 319, App
437	16	0.5	458	5	US-09-531-113-43241	Sequence 43241, App	510	16	0.5	837	5	US-09-134-000C-319	Sequence 319, App
438	16	0.5	463	6	US-10-071-510-10	Sequence 10, Appl	511	16	0.5	844	5	US-10-264-237-551	Sequence 551, App
439	16	0.5	465	5	US-09-531-113-29074	Sequence 29074, A	512	16	0.5	855	5	US-09-724-676-25411	Sequence 25411, A
440	16	0.5	465	6	US-10-203-138A-664	Sequence 664, App	513	16	0.5	855	5	US-09-724-676-25411	Sequence 25411, A
441	16	0.5	466	5	US-10-203-138A-3339	Sequence 3339, App	514	16	0.5	881	6	US-10-264-237-428	Sequence 428, App
442	16	0.5	466	5	US-09-724-676-30389	Sequence 30389, A	515	16	0.5	881	6	US-10-264-237-428	Sequence 428, App
443	16	0.5	466	5	US-09-724-676-30389	Sequence 30389, A	516	16	0.5	887	6	US-10-240-425-658	Sequence 658, App
444	16	0.5	467	6	US-10-203-138A-3514	Sequence 3514, App	517	16	0.5	901	5	US-09-620-312B-814	Sequence 814, App
445	16	0.5	469	6	US-10-203-138A-2929	Sequence 2929, App	518	16	0.5	915	6	US-10-329-624-739	Sequence 739, App
446	16	0.5	471	6	US-10-203-138A-2441	Sequence 2441, App	519	16	0.5	943	6	US-10-017-161-1851	Sequence 1851, App
447	16	0.5	474	6	US-10-203-138A-1734	Sequence 1734, App	520	16	0.5	962	5	US-09-724-676-15881	Sequence 15881, A
448	16	0.5	475	6	US-10-203-138A-2608	Sequence 2608, App	521	16	0.5	972	6	US-09-724-676A-15881	Sequence 15881, A
449	16	0.5	477	6	US-10-203-138A-147	Sequence 147, App	522	16	0.5	993	5	US-10-203-138A-2107	Sequence 2107, App
450	16	0.5	482	6	US-09-949-002-6986	Sequence 6986, App	523	16	0.5	998	6	US-09-950-084-2296	Sequence 2296, App
451	16	0.5	482	6	US-10-203-138A-9245	Sequence 9245, App	524	16	0.5	998	6	US-10-278-173-147	Sequence 147, App
452	16	0.5	491	6	US-10-266-131-2388	Sequence 2388, App	525	16	0.5	998	6	US-10-278-173-147	Sequence 147, App
453	16	0.5	492	5	US-09-534-850-23347	Sequence 23347, A	526	16	0.5	1044	6	US-10-278-536A-91	Sequence 91, Appl
454	16	0.5	495	6	US-10-152-319A-57	Sequence 57, Appl	527	16	0.5	1050	1	PCT-US02-35606-39	Sequence 39, Appl
455	16	0.5	502	5	US-09-534-850-23348	Sequence 23348, A	528	16	0.5	1057	6	PCT-US02-18666-9	Sequence 9, Appl
456	16	0.5	504	6	US-10-321-854-3709	Sequence 3709, App	529	16	0.5	1073	1	PCT-US02-18666-9	Sequence 9, Appl
457	16	0.5	504	6	US-10-321-854-3709	Sequence 3709, App	530	16	0.5	1084	6	US-10-152-319A-1992	Sequence 1992, App
458	16	0.5	506	7	US-60-422-176-1544	Sequence 1544, App	531	16	0.5	1089	5	US-09-724-676-40650	Sequence 40650, A
459	16	0.5	510	6	US-09-531-113-4372	Sequence 4372, App	532	16	0.5	1089	5	US-09-724-676A-40650	Sequence 40650, A
460	16	0.5	511	6	US-10-327-713-82	Sequence 82, Appl	533	16	0.5	1089	6	US-10-095-720-1381	Sequence 1381, App
461	16	0.5	514	5	US-09-534-850-23355	Sequence 23355, A	534	16	0.5	1113	6	US-10-092-411A-586	Sequence 586, App
462	16	0.5	524	5	US-09-531-113-12563	Sequence 12563, A	535	16	0.5	1120	6	US-10-017-161-2355	Sequence 2355, App
463	16	0.5	529	5	US-09-534-850-22737	Sequence 22737, A	536	16	0.5	1134	6	US-10-302-267-119	Sequence 119, App
464	16	0.5	536	5	US-09-531-113-30061	Sequence 30061, A	537	16	0.5	1134	6	US-10-302-267-119	Sequence 119, App



538	16	0.5	1138	5	US-09-724-676-35837	Sequence 35837, A	c 611	16	0.5	1762	5	US-09-724-676A-23874	Sequence 23874, A
539	16	0.5	1138	5	US-09-724-676A-35837	Sequence 35837, A	612	16	0.5	1788	6	US-10-276-774-1080	Sequence 1080, Ap
540	16	0.5	1146	5	US-09-134-000C-1824	Sequence 1824, Ap	613	16	0.5	1811	6	US-10-131-985-52	Sequence 52, Appl
541	16	0.5	1146	5	US-09-134-000C-1824	Sequence 1824, Ap	614	16	0.5	1840	6	US-10-305-720-1367	Sequence 1367, Ap
542	16	0.5	1149	5	US-09-134-000C-1632	Sequence 1632, Ap	615	16	0.5	1858	5	US-09-724-676-25412	Sequence 25412, A
543	16	0.5	1149	5	US-09-134-000C-1632	Sequence 1632, Ap	616	16	0.5	1858	5	US-09-724-676A-23412	Sequence 23412, A
c 544	16	0.5	1171	1	PCT-US02-18666-11	Sequence 11, Appl	c 617	16	0.5	1870	5	US-09-724-676A-23904	Sequence 23904, A
545	16	0.5	1232	6	US-09-620-312D-672	Sequence 672, App	c 618	16	0.5	1870	5	US-09-724-676A-23904	Sequence 23904, A
546	16	0.5	1233	6	US-10-202-138A-8047	Sequence 195, App	619	16	0.5	1874	5	US-09-724-676-20569	Sequence 20569, A
547	16	0.5	1233	6	US-10-203-138A-8047	Sequence 8047, App	620	16	0.5	1874	5	US-09-724-676A-20569	Sequence 20569, A
c 548	16	0.5	1279	5	US-09-724-676A-11678	Sequence 11678, A	c 621	16	0.5	1875	5	US-09-724-676-14582	Sequence 14582, A
c 549	16	0.5	1279	5	US-09-724-676A-11678	Sequence 11678, A	c 622	16	0.5	1875	5	US-09-724-676A-14582	Sequence 14582, A
550	16	0.5	1305	5	US-09-724-676-30638	Sequence 30638, A	c 623	16	0.5	1876	5	US-09-724-676-47490	Sequence 47490, A
551	16	0.5	1305	5	US-09-724-676-30638	Sequence 30638, A	c 624	16	0.5	1876	5	US-09-724-676A-47490	Sequence 47490, A
c 552	16	0.5	1311	6	US-10-092-411A-386	Sequence 386, App	c 625	16	0.5	1888	6	US-10-315-664-38	Sequence 38, Appl
553	16	0.5	1311	6	US-10-304-105-4	Sequence 4, Appli	626	16	0.5	1888	6	US-10-315-664-38	Sequence 38, Appl
554	16	0.5	1321	5	US-09-724-676-17163	Sequence 17163, A	627	16	0.5	1893	5	US-09-724-676-15888	Sequence 15888, A
555	16	0.5	1321	5	US-09-724-676A-17163	Sequence 17163, A	c 628	16	0.5	1901	5	US-09-724-676A-15888	Sequence 15888, A
556	16	0.5	1322	7	US-60-427-982-120	Sequence 120, App	c 629	16	0.5	1901	5	US-09-724-676-14581	Sequence 14581, A
557	16	0.5	1333	6	US-10-017-161-545	Sequence 545, App	630	16	0.5	1906	5	US-09-724-676-30384	Sequence 30384, A
c 558	16	0.5	1339	5	US-09-724-676-11676	Sequence 11676, A	631	16	0.5	1906	5	US-09-724-676A-30384	Sequence 30384, A
c 559	16	0.5	1339	5	US-09-724-676A-11676	Sequence 11676, A	c 632	16	0.5	1914	6	US-10-287-818-1298	Sequence 1298, Ap
560	16	0.5	1339	6	US-10-264-237-1242	Sequence 1242, Ap	633	16	0.5	1915	6	US-10-325-899-9261	Sequence 9261, Ap
c 561	16	0.5	1350	5	US-09-950-084-1603	Sequence 1603, Ap	c 634	16	0.5	1924	5	US-09-724-676-23909	Sequence 23909, A
562	16	0.5	1352	6	US-10-218-140-2879	Sequence 2879, Ap	c 635	16	0.5	1924	5	US-09-724-676A-23909	Sequence 23909, A
563	16	0.5	1363	5	US-09-724-676A-15890	Sequence 15890, A	636	16	0.5	1928	6	US-10-218-140-4309	Sequence 4309, Ap
564	16	0.5	1363	5	US-09-724-676A-15890	Sequence 15890, A	c 637	16	0.5	1951	6	US-10-278-536-45	Sequence 45, Appl
c 565	16	0.5	1380	6	US-10-288-252-22	Sequence 22, Appl	c 638	16	0.5	1951	6	US-10-278-536A-45	Sequence 45, Appl
c 566	16	0.5	1380	6	US-09-724-676-11683	Sequence 11683, A	c 639	16	0.5	1951	6	US-10-203-138A-2893	Sequence 2893, Ap
c 567	16	0.5	1390	5	US-09-724-676-11683	Sequence 11683, A	c 640	16	0.5	1964	5	US-09-911-514-1	Sequence 1, Appli
568	16	0.5	1394	5	US-09-620-312D-364	Sequence 364, App	c 641	16	0.5	1966	7	US-60-427-982-109	Sequence 109, App
569	16	0.5	1404	5	US-09-948-124-146	Sequence 146, App	c 642	16	0.5	1969	6	US-10-203-138A-3479	Sequence 3479, Ap
c 570	16	0.5	1422	7	US-60-427-045-147	Sequence 147, App	c 643	16	0.5	1972	6	US-10-203-138A-5151	Sequence 5151, Ap
c 571	16	0.5	1450	5	US-09-724-676-11681	Sequence 11681, A	c 644	16	0.5	1988	5	US-09-724-676-23894	Sequence 23894, A
c 572	16	0.5	1450	6	US-09-724-676A-11681	Sequence 11681, A	c 645	16	0.5	1988	5	US-09-724-676A-23894	Sequence 23894, A
c 573	16	0.5	1455	6	US-10-305-720-1287	Sequence 1287, Ap	646	16	0.5	1989	6	US-10-218-140-5283	Sequence 5283, Ap
c 574	16	0.5	1458	5	US-09-724-676-12266	Sequence 12266, A	c 647	16	0.5	2042	5	US-09-724-676-23899	Sequence 23899, A
c 575	16	0.5	1458	5	US-09-724-676-23875	Sequence 23875, A	c 648	16	0.5	2042	5	US-09-724-676A-23899	Sequence 23899, A
c 576	16	0.5	1500	6	US-10-209-582-40	Sequence 40, Appl	c 649	16	0.5	2047	6	US-10-203-138A-8620	Sequence 8620, Ap
c 577	16	0.5	1513	6	US-10-218-140-5481	Sequence 5481, Ap	650	16	0.5	2050	6	US-10-264-237-1009	Sequence 1009, Ap
578	16	0.5	1523	5	US-09-724-676-12266	Sequence 12266, A	c 651	16	0.5	2070	1	PCT-US02-29560-44	Sequence 44, Appl
579	16	0.5	1523	5	US-09-724-676A-12266	Sequence 12266, A	c 652	16	0.5	2070	6	US-10-245-882-44	Sequence 44, Appl
c 580	16	0.5	1551	6	US-10-029-397B-29	Sequence 29, Appl	c 653	16	0.5	2076	5	US-09-724-676-23905	Sequence 23905, A
c 581	16	0.5	1573	5	US-09-620-312D-399	Sequence 399, App	c 654	16	0.5	2076	5	US-09-724-676A-23905	Sequence 23905, A
582	16	0.5	1574	5	US-09-724-676-12272	Sequence 12272, A	655	16	0.5	2078	5	US-09-724-676-12269	Sequence 12269, A
583	16	0.5	1574	5	US-09-724-676A-12272	Sequence 12272, A	656	16	0.5	2078	5	US-09-724-676A-12269	Sequence 12269, A
584	16	0.5	1594	5	US-09-724-676-33114	Sequence 33114, A	c 657	16	0.5	2088	6	US-10-287-818-1312	Sequence 1312, Ap
585	16	0.5	1594	5	US-09-724-676A-33114	Sequence 33114, A	c 658	16	0.5	2104	5	US-09-724-676-30364	Sequence 30364, A
c 586	16	0.5	1597	5	US-09-921-406C-39	Sequence 39, Appl	c 659	16	0.5	2104	5	US-09-724-676A-30364	Sequence 30364, A
587	16	0.5	1599	5	US-09-724-676-12268	Sequence 12268, A	c 660	16	0.5	2110	6	US-10-287-818-1313	Sequence 1313, Ap
c 588	16	0.5	1599	5	US-09-724-676-12268	Sequence 12268, A	c 661	16	0.5	2115	5	US-09-724-676-23902	Sequence 23902, A
c 589	16	0.5	1618	5	US-09-814-915A-48	Sequence 48, Appl	c 662	16	0.5	2115	5	US-09-724-676A-23902	Sequence 23902, A
c 590	16	0.5	1636	5	US-09-911-514-7	Sequence 7, Appli	c 663	16	0.5	2125	5	US-09-724-676-34195	Sequence 34195, A
c 591	16	0.5	1642	5	US-09-911-514-5	Sequence 5, Appli	c 664	16	0.5	2125	5	US-09-724-676A-34195	Sequence 34195, A
c 592	16	0.5	1642	5	US-09-911-514-9	Sequence 9, Appli	665	16	0.5	2128	5	US-09-724-676-12267	Sequence 12267, A
c 593	16	0.5	1643	5	US-09-911-514-3	Sequence 3, Appli	666	16	0.5	2128	5	US-09-724-676A-12267	Sequence 12267, A
594	16	0.5	1650	5	US-09-724-676-12275	Sequence 12275, A	667	16	0.5	2129	5	US-09-724-676-12261	Sequence 12261, A
595	16	0.5	1650	5	US-09-724-676A-12275	Sequence 12275, A	668	16	0.5	2129	5	US-09-724-676A-12261	Sequence 12261, A
c 596	16	0.5	1655	5	US-09-724-676-27588	Sequence 27588, A	c 669	16	0.5	2130	5	US-09-724-676-23910	Sequence 23910, A
c 597	16	0.5	1655	5	US-09-724-676A-27588	Sequence 27588, A	c 670	16	0.5	2130	5	US-09-724-676A-23910	Sequence 23910, A
c 598	16	0.5	1664	5	US-09-724-676-23876	Sequence 23876, A	671	16	0.5	2151	5	US-09-724-676-12264	Sequence 12264, A
c 599	16	0.5	1664	5	US-09-724-676A-23876	Sequence 23876, A	672	16	0.5	2151	5	US-09-724-676A-12264	Sequence 12264, A
600	16	0.5	1672	5	US-09-724-676-12263	Sequence 12263, A	c 673	16	0.5	2163	1	PCT-US02-40225-2287	Sequence 2287, Ap
601	16	0.5	1672	6	US-09-724-676A-12263	Sequence 12263, A	c 674	16	0.5	2163	6	US-10-320-797-2287	Sequence 2287, Ap
c 602	16	0.5	1678	5	US-10-218-140-1593	Sequence 1593, Ap	c 675	16	0.5	2169	5	US-09-724-676-23907	Sequence 23907, A
c 603	16	0.5	1703	5	US-09-724-676-23873	Sequence 23873, A	c 676	16	0.5	2169	5	US-09-724-676A-23907	Sequence 23907, A
c 604	16	0.5	1703	5	US-09-724-676A-23873	Sequence 23873, A	c 677	16	0.5	2174	5	US-09-724-676-23903	Sequence 23903, A
605	16	0.5	1723	5	US-09-724-676-12273	Sequence 12273, A	c 678	16	0.5	2174	5	US-09-724-676A-23903	Sequence 23903, A
606	16	0.5	1728	5	US-09-724-676A-12273	Sequence 12273, A	679	16	0.5	2179	5	US-09-724-676-12270	Sequence 12270, A
c 607	16	0.5	1735	1	US-10-210-120-23	Sequence 23, Appl	680	16	0.5	2179	5	US-09-724-676A-12270	Sequence 12270, A
c 608	16	0.5	1735	1	PCT-US02-18666-3	Sequence 3, Appli	681	16	0.5	2184	5	US-09-134-000C-3320	Sequence 3320, Ap
c 609	16	0.5	1740	5	US-09-950-084-2114	Sequence 2114, Ap	682	16	0.5	2184	5	US-09-134-000C-3320	Sequence 3320, Ap
c 610	16	0.5	1762	5	US-09-724-676-23874	Sequence 23874, A	c 683	16	0.5	2194	5	US-09-724-676-23895	Sequence 23895, A

c 684	16	0.5	2194	5	US-09-724-676A-23895	Sequence 23895, A	757	16	0.5	2677	5	US-09-724-676A-20568	Sequence 20568, A
c 685	16	0.5	2200	5	US-09-949-004-2022	Sequence 202, App	758	16	0.5	2678	6	US-10-017-161-1647	Sequence 1647, App
c 686	16	0.5	2201	5	US-09-724-676-12262	Sequence 12262, A	759	16	0.5	2681	6	US-10-152-319A-1631	Sequence 1631, App
c 687	16	0.5	2201	5	US-09-724-676A-12262	Sequence 12262, A	760	16	0.5	2686	5	US-09-724-676A-30503	Sequence 30503, A
c 688	16	0.5	2202	5	US-09-724-676-12274	Sequence 12274, A	761	16	0.5	2686	5	US-09-724-676A-30503	Sequence 30503, A
c 689	16	0.5	2202	5	US-09-724-676A-12274	Sequence 12274, A	c 762	16	0.5	2705	1	PCT-US02-40225-1287	Sequence 1287, App
c 690	16	0.5	2205	5	US-09-724-676-29646	Sequence 29646, A	c 763	16	0.5	2705	6	US-10-320-797-1287	Sequence 1287, App
c 691	16	0.5	2205	5	US-09-724-676A-29646	Sequence 29646, A	c 764	16	0.5	2723	5	US-09-724-676-30536	Sequence 30536, A
c 692	16	0.5	2222	6	US-10-324-130-1	Sequence 1, Appl1	765	16	0.5	2723	5	US-09-724-676A-30536	Sequence 30536, A
c 693	16	0.5	2228	5	US-09-724-676-23908	Sequence 23908, A	766	16	0.5	2738	5	US-09-724-676A-30509	Sequence 30509, A
c 694	16	0.5	2228	5	US-09-724-676A-23908	Sequence 23908, A	767	16	0.5	2738	5	US-09-724-676A-30509	Sequence 30509, A
c 695	16	0.5	2233	5	US-09-724-676-23892	Sequence 23892, A	768	16	0.5	2742	1	PCT-US02-21420-20	Sequence 20, Appl1
c 696	16	0.5	2233	5	US-09-724-676A-23892	Sequence 23892, A	769	16	0.5	2742	6	US-10-190-305A-15	Sequence 15, Appl1
c 697	16	0.5	2239	5	US-09-724-676-40652	Sequence 40652, A	770	16	0.5	2742	6	US-10-190-435-20	Sequence 20, Appl1
c 698	16	0.5	2239	5	US-09-724-676A-40652	Sequence 40652, A	c 771	16	0.5	2748	5	US-09-724-676-47489	Sequence 47489, A
c 699	16	0.5	2248	5	US-09-724-676-23900	Sequence 23900, A	c 772	16	0.5	2748	5	US-09-724-676A-47489	Sequence 47489, A
c 700	16	0.5	2248	5	US-09-724-676A-23900	Sequence 23900, A	c 773	16	0.5	2762	5	US-09-724-676-30511	Sequence 30511, A
c 701	16	0.5	2253	6	US-10-171-404A-1	Sequence 1, Appl1	c 774	16	0.5	2762	5	US-09-724-676A-30511	Sequence 30511, A
c 702	16	0.5	2277	6	US-10-276-774-97	Sequence 97, Appl1	c 775	16	0.5	2775	5	US-09-724-676-23880	Sequence 23880, A
c 703	16	0.5	2279	1	PCT-US02-28859-6	Sequence 6, Appl1	c 776	16	0.5	2775	5	US-09-724-676A-23880	Sequence 23880, A
c 704	16	0.5	2279	6	US-10-241-220-6	Sequence 6, Appl1	c 777	16	0.5	2814	5	US-09-724-676-30522	Sequence 30522, A
c 705	16	0.5	2287	5	US-09-724-676-23897	Sequence 23897, A	c 778	16	0.5	2814	5	US-09-724-676A-30522	Sequence 30522, A
c 706	16	0.5	2287	5	US-09-724-676A-23897	Sequence 23897, A	c 779	16	0.5	2818	5	US-09-724-676-30520	Sequence 30520, A
c 707	16	0.5	2291	5	US-09-724-676-8957	Sequence 8957, App	c 780	16	0.5	2818	5	US-09-724-676A-30520	Sequence 30520, A
c 708	16	0.5	2291	5	US-09-724-676A-8957	Sequence 8957, App	c 781	16	0.5	2818	5	US-09-724-676A-30513	Sequence 30513, A
c 709	16	0.5	2292	5	US-09-724-676-23893	Sequence 23893, A	c 782	16	0.5	2818	5	US-09-724-676A-30513	Sequence 30513, A
c 710	16	0.5	2307	5	US-09-724-676A-23893	Sequence 23893, A	c 783	16	0.5	2829	5	US-09-724-676A-30520	Sequence 30520, A
c 711	16	0.5	2307	5	US-09-724-676-34193	Sequence 34193, A	c 784	16	0.5	2829	5	US-09-724-676A-30520	Sequence 30520, A
c 712	16	0.5	2307	5	US-09-724-676-34193	Sequence 34193, A	c 785	16	0.5	2835	5	US-09-724-676A-23885	Sequence 23885, A
c 713	16	0.5	2346	5	US-09-724-676A-34193	Sequence 34193, A	c 786	16	0.5	2835	5	US-10-240-965-126	Sequence 126, App
c 714	16	0.5	2346	5	US-09-724-676A-34193	Sequence 34193, A	c 787	16	0.5	2840	6	US-10-152-319A-1540	Sequence 1540, App
c 715	16	0.5	2356	5	US-09-724-676A-23898	Sequence 23898, A	c 788	16	0.5	2870	5	US-09-724-676-30530	Sequence 30530, A
c 716	16	0.5	2356	5	US-09-136-159-68	Sequence 68, Appl1	c 789	16	0.5	2870	5	US-09-724-676A-30530	Sequence 30530, A
c 717	16	0.5	2356	6	US-10-136-159A-68	Sequence 68, Appl1	c 790	16	0.5	2870	5	US-09-724-676A-30530	Sequence 30530, A
c 718	16	0.5	2367	5	US-09-724-676-30518	Sequence 30518, A	c 791	16	0.5	2870	5	US-09-724-676A-30538	Sequence 30538, A
c 719	16	0.5	2367	5	US-09-724-676A-30518	Sequence 30518, A	c 792	16	0.5	2874	5	US-09-724-676A-30538	Sequence 30538, A
c 720	16	0.5	2375	5	US-09-724-676-14580	Sequence 14580, A	c 793	16	0.5	2874	5	US-09-724-676A-30523	Sequence 30523, A
c 721	16	0.5	2375	5	US-09-724-676A-14580	Sequence 14580, A	c 794	16	0.5	2878	5	US-09-724-676A-30501	Sequence 30501, A
c 722	16	0.5	2401	5	US-09-724-676-14579	Sequence 14579, A	c 795	16	0.5	2900	6	US-10-276-774-892	Sequence 892, App
c 723	16	0.5	2401	5	US-09-724-676A-14579	Sequence 14579, A	c 796	16	0.5	2926	5	US-09-724-676-30532	Sequence 30532, A
c 724	16	0.5	2419	5	US-09-724-676-30498	Sequence 30498, A	c 797	16	0.5	2926	5	US-09-724-676A-30532	Sequence 30532, A
c 725	16	0.5	2419	5	US-09-724-676A-30498	Sequence 30498, A	c 798	16	0.5	2930	5	US-09-724-676-30507	Sequence 30507, A
c 726	16	0.5	2423	5	US-09-724-676-30528	Sequence 30528, A	c 799	16	0.5	2930	5	US-09-724-676A-30507	Sequence 30507, A
c 727	16	0.5	2423	7	US-60-427-313-157	Sequence 157, App	c 800	16	0.5	2934	5	US-09-724-676-30502	Sequence 30502, A
c 728	16	0.5	2423	7	US-09-724-676-30537	Sequence 30537, A	c 801	16	0.5	2934	5	US-09-724-676A-30502	Sequence 30502, A
c 729	16	0.5	2475	5	US-09-724-676A-30537	Sequence 30537, A	c 802	16	0.5	2977	5	US-09-724-676-34198	Sequence 34198, A
c 730	16	0.5	2475	5	US-09-724-676A-30537	Sequence 30537, A	c 803	16	0.5	2977	5	US-09-724-676A-34198	Sequence 34198, A
c 731	16	0.5	2494	5	US-09-724-676-30372	Sequence 30372, A	c 804	16	0.5	2981	5	US-09-724-676A-23881	Sequence 23881, A
c 732	16	0.5	2494	5	US-09-724-676-30372	Sequence 30372, A	c 805	16	0.5	2981	5	US-09-724-676A-23881	Sequence 23881, A
c 733	16	0.5	2526	5	US-09-864-636A-391	Sequence 391, App	c 806	16	0.5	2986	5	US-09-724-676-30508	Sequence 30508, A
c 734	16	0.5	2526	5	US-09-864-636A-459	Sequence 459, App	c 807	16	0.5	2986	5	US-09-724-676A-30508	Sequence 30508, A
c 735	16	0.5	2526	6	US-10-084-839-459	Sequence 459, App	c 808	16	0.5	3001	5	US-09-539-333D-146	Sequence 146, App
c 736	16	0.5	2526	6	US-10-084-839-459	Sequence 459, App	c 809	16	0.5	3001	5	US-09-539-333D-146	Sequence 146, App
c 737	16	0.5	2526	6	US-10-084-839-2731	Sequence 2731, App	c 810	16	0.5	3012	5	US-09-724-676-1434	Sequence 1434, App
c 738	16	0.5	2526	6	US-10-084-839-2731	Sequence 2731, App	c 811	16	0.5	3012	5	US-09-724-676A-1434	Sequence 1434, App
c 739	16	0.5	2529	5	US-09-620-312D-688	Sequence 688, App	c 812	16	0.5	3018	1	PCT-US02-40102-2	Sequence 2, Appl1
c 740	16	0.5	2559	5	US-09-724-676-30515	Sequence 30515, A	c 813	16	0.5	3020	5	US-09-724-676-23878	Sequence 23878, A
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## ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; NUMBER OF SEQ ID NOS: 14
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841 ACTGAG:TCGCTGAGGACATACACGAGCTTGGTGCCTGACTGCTGAGGTGGGGATATG 900
Qy 901 ACAGAA:JACAGCGCCAGGCTCTCATCCGAGAGTGTCTGATCAAGGAGCTTGTCTGAAGGC 960
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
901 ACAGAA:JACAGCGCCAGGCTCTCATCCGAGAGTGTCTGATCAAGGAGCTTGTCTGAAGGC 960
Qy 961 TTGTTG:TTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
961 TTGTTG:TTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
Qy 1021 GTGTCI:TCACATACCTTCTATGATCTGTGATACAGAAAAACAACACATAAAGGT 1080
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1021 GTGTCI:TCACATACCTTCTATGATCTGTGATACAGAAAAACAACACATAAAGGT 1080
Qy 1081 ACGCTG:TTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1140
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1081 ACGCTG:TTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1140
Qy 1141 GTGCTC:CAAGTGACTTTCATTCGAGGCTGGACCATCTGCGAGACCTAGCTCTGAGGCT 1200
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1141 GTGCTC:CAAGTGACTTTCATTCGAGGCTGGACCATCTGCGAGACCTAGCTCTGAGGCT 1200
Qy 1201 GTGCTC:CCCAACAGTTTGAATTCGAACCTGAGGATGCTCCAGGCTGAATGAGGATGTC 1260
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1201 GTGCTC:CCCAACAGTTTGAATTCGAACCTGAGGATGCTCCAGGCTGAATGAGGATGTC 1260
Qy 1261 CTGCTG:CAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCCAAGATATAA 1320
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1261 CTGCTG:CAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCCAAGATATAA 1320
Qy 1321 TTTCTTC:ACAAGTCAATTCAGGAGTACACAGCAGGACGAGACTTCAGCAGTTTATGAGC 1380
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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Db 1321 TTCTTTCACAAGATTCATCCAGGAGTACACAGCAGGAGCAAGACTCAGCAGCTTTATTGACG 1380
QY 1381 TCTCATGACCCAGAGAGGTGACCAAGGGAATGGTTACTTGCAGAAAATGGTTTCCATT 1440
Db 1381 TCTCATGACCCAGAGAGGTGACCAAGGGAATGGTTACTTGCAGAAAATGGTTTCCATT 1440
QY 1441 TCGGACATACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTGATCTGTGGAA 1500
Db 1441 TCGGACATACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTGATCTGTGGAA 1500
QY 1501 GCCACAGGGCTGTTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCCCTTCGGGA 1560
Db 1501 GCCACAGGGCTGTTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCCCTTCGGGA 1560
QY 1561 CTTTTCATCCCAAGAGGCTCTCTCGAGACAGGAATCTTTGCAAAAGTGTGAAAACACC 1620
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QY 1621 ACTGAGCAAGAAATCTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
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QY 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTTCTTTCAA 1740
Db 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTTCTTTCAA 1740
QY 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTGTACTTCTTTGAA 1800
Db 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTGTACTTCTTTGAA 1800
QY 1801 CATTGTGCCAATGTGCAAGTCTGAGACTTCATTAAGCTGGACTTTTATGGGGAGCT 1860
Db 1801 CATTGTGCCAATGTGCAAGTCTGAGACTTCATTAAGCTGGACTTTTATGGGGAGCT 1860
QY 1861 ATGCTTTCATGGAAGAGCTGAGAGACACAGGTGGAATCCACATGGAAGAGCCCCA 1920
Db 1861 ATGCTTTCATGGAAGAGCTGAGAGACACAGGTGGAATCCACATGGAAGAGCCCCA 1920
QY 1921 GAAACCTACATTCGCCAGCGGCTGTATCTTCTTCACTGGAAGCAGGAATTCAGG 1980
Db 1921 GAAACCTACATTCGCCAGCGGCTGTATCTTCTTCACTGGAAGCAGGAATTCAGG 1980
QY 1981 ACTCTGGAGTCACTCCGGGATTTGAGCAAGTTGAATGAAGCAAGATFACATATCTG 2040
Db 1981 ACTCTGGAGTCACTCCGGGATTTGAGCAAGTTGAATGAAGCAAGATFACATATCTG 2040
QY 2041 GGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTGCTGGTG 2100
Db 2041 GGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTGCTGGTG 2100
QY 2101 GCTGGAAGCCTCAGTTTGGTTCCTCAGCACCTGTAAAGCAATTTATCTCTCATGGTGGAA 2160
Db 2101 GCTGGAAGCCTCAGTTTGGTTCCTCAGCACCTGTAAAGCAATTTATCTCTCATGGTGGAA 2160
QY 2161 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCACATCTGTAAACAACTGAAAAACC 2220
Db 2161 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCACATCTGTAAACAACTGAAAAACC 2220
QY 2221 TTGAGTATTCATGACCTACAGATCAACGGCTGCCGGTGGTCTGACTGACACCTTGGGT 2280
Db 2221 TTGAGTATTCATGACCTACAGATCAACGGCTGCCGGTGGTCTGACTGACACCTTGGGT 2280
QY 2281 AACTTGAAGAACCTTCAAAAGCTCATTAATGATAAAGATGAATGAAGAGATGCT 2340
Db 2281 AACTTGAAGAACCTTCAAAAGCTCATTAATGATAAAGATGAATGAAGAGATGCT 2340
QY 2341 ATAAACTAGCTGAAGGCCCTGAAAAACCTGGAAGAAGATGTGTTTATTTCAATTTGACCCAC 2400
Db 2341 ATAAACTAGCTGAAGGCCCTGAAAAACCTGGAAGAAGATGTGTTTATTTCAATTTGACCCAC 2400
QY 2401 TTGCTGACATTTGAGAGGGAATGGATTTACATAGTCAAGTCTCTGCAAGTGAACCCGTG 2460
Db 2401 TTGCTGACATTTGAGAGGGAATGGATTTACATAGTCAAGTCTCTGCAAGTGAACCCGTG 2460
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QY 2461 GACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGTCTCAAAATGCAGTGAATACTCTA 2520
Db 2461 GACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGTCTCAAAATGCAGTGAATACTCTA 2520
QY 2521 GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATCTTGTATTATCAGAAAAATTACCTG 2580
Db 2521 GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATCTTGTATTATCAGAAAAATTACCTG 2580
QY 2581 GAAAAAGATGGAATGAAGCTCTTCATGAATGATCGACAGGATGAACGTGCTAGAACAG 2640
Db 2581 GAAAAAGATGGAATGAAGCTCTTCATGAATGATCGACAGGATGAACGTGCTAGAACAG 2640
QY 2641 CTCACGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCCTGAGCAGCCTGTTG 2700
Db 2641 CTCACGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCCTGAGCAGCCTGTTG 2700
QY 2701 AAACATTTGGAGAGGTGCCCAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2760
Db 2701 AAACATTTGGAGAGGTGCCCAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2760
QY 2761 GATACAGAGATTAGAATTTTAGCTGGCATTTTGGAAAGAACCTCTGAAAAACTTCCAG 2820
Db 2761 GATACAGAGATTAGAATTTTAGCTGGCATTTTGGAAAGAACCTCTGAAAAACTTCCAG 2820
QY 2821 CAGTTGAATTTGGCGGAAATCGTGACGAGTGTGATGGCTTGCCTTCATGGGTGTA 2880
Db 2821 CAGTTGAATTTGGCGGAAATCGTGACGAGTGTGATGGCTTGCCTTCATGGGTGTA 2880
QY 2881 TTTGAGAACTTAAAGCAATTTAGTGTGTTTGGACTTTAGTACTAAAGAAATTTCTACCTGAT 2940
Db 2881 TTTGAGAACTTAAAGCAATTTAGTGTGTTTGGACTTTAGTACTAAAGAAATTTCTACCTGAT 2940
QY 2941 CCAGCATTTAGTCAAGAACTTACCCAGTGTATCCAAAGTAACTTTCTCGCAAGAGCT 3000
Db 2941 CCAGCATTTAGTCAAGAACTTACCCAGTGTATCCAAAGTAACTTTCTCGCAAGAGCT 3000
QY 3001 AGCTTGTGGTGGCAATTTGATGATGATCTCAGTGTATTACAGTGTCTTTTAA 3060
Db 3001 AGCTTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGTGTCTTTTAA 3060
QY 3061 CTAGTAACTGCT 3072
Db 3061 CTAGTAACTGCT 3072
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RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21946A-14
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Query Match 95.0%; Score 2919; DB 1; Length 3219;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATCAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAAATGGGAATGACTGTATTATA 60
Db 145 ATGAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAAATGGGAATGACTGTATTATA 204
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QY 61 AAGCAATCACAGATGACCTATTGTTGATCGAATGTTCTGAATCGCGAAGAAAGTAACATC 120  
|||||  
Db 205 AAGCAATCACAGATGACCTATTGTTGATCGAATGTTCTGAATCGCGAAGAAAGTAACATC 264  
QY 121 ATTGCTCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 180  
|||||  
Db 265 ATTGCTCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 324  
QY 181 AAGGGTTACAGATGCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 240  
Db 325 AAGGGTTACAGATGCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 384  
QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGGACTTGGACGAT 300  
Db 385 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGGACTTGGACGAT 444  
QY 301 TTGGCTCAGGATTTAAAGACTTGTACCATACCCCATCTTTCTGAACCTTTTATCCCTT 360  
Db 445 TTGGCTCAGGATTTAAAGACTTGTACCATACCCCATCTTTCTGAACCTTTTATCCCTT 504  
QY 361 GGTGAAGATATGACATTAATTTTAACTTGAAGACCTTTCAGAGACCTGCTCGTGG 420  
Db 505 GGTGAAGATATGACATTAATTTTAACTTGAAGACCTTTCAGAGACCTGCTCGTGG 564  
QY 421 AGAAGGACCAACACATCACCCTGGAGCAGCTGACCTGAATGGCTCTCTGAGGCT 480  
Db 565 AGAAGGACCAACACATCACCCTGGAGCAGCTGACCTGAATGGCTCTCTGAGGCT 624  
QY 481 CTTACAGACCCCTGCATCATTGAAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGCAG 540  
Db 625 CTTACAGACCCCTGCATCATTGAAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGCAG 684  
QY 541 CGCATTTGCCATGCTCTGGGGCTCCGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC 600  
Db 685 CGAATTTGCCATGCTCTGGGGCTCCGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC 744  
QY 601 TTCTTCTCCCTGCTCAGACAGGCCCCAGGGTGGACTTTTGAACCTCTCTGTATCAACTC 660  
Db 745 TTCTTCTCCCTGCTCAGACAGGCCCCAGGGTGGACTTTTGAACCTCTCTGTATCAACTC 804  
QY 661 CTGGATATACCTGGCACATCAGGAAGCAGACATTCATGCGCCATGCTGTAAGCTGGG 720  
Db 805 CTGGATATACCTGGCACATCAGGAAGCAGACATTCATGCGCCATGCTGTAAGCTGGG 864  
QY 721 CAGAGGGTTCTTTTCTTCTGATGCTACATGAATTCAGCCCCCAGAACTGCCCAGAA 924  
Db 865 CAGAGGGTTCTTTTCTTCTGATGCTACATGAATTCAGCCCCCAGAACTGCCCAGAA 984  
QY 781 ATCGAAGCCCTGATTAAGGAAACACCCGCTTCAGAACATGCTGTCACACTACC 840  
Db 925 ATCGAAGCCCTGATTAAGGAAACACCCGCTTCAGAACATGCTGTCACACTACC 984  
QY 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGATATG 900  
Db 985 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGATATG 1044  
QY 901 ACAGAAGCAGCGCCAGGCTCTCATCCGAGAAGTGCCTGATCAAGGACTTGCCTGAAGGC 960  
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QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATTCATGAAGACCCCTCTCTT 1020  
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QY 1021 GTGGTCTATCATTGTGCAATCCAGATGGGTGAAAGTGAAGTTCACCTCTCACACACAAACA 1080  
Db 1165 GTGGTCTATCATTGTGCAATCCAGATGGGTGAAAGTGAAGTTCACCTCTCACACACAAACA 1224  
QY 1081 ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAATAAAGGT 1140  
Db 1225 ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAATAAAGGT 1284  
QY 1141 GTGGCTGCAAGTGACTTTCATTGGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGT 1200  
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Db 1285 GTGGCTGCAAGTGACTTTCATTCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGT 1344  
QY 1201 GTGTTTTCGCCACAAGTTTGATTTCCGAATGCAAGGATGTGCCAGGTGAATGAGGATGTC 1260  
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Db 1345 GTGTTTTCGCCACAAGTTTGATTTCCGAATGCAAGGATGTGCCAGGTGAATGAGGATGTC 1404  
QY 1261 CTGCTTACAACTGGGCTCCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGATATAA 1320  
Db 1405 CTGCTTACAACTGGGCTCCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGATATAA 1464  
QY 1321 TTCTTTTCACAAGTCAATCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGTTTATTGAGC 1380  
Db 1465 TTCTTTTCACAAGTCAATCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGTTTATTGAGC 1524  
QY 1381 TCTCAAGAGGAGGTGACCAAGGGGAATGTTACTTTCAGANAATGTTTCCATT 1440  
Db 1525 TCTCAAGAGGAGGTGACCAAGGGGAATGTTACTTTCAGANAATGTTTCCATT 1584  
QY 1441 TCGGAATTATACATTCACATTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAA 1500  
Db 1585 TCGGAATTATACATTCACATTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAA 1644  
QY 1501 GCCACTAGGCTGTTATGAAGCACCCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA 1560  
Db 1645 GCCACTAGGCTGTTATGAAGCACCCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA 1704  
QY 1561 CTTTCCATCGGCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACC 1620  
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QY 1621 ACTGAACAAGAAATCTGAAAGCCATTAACATCAATCTCTTTGTAGAGTGTGGCATCCAT 1680  
Db 1765 ACTGAACAAGAAATCTGAAAGCCATTAACATCAATCTCTTTGTAGAGTGTGGCATCCAT 1824  
QY 1681 TTATATTAAGAGATACATCCAAATCAGCCCTGAGCAGGAATTTGAAGCTTCTTTTCAA 1740  
Db 1825 TTATATTAAGAGATACATCCAAATCAGCCCTGAGCAGGAATTTGAAGCTTCTTTTCAA 1884  
QY 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATCTACTTATTTGACTTCTTTGAA 1800  
Db 1885 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATCTACTTATTTGACTTCTTTGAA 1944  
QY 1801 CATTGTCCAAATGTGCAAGTCTCTGGACTTCATTAACCTGAGCTTTTATGGGAGCT 1860  
Db 1945 CATTGTCCAAATGTGCAAGTCTCTGGACTTCATTAACCTGAGCTTTTATGGGAGCT 2004  
QY 1861 ATGGCTTCATGGGAAAGGCTCGAGAAGACACAGTGGNATCCATGGAAGAGGCCCA 1920  
Db 2005 ATGGCTTCATGGGAAAGGCTCGAGAAGACACAGTGGNATCCATGGAAGAGGCCCA 2064  
QY 1921 GAAACCACATTCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAG 1980  
Db 2065 GAAACCACATTCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAG 2124  
QY 1981 ACTCTGAGGTCACACTCCGGGATTTCAAGCAAGTTGAATAAGCAAGATATCATATCTG 2040  
Db 2125 ACTCTGAGGTCACACTCCGGGATTTCAAGCAAGTTGAATAAGCAAGATATCATATCTG 2184  
QY 2041 GGGAAATATTTCAGCTCTGCCACAAGCCCTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2100  
Db 2185 GGGAAATATTTCAGCTCTGCCACAAGCCCTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2244  
QY 2101 GCTGGAGCCCTCAGTTTGGTCTCAGCACCCTGTAAGAACATTTATCTCTCATGTGGAA 2160  
Db 2245 GCTGGAGCCCTCAGTTTGGTCTCAGCACCCTGTAAGAACATTTATCTCTCATGTGGAA 2304  
QY 2161 GCCAGTCCCTCACCATAGAAGATGAGAGGACATCAGATCTGTAAACAACTGAAACC 2220  
Db 2305 GCCAGTCCCTCACCATAGAAGATGAGAGGACATCAGATCTGTAAACAACTGAAACC 2364  
QY 2221 TTGAGTATTCATGACCTACAGAACTAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2280  
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Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020  
Db 1192 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1251  
Qy 1021 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACAACA 1080  
Db 1252 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACAACA 1311  
Qy 1081 ACGTGTTCCATACCTTCTATGATCTGTGTGATACAGAAAAACAACAACAATAAAGGT 1140  
Db 1312 ACGTGTTCCATACCTTCTATGATCTGTGTGATACAGAAAAACAACAACAATAAAGGT 1371  
Qy 1141 GTGGTCGAAGTGACTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 1200  
Db 1372 GTGGTCGAAGTGACTTCATTCGGAGCCTGGACCACTGTGGATACCTAGCTCTGGAGGT 1431  
Qy 1201 GTGGTCGCCCAAGTTTGATTTCCAGACTGCAGATGTGTCAGGGTGAATGAGATGTC 1260  
Db 1432 GTGGTCGCCCAAGTTTGATTTCCAGACTGCAGATGTGTCAGGGTGAATGAGATGTC 1491  
Qy 1261 GTGGTCGACAACTGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1320  
Db 1492 GTGGTCGACAACTGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1551  
Qy 1321 TTCTTTTCAAGTCAATCCAGAGGTACACAGCAGGAGCAAGACTCAGCAGTTTATGAGC 1380  
Db 1552 TTCTTTTCAAGTCAATCCAGAGGTACACAGCAGGAGCAAGACTCAGCAGTTTATGAGC 1611  
Qy 1381 TCTCATGACGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAAATGGTTTCCATT 1440  
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Qy 1441 TCGGACATTACATCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCACTCTGTGGAA 1500  
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Qy 1561 CTTTCCATCGCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620  
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Db 1852 ACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1911  
Qy 1681 TTATATCAAGAGTACATCAAAATCAGCCCTGAGCCAGAAATTTGAAGCTTCTTTCAA 1740  
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Qy 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTTGACTTCTTTGAA 1800  
Db 1972 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTTGACTTCTTTGAA 2031  
Qy 1801 CATTTGCCCAATTTGCAAGTGCTCTGGACTTCATTAACACTGGACTTTTATGGGGGAGCT 1860  
Db 2032 CATTTGCCCAATTTGCAAGTGCTCTGGACTTCATTAACACTGGCTTTTATGGGGGAGCT 2091  
Qy 1861 ATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
Db 2092 ATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 2151  
Qy 1921 GAAACCTACATCCACAGGCTGTATCTTTGTCTTCACTGGAAGCAGGAATTCAGG 1980  
Db 2152 GAAACCTACATCCACAGGCTGTATCTTTGTCTTCACTGGAAGCAGGAATTCAGG 2211  
Qy 1981 ACTCTGGAGGTCACACTCCGGATTTTCAGCAAGTTTGAATAAGCAAGATATCAGATATCTG 2040  
Db 2212 ACTCTGGAGGTCACACTCCGGATTTTCAGCAAGTTTGAATAAGCAAGATATCAGATATCTG 2271

Qy 2041 GGGAAJATATTTACGCTTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGCTGGTGTG 2100  
Db 2272 GGGAAJATATTTACGCTTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGCTGGTGTG 2331  
Qy 2101 GCTGGJAGCCTCAGCTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCTCATGGTGAA 2160  
Db 2332 GCTGGJAGCCTCAGCTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCTCATGGTGAA 2391  
Qy 2161 GCCAGJCCCTCCACCATAGAAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAAAC 2220  
Db 2392 GCCAGJCCCTCCACCATAGAAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAAAC 2451  
Qy 2221 TTGAGJATTTATGATGACCTTACAGAATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGT 2280  
Db 2452 TTGAGJATTTATGATGACCTTACAGAATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGT 2511  
Qy 2281 AACTTGAAGACCTTACAAAAGCTCATATGATGATACATTAAGATGAATGAAGAGAGTCT 2340  
Db 2512 AACTTGAAGACCTTACAAAAGCTCATATGATGATACATTAAGATGAATGAAGAGAGTCT 2571  
Qy 2341 ATAAAAJTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTTCATTTCACCCAC 2400  
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Qy 2401 TTGTCTJACATTTGAGAGGGAATGGATTAATAGTCAAGTCTCTGTCGAAAGTGAACCTGT 2460  
Db 2632 TTGTCTJACATTTGAGAGGGAATGGATTAATAGTCAAGTCTCTGTCGAAAGTGAACCTGT 2691  
Qy 2461 GACCTTJAAAGAAATTCAAATTAGTCTCTCTGCTGCTGTCGCAAAATGCAAGTGAAGAAATCCTA 2520  
Db 2692 GACCTTJAAAGAAATTCAAATTAGTCTCTCTGCTGCTGTCGCAAAATGCAAGTGAAGAAATCCTA 2751  
Qy 2521 GCTCAGJATCTTCAACAATTTGGTCAAACTGAGCATCTTGTGATTTATCAGAAAAATTACCTG 2580  
Db 2752 GCTCAGJATCTTCAACAATTTGGTCAAACTGAGCATCTTGTGATTTATCAGAAAAATTACCTG 2811  
Qy 2581 GAAAAAJATGGAATGAAGCTCTTTCATGAACATGATCAGCAGAGTGAAGTCTAGAACAG 2640  
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Qy 2641 CTCACJCACTGATGCTGCCCTGGGCTGTGACCTGCAAGCGCAGCTGAGCAGCTGTTG 2700  
Db 2872 CTCACJCACTGATGCTGCCCTGGGCTGTGACCTGCAAGCGCAGCTGAGCAGCTGTTG 2931  
Qy 2701 AAACATJTGAGAGGTCACCAACTCTCAAGCTTGGGTGAAAACTGGAGACTCACA 2760  
Db 2932 AAACATJTGAGAGGTCACCAACTCTCAAGCTTGGGTGAAAACTGGAGACTCACA 2991  
Qy 2761 GATACAGATTAGAAATTTTAGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCAG 2820  
Db 2992 GATACAGATTAGAAATTTTAGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCAG 3051  
Qy 2821 CAGTTGAATTTGGCGGAAATFCGTGTGAGCAGTGAATGGATGGCTTGCCCTTCATGGGTGA 2880  
Db 3052 CAGTTGAATTTGGCGGAAATFCGTGTGAGCAGTGAATGGATGGCTTGCCCTTCATGGGTGA 3111  
Qy 2881 TTTGAGATCTTAAAGCAATTAGTGTTTTGGACTTTTAGTACTAAGAAATTTTCTACCTGAT 2940  
Db 3112 TTTGAGATCTTAAAGCAATTAGTGTTTTGGACTTTTAGTACTAAGAAATTTTCTACCTGAT 3171  
Qy 2941 CCAGCATTAGTCAGAAAACTTAGCACAAGTGTATCCAAGTTAACTTTCTGCAAGAGCT 3000  
Db 3172 CCAGCATTAGTCAGAAAACTTAGCACAAGTGTATCCAAGTTAACTTTCTGCAAGAGCT 3231  
Qy 3001 AGGCTTGCTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGGCTGCTTTTAAA 3060  
Db 3232 AGGCTTGCTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGGCTGCTTTTAAA 3291  
Qy 3061 CTAGTAATTCGT 3072  
Db 3292 CTAGTAATTCGT 3303



## RESULT 4

```

US-10-203-138A-4307
; Sequence 4307, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Ranzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4307
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011232.3
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; US-10-203-138A-4307

```

Query Match	7.9%	Score 242;	DB 6;	Length 421;
Best Local Similarity	100.0%;	Pred. No. 1.3e-115;		
Matches 242;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 2781	AGGTGCATTTTTTTGGAAAGAACCCCTCTGAAAAAACCTTCCAGCAGTTGAAATTTGGCGGGAAA	2840		
Db				
180	AGGTGCATTTTTTTGGAAAGAACCCCTCTGAAAAAACCTTCCAGCAGTTGAAATTTGGCGGGAAA	239		
QY 2841	TCGTGTGAGCAGTCATGGATGGCTTGCCCTCATCGGGTGTAATTTGAGAAATCATTAGCAAAAT	2900		
Db				
240	TCGTGTGAGCAGTCATGGATGGCTTGCCCTCATCGGGTGTAATTTGAGAAATCATTAGCAAAAT	299		
QY 2901	AGTGTTTTTTTTGACATTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAAC	2960		
Db				
300	AGTGTTTTTTTTGACATTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAAC	359		
QY 2961	TAGCCAAAGTCGTTATCCCAAGTTAACTTTTCTGCRAAGAGCTAGGCTTGTTGGTGGCAAT	3020		
Db				
360	TAGCCAAAGTCGTTATCCCAAGTTAACTTTTCTGCRAAGAGCTAGGCTTGTTGGTGGCAAT	419		
QY 3021	TG 3022			
Db				
Db 420	TG 421			

SECRET 5

RESULT 3  
 US-10-203-138A-9429  
 ; Sequence 9429, Application US/10203138A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Molecular Dynamics, Inc.  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ;  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: CL000848  
 ; CURRENT APPLICATION NUMBER: US/09/949,004  
 ; CURRENT FILING DATE: 2002-12-20  
 ; PRIOR APPLICATION NUMBER: 60/232.045  
 ; PRIOR FILING DATE: 2000-09-13  
 ; NUMBER OF SEQ ID NOS: 6961

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6715  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-004-6715

Query Match 0.7%; Score 20; DB 5; Length 601;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 693 ATTATGGCCATGCTGCTGA 712  
|||||

Db 140 ATTATGGCCATGCTGCTGA 159

RESULT 7  
; Sequence 693, Application US/09949004  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: C1000848  
; CURRENT APPLICATION NUMBER: US/09/949,004  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 60/232,045  
; PRIOR FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 6961  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 693  
; LENGTH: 209798  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-004-693

Query Match 0.7%; Score 20; DB 5; Length 209798;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 693 ATTATGGCCATGCTGCTGA 712  
|||||

Db 102520 ATTATGGCCATGCTGCTGA 102539

RESULT 8  
US-09-531-113-38966/c  
; Sequence 38966, Application US/09531113  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Gregory R.  
; APPLICANT: Heck, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15761)B  
; CURRENT APPLICATION NUMBER: US/09/531,113  
; CURRENT FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 48629  
; SEQ ID NO 38966  
; LENGTH: 230  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700943742H1  
US-09-531-113-38966

Query Match 0.6%; Score 19; DB 5; Length 230;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 TCGTTGAGGAATCTCATGA 1006  
|||||

Db 23 TCGTTGAGGAATCTCATGA 5

RESULT 9  
US-10-240-425-462  
; Sequence 462, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Folland, Joseph F.  
; APPLICANT: Ford, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 462  
; LENGTH: 369  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AI082708  
US-10-240-425-462

Query Match 0.6%; Score 19; DB 6; Length 369;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2193 CATCACCTCTCTAACAAAC 2211  
|||||

Db 346 CATCACCTCTCTAACAAAC 364

RESULT 10  
US-09-724-676-1613/c  
; Sequence 16013, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: Patent In version 3.2  
; SEQ ID NO 16013  
; LENGTH: 5513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-16013

Query Match 0.6%; Score 19; DB 5; Length 5513;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 AGGCCTCTCTGGAGACAGG 1594  
|||||

Db 1853 AGGCCTCTCTGGAGACAGG 1835

RESULT 11  
US-09-724-676A-16013/c  
; Sequence 16013, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16013  
; LENGTH: 5513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-16013

Query Match 0.6%; Score 19; DB 5; Length 5513;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 AGGCCTCTGAGACAGG 1594  
|||||  
DB 1853 AGGCCTCTGAGACAGG 1835

RESULT 12  
PCT-US02-32727-122/c  
; Sequence 122, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Fanni  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne  
; FILE REFERENCE: 210121.514c1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 122  
; LENGTH: 8632  
; TYPE: DNA  
; ORGANISM: Propioni acnes  
PCT-US02-32727-122

Query Match 0.6%; Score 19; DB 1; Length 8632;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1612 AAAACACCCTGAGCAAG 1630  
|||||  
DB 8118 AAAACACCCTGAGCAAG 8100

RESULT 13  
US-10-057-498-122/c  
; Sequence 122, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 122  
; LENGTH: 8632  
; TYPE: DNA  
; ORGANISM: Propioni acnes

US-10-057-498-122

Query Match 0.6%; Score 19; DB 6; Length 8632;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1612 AAAACACCCTGAGCAAG 1630  
|||||  
DB 8118 AAAACACCCTGAGCAAG 8100

RESULT 14  
US-10-293-783-96/c  
; Sequence 96, Application US/10293783  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST E  
; FILE REFERENCE: ISPH-0544  
; CURRENT APPLICATION NUMBER: US/10/293,783  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US/09/800,631  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US/09/657,346  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 175  
; SEQ ID NO 96  
; LENGTH: 30310  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (19791)...(19802)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (21160)...(21370)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (24168)...(24307)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25696)...(25908)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27235)...(27246)  
US-10-293-783-96

Query Match 0.6%; Score 19; DB 6; Length 30310;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 TGACAACTGGCTCTCTG 1283  
|||||  
DB 13062 TGACAACTGGCTCTCTG 13044

RESULT 15  
PCT-US02-32700-8  
; Sequence 8, Application PC/TUS0232700  
; GENERAL INFORMATION:  
; APPLICANT: Keith, Tim  
; APPLICANT: Little, Randall D.  
; APPLICANT: Van Eerdewegh, Paul  
; APPLICANT: Dupuis, Josee  
; APPLICANT: Del Mastro, Richard G.  
; APPLICANT: Allen, Kristina  
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY  
; FILE REFERENCE: 2976-4045  
; CURRENT APPLICATION NUMBER: PCT/US02/32700  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/328,424  
; PRIOR FILING DATE: 2001-10-11

```
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 302603
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US02-32700-8
```

```
Query Match 0.6%; Score 19; DB 1; Length 302603;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2192 ACATCACATCTCTGTACAAA 2210
|||||
Db 156828 ACATCACATCTGTACAAA 156846
```

```
RESULT 16
US-10-271-416-8
; Sequence 8, Application US/10271416
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 302603
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-271-416-8
```

```
Query Match 0.6%; Score 19; DB 6; Length 302603;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2192 ACATCACATCTGTGTACAAA 2210
|||||
Db 156828 ACATCACATCTGTGTACAAA 156846
```

```
RESULT 17
US-09-948-124-119/c
; Sequence 119, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; TITLE OF INVENTION: Y, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001301
; CURRENT APPLICATION NUMBER: US/09/948,124
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 183
; SEQ ID NO 119
; LENGTH: 428573
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(428573)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-124-119
```

```
Query Match 0.6%; Score 19; DB 5; Length 428573;
```

```
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1496 TGGAA(C)CCACCAGGGCTGT 1514
|||||
Db 166944 TGGAA(C)CCACCAGGGCTGT 166926
```

```
RESULT 18
US-10-303-778-1:466
; Sequence 1546, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: Rcssetagenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1546
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-1:466
```

```
Query Match 0.6%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ATGAATTCATTAAGGAC 18
|||||
Db 1 ATGAATTCATTAAGGAC 18
```

```
RESULT 19
US-10-310-188-29161
; Sequence 29161, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: Rcssetagenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86941
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29161
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-29161
```

```
Query Match 0.6%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ATGAATTCATTAAGGAC 18
|||||
Db 1 ATGAATTCATTAAGGAC 18
```

```
RESULT 20
US-60-427-836-33174/c
; Sequence 33474, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xu, Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

; SEQ ID NO 33474  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-60-427-836-33474

Query Match 0.6%; Score 18; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 TCCAGGAGTACACAGCAG 1354  
Db 24 TCCAGGAGTACACAGCAG 7

RESULT 21  
US-09-513-999C-19061  
; Sequence 19061, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 19061  
; LENGTH: 116  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-19061

Query Match 0.6%; Score 18; DB 5; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 AGCAATACACATGACCC 79  
Db 47 AGCAATACACATGACCC 64

RESULT 22  
US-10-286-136-502/C  
; Sequence 502, Application US/10286136  
; GENERAL INFORMATION:  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags  
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags  
; FILE REFERENCE: LEX-0049-USA  
; CURRENT APPLICATION NUMBER: US/10/286,136  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US/09/677,367  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US 60/157,364  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 1000  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 502  
; LENGTH: 124  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-10-286-136-502

Query Match 0.6%; Score 18; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2378 TCTGTATTATTCATTGA 2395  
Db 99 TCTGTATTATTCATTGA 82

RESULT 23  
US-10-266-131-1575  
; Sequence 1575, Application US/10266131  
; GENERAL INFORMATION:  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and  
; TITLE OF INVENTION: Mutant Cells and Mutant Animals Defined Thereby  
; FILE REFERENCE: LEX-0030-USA  
; CURRENT APPLICATION NUMBER: US/10/266,131  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: US/09/617,675  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/143,878  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 2908  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1575  
; LENGTH: 143  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-266-131-1575

Query Match 0.6%; Score 18; DB 6; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2411 TTGGAGAGGGAATGGATT 2428  
Db 52 TTGGAGAGGGAATGGATT 69

RESULT 24  
US-09-531-113-19390/C  
; Sequence 19390, Application US/09531113  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15761)B  
; CURRENT APPLICATION NUMBER: US/09/531,113  
; CURRENT FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 48629  
; SEQ ID NO 19390  
; LENGTH: 199  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700957045H1  
US-09-531-113-19390

Query Match 0.6%; Score 18; DB 5; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2746 AACTGGAGACTCACAGAT 2763  
Db 124 AACTGGAGACTCACAGAT 107

RESULT 25  
US-09-531-113-22263/C  
; Sequence 22263, Application US/09531113  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.

; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15761)B  
; CURRENT APPLICATION NUMBER: US/09/531,113  
; CURRENT FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 48629  
; SEQ ID NO 22263  
; LENGTH: 246  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700952841H1  
US-09-531-113-22263

Query Match 0.6%; Score 18; DB 5; Length 246;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3016 CAATTGTGATGATGAT 3033  
|||||  
Db 145 CAATTGTGATGATGAT 128

RESULT 26  
US-09-531-113-25999/c  
; Sequence 25999, Application US/09531113  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Gregory R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15761)B  
; CURRENT APPLICATION NUMBER: US/09/531,113  
; CURRENT FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 48629  
; SEQ ID NO 25999  
; LENGTH: 256  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 700905370H1  
US-09-531-113-25999

Query Match 0.6%; Score 18; DB 5; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 915 CCAGGCTCTATCCGAGA 932  
|||||  
Db 164 CCAGGCTCTATCCGAGA 147

RESULT 27  
US-09-531-113-37454  
; Sequence 37454, Application US/09531113  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Gregory R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15761)B  
; CURRENT APPLICATION NUMBER: US/09/531,113  
; CURRENT FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 48629  
; SEQ ID NO 37454  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700945701H1  
US-09-531-113-37454

Query Match 0.6%; Score 18; DB 5; Length 270;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TGGAACTATCCTCTATTT 243  
|||||  
Db 215 TGGAACTATCCTCTATTT 232

RESULT 28  
US-09-513-999C-13408/c  
; Sequence 13408, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Luciert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13408  
; LENGTH: 446  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 123  
; OTHER INFORMATION: y=c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 130  
; OTHER INFORMATION: k=g or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 425  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 423  
; OTHER INFORMATION: r=a or g  
US-09-513-999C-13408

Query Match 0.6%; Score 18; DB 5; Length 446;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATAAAGGAC 18  
|||||  
Db 106 ATGAATTCATAAAGGAC 89

RESULT 29  
US-10-203-138A-4790/c  
; Sequence 4790, Application US/10203138A  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Ruck, David R.  
; APPLICANT: Huzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; FILE REFERENCE: PB 0004 WO 8  
; CURRENT APPLICATION NUMBER: US/10/203,138A  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456

```
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4790
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109823.11
;
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
US-10-203-138A-4790

Query Match          0.6%; Score 18; DB 6; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 GGGGAATCGCAAGGC 522
DB 29 GGGGAATCGCAAGGC 12

RESULT 30
US-09-513-999C-1807
; Sequence 1807, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1807
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 300..464
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 127
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 139
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 455
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 456
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 53
```

```
; OTHER INFORMATION: Xaa=ile or Leu
US-09-513-999C-1807

Query Match          0.6%; Score 18; DB 5; Length 466;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 TTTTCCTTCTTGATGCT 748
DB 220 TTTTCCTTCTTGATGCT 237

RESULT 31
US-10-203-138A-1760
; Sequence 1760, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 1760
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010087.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
US-10-203-138A-1760

Query Match          0.6%; Score 18; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 AGAAGGTGGAGCAGGATG 148
DB 143 AGAAGGTGGAGCAGGATG 160

RESULT 32
US-09-747-358A-688/c
; Sequence 888, Application US/09747358A
; GENERAL INFORMATION:
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Polynucleotides and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0112-USA
; CURRENT APPLICATION NUMBER: US/09/747,358A
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/174,283
```

; PRIOR FILING DATE: 2000-01-03  
; NUMBER OF SEQ ID NOS: 1008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 688  
; LENGTH: 481  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(481)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-747-358A-688

Query Match 0.6%; Score 18; DB 5; Length 481;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 379 ATTTTAACTGAAAGC 396  
|||||  
Db 253 ATTTTAACTGAAAGC 236

## RESULT 33

US-09-949-002-8756/c  
; Sequence 8756, Application US/09949002  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8756  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-002-8756

Query Match 0.6%; Score 18; DB 5; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3025 GATGATGATCTCAGTGT 3042  
|||||  
Db 256 GATGATGATCTCAGTGT 239

## RESULT 34

US-09-949-002-8757/c  
; Sequence 8757, Application US/09949002  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8757  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-002-8757

Query Match 0.6%; Score 18; DB 5; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3025 GATGATGATCTCAGTGT 3042  
|||||  
Db 350 GATGATGATCTCAGTGT 333

## RESULT 35

US-09-134-000C-1076  
; Sequence 1076, Application US/09134000C  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1076  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-1076

Query Match 0.6%; Score 18; DB 5; Length 885;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2492 GCTTGT.TGCAAAATGCAG 2509  
|||||  
Db 107 GCTTGT.TGCAAAATGCAG 124

## RESULT 36

US-09-134-000C-1076  
; Sequence 1076, Application US/09134000C  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1076  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-1076

Query Match 0.6%; Score 18; DB 5; Length 885;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2492 GCTTGT.TGCAAAATGCAG 2509  
|||||  
Db 107 GCTTGT.TGCAAAATGCAG 124

## RESULT 37

US-09-724-676-3618/c  
; Sequence 3688, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing



; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3688  
; LENGTH: 986  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-3688

Query Match 0.6%; Score 18; DB 5; Length 986;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18  
|||||  
Db 630 ATGAATTTTCATAAAGGAC 613

RESULT 38  
US-09-724-676-3693/c  
; Sequence 3693, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3693  
; LENGTH: 986  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-3693

Query Match 0.6%; Score 18; DB 5; Length 986;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18  
|||||  
Db 630 ATGAATTTTCATAAAGGAC 613

RESULT 39  
US-09-724-676A-3688/c  
; Sequence 3688, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3688  
; LENGTH: 986  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-3688

Query Match 0.6%; Score 18; DB 5; Length 986;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18  
|||||  
Db 630 ATGAATTTTCATAAAGGAC 613

RESULT 40

US-09-724-676A-3693/c  
; Sequence 3693, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3693  
; LENGTH: 986  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-3693

Query Match 0.6%; Score 18; DB 5; Length 986;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18  
|||||  
Db 630 ATGAATTTTCATAAAGGAC 613

RESULT 41  
US-09-724-676-3689/c  
; Sequence 3689, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3689  
; LENGTH: 998  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-3689

Query Match 0.6%; Score 18; DB 5; Length 998;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18  
|||||  
Db 630 ATGAATTTTCATAAAGGAC 613

RESULT 42  
US-09-724-676-3694/c  
; Sequence 3694, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3694  
; LENGTH: 998  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-3694

Query Match 0.6%; Score 18; DB 5; Length 998;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18

Db 630 ATGAATTCATAAAGGAC 613  
|||||

## RESULT 43

US-09-724-676A-3689/c

; Sequence 3689, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724.676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3689

; LENGTH: 998

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-3689

Query Match 0.6%; Score 18; DB 5; Length 998;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATAAAGGAC 18

|||||

Db 630 ATGAATTCATAAAGGAC 613

## RESULT 44

US-09-724-676A-3694/c

; Sequence 3694, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724.676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3694

; LENGTH: 998

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-3694

Query Match 0.6%; Score 18; DB 5; Length 998;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATAAAGGAC 18

|||||

Db 630 ATGAATTCATAAAGGAC 613

## RESULT 45

US-10-264-237-181/c

; Sequence 181, Application US/10264237

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: P131P1

; CURRENT APPLICATION NUMBER: US/10/264.237

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/16450

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 2876

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 181

; LENGTH: 1243

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-264-237-181

## Query Match

Best Local Similarity 100.0%; Score 18; DB 6; Length 1243;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 415 CTGTGK AGGAAGGACCA 432

|||||

Db 474 CTGTGK AGGAAGGACCA 457

## RESULT 46

PCT-US02-38446-58

; Sequence 98, Application PC/YUS0238446

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: TANG, Y. Tom

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: IU, Dyung Aina M.

; APPLICANT: PHAN, Farrah A.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: SWARNAKAR, Anita

; APPLICANT: FZIMZAI, Yalda

; APPLICANT: PARQUIS, Joseph P.

; APPLICANT: PRAGUE, William W.

; APPLICANT: EMERLING, Brooke M.

; APPLICANT: YUE, Henry

; APPLICANT: EOROWSKY, Mark L.

; APPLICANT: ECHA, Shaoya D.

; APPLICANT: ISON, Craig H.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: KING, Huijun Z.

; APPLICANT: WARREN, Bridget A.

; APPLICANT: GRIETZEN, Kimberly J.

; APPLICANT: IRAN, Uyen K.

; APPLICANT: LEE, Soo Yeun

; APPLICANT: LEE, Ernestine A.

; APPLICANT: RICHARDSON, Thomas W.

; APPLICANT: KABLE, Amy E.

; APPLICANT: BURFORD, Neil

; APPLICANT: LEHR-MASON, Patricia M.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: LEE, Sally

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HONCHELL, Cynthia D.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: CHIEN, David

; APPLICANT: JIN, Pei

; APPLICANT: CHANG, Hsin-Ru

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: NUJEN, Dannel B.

; APPLICANT: KHARE, Reena

; APPLICANT: BHATIA, Umesh

; APPLICANT: BURRILL, John D.

; APPLICANT: HJ, Anne

; APPLICANT: ZHENG, Wenjin

; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT

; FILE REFERENCE: P1-1302 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/38446

; CURRENT FILING DATE: 2002-11-25

; PRIOR APPLICATION NUMBER: US 60/334,182

; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: US 60/342,052

; PRIOR FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: US 60/350,410

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US 60/353,284

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: US 60/363,649

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; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 98
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
; PCN-US02-38446-98

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Query Match 0.6%; Score 18; DB 1; Length 1297;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0 Indels

Qy 2362 AAAAACCTGAAGAAGATG 2379  
 Db 824 AAAAACCTGAAGAAGATG 841

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RESULT 47
US-09-724-676-3691/c
; Sequence 3691, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alter
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3691
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-3691

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```
Query Match      0.6%;   Score 18;   DB 5;   Length 1610;
Best Local Similarity 100.0%;   Pred. No. 1.3e+02;
Matches 18;   Conservative 0;   Mismatches 0;   Indels
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Qy 1 ATGAATTTCATAAAGGAC 18  
Db 1254 ATGAATTTCATAAAGGAC 1237

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RESULT 48
US-09-724-676A-3691/c
; Sequence 3691, Application US/09724676A-
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alterna
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724, 6
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3691
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-3691

```

```
Query Match      0.6%; Score 18; DB 5; Length 1610;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Qy 1 ATGAATTTCATAAAGGAC 18  
 |||  
 Db 1254 ATGAATTTCATAAAGGAC 1237

```

RESULT 49
US-09-743-247A-23/c
; Sequence 23, Application US/09743247A
; GENERAL INFORMATION:
; APPLICANT: Sagami Chemical Research Center
; TITLE OF INVENTION: Human Proteins Having
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 1997.13300
; CURRENT APPLICATION NUMBER: US/09/743,247A
; CURRENT FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: JP 10-208820
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: JP 10-224105
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: JP 10-238116
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: JP 10-254736
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: JP 10-275505
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Windows 95 (Word 98)
; SEQ ID NO 23
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (287)...(1015)
US-09-743-247A-23

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Query Match 0.6%; Score 18; DB 5; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels

Qy 1 ATGAATTCATAAAGGAC 18  
 |||||  
 Db 1277 ATGAATTCATAAAGGAC 1260

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RESULT 50
US-09-724-676-3692/c
; Sequence 3692, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3692
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-3692

```

Query Match 0.6%; Score 18; DB 5; Length 1622;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels

Qy 1 ATGAATTTCATAAAGGAC 18  
 |||||  
 Db 1254 ATGAATTTCATAAAGGAC 1237

Search completed: January 31, 2003, 04:39:30  
Job time : 1949 secs

